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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:06:05 ; Search time 65.3214 Seconds  
(without alignments)  
2468.595 Million cell updates/sec

Title: US-09-868-131A-1  
Perfect score: 1954  
Sequence: 1 MNSSPAGTPSPQPSRANGNI.....ASSAFLGFSVAPEDDILDC 367

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues  
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1954	100.0	367	3 AAY95275	Aay95275 Human ser
2	1954	100.0	367	4 AAU28087	Aau28087 Novel hum
3	1954	100.0	367	5 AAE22765	Aae22765 Human ser
4	1954	100.0	367	7 ADD45799	Add45799 Human pro
5	1954	100.0	367	8 ADI29317	Adi29317 Human MAR
6	1954	100.0	367	8 ADJ45521	Adj45521 LXR-ligan
7	1954	100.0	382	4 AAM25594	Aam25594 Human pro
8	1954	100.0	396	9 ADY37607	Ady37607 Lung canc
9	1954	100.0	427	3 AAY95276	Aay95276 Human ser
10	1954	100.0	427	8 ADQ88284	Adq88284 Human 549
11	1952	99.9	367	4 AAB65708	Aab65708 Novel ser
12	1848	94.6	367	3 AAY95277	Aay95277 Mouse ser
13	1848	94.6	367	7 ADG45797	Adg45797 Rat Prote
14	1767	5	90.5	6 ADA05780	Ada05780 Human NOV
15	1748	5	89.5	8 ADN2944	Adn2944 Human NOV
16	1691	86.5	319	4 AAB99838	Aab99838 AGC prote
17	1691	86.5	319	8 ADJ38886	Adj38886 SGK2 amin
18	1677	85.8	335	8 ADP29822	Adp29822 Human sec
19	1665	85.2	330	8 ADN61463	Adn61463 Human Kpp
20	1413	72.3	431	3 AAB24116	Aab24116 Rat serum
21	1413	72.3	431	3 AAY93530	Aay93530 A rat ser
22	1411	72.2	407	7 ADC69794	Adc69794 Human ser
23	1411	72.2	431	2 AAW90139	Aaw90139 Human sgk
24	1411	72.2	431	6 ADA10889	Ada10889 Human cdn

25	1411	72.2	431	7 ADG31708	Adg31708 Human pro
26	1411	72.2	431	7 ADK50982	Adk50982 Human NOV
27	1411	72.2	431	7 ADK50984	Adk50984 Human NOV
28	1411	72.2	431	8 ADO55118	Ado55118 Protein #
29	1411	72.2	431	9 ADY14632	Ady14632 PRO polyp
30	1411	72.2	431	9 ADY19878	Ady19878 PRO polyp
31	1411	72.2	431	9 AEA04529	Aea04529 Human pro
32	1411	72.2	442	7 ADG31706	Adg31706 Human pro
33	1411	72.2	445	7 ADC69792	Adc69792 Human pro
34	1411	72.2	526	6 ADA54293	Ada54293 Human pro
35	1411	72.2	526	7 ADG31710	Adg31710 Human pro
36	1411	72.2	788	7 ADD93289	Add93289 p53-SGK(6
37	1409	72.1	431	8 ADO60030	Ado60030 CRH signa
38	1409	72.1	431	8 ADO44573	Ado44573 Serum/glu
39	1407	72.0	373	4 AAB99815	Aab99815 AGC prote
40	1407	72.0	430	2 ADN95921	Adn95921 Human BEC
41	1407	72.0	431	2 AAW77217	Aaw77217 Human cel
42	1407	72.0	431	3 AAY95279	Aay95279 Human ser
43	1407	72.0	431	3 AAB24115	Aab24115 Human ser
44	1407	72.0	431	4 AAB65613	Aab65613 Novel pro
45	1407	72.0	431	7 ADD14174	Add14174 Human src

ALIGNMENTS

RESULT 1  
AAY95275  
ID AAY95275 standard; protein; 367 AA.  
XX  
AC AAY95275;  
XX  
DT 12-SRP-2000 (first entry)  
XX  
DE Human serum and glucocorticoid-induced protein kinase 2-alpha.  
XX  
KW Serum and glucocorticoid-induced protein kinase 2; SGK2-alpha; human;  
KW phosphorylation; cancer; diabetes; ischaemia; therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 279  
FT /note= "O-phosphorylated"  
FT Modified-site 334  
FT /note= "O-phosphorylated"  
XX  
PN WO200035946-A1.  
XX  
PD 22-JUN-2000.  
XX  
PF 14-DEC-1999; 99WO-GB004232.  
XX  
PR 14-DEC-1998; 98US-0112217P.  
PR 19-AUG-1999; 99GB-00019676.  
XX  
PA (UYDU-) UNIV DUNDEE.  
XX  
PI Cohen P, Kobayashi T, Deak M;  
XX  
DR WPI; 2000-442364/38.  
DR N-PSDB; AAA27856.  
XX  
PT Modulation of serum and glucocorticoid-induced protein kinase (SGK) by  
PT phosphorylation with 3-phosphoinositide-dependent protein kinase-1 (PDK1)  
PT or dephosphorylation, useful for treatment of cancer, diabetes and  
XX ischemic diseases.  
PS Disclosure; Page 6; 127pp; English.  
XX  
CC The present sequence is that of human serum and glucocorticoid-induced  
CC protein kinase (SGK) isoform 2-alpha. SGK (see AAY95279) was initially  
CC identified as a glucocorticoid and osmotic stress-responsive gene. Novel

CC isoforms, SGK2 and SGK3, were isolated from EST database searches, and 2  
CC splice variants of SGK2, i.e. SGK2-alpha and -beta (see AY95276), which  
CC contains an extra 60 N-terminal residues, were identified. SGK2-alpha is  
CC expressed in liver, kidney, pancreas and brain. It is activated by  
CC phosphorylation in a similar manner to SGK. The invention provides  
CC methods of activating SGK activity by phosphorylation using 3-  
CC phosphoinositide-dependent protein kinase-1 (PDK1), and of reducing the  
CC activity of SGK by dephosphorylation. The invention also provides a  
CC method of identifying a compound that modulates the activity of SGK. Such  
CC compounds are useful for treating patients requiring modulation of SGK,  
CC such as patients with cancer, diabetes or ischaemic disease  
XX  
SQ Sequence 367 AA;

Query Match 100.0%; Score 1954; DB 3; Length 367;  
Best Local Similarity 100.0%; Pred. No. 1.3e-180;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNSSPAGTSPQPSRANGINILGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSDDGAF 60  
Db 1 MNSSPAGTSPQPSRANGINILGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSDDGAF 60  
QY 61 YAVKVLQKKSILKKKEQSHIMAEVSLLKNVRHPFLVGLRYSFQTPPEKLYFVLDYVNGGE 120  
Db 61 YAVKVLQKKSILKKKEQSHIMAEVSLLKNVRHPFLVGLRYSFQTPPEKLYFVLDYVNGGE 120  
QY 121 LFFHLQRRERFLEPRARFVAEVAISGVLHSLNIIYRDLKPNILLLDCCQGHVLTDFGL 180  
Db 121 LFFHLQRRERFLEPRARFVAEVAISGVLHSLNIIYRDLKPNILLLDCCQGHVLTDFGL 180  
QY 181 CKEGVEPEDTTFCTGPEYLAPEVLKPEYDRAVDWVGLGAVLYEMLHGLPPFVSQDVS 240  
Db 181 CKEGVEPEDTTFCTGPEYLAPEVLKPEYDRAVDWVGLGAVLYEMLHGLPPFVSQDVS 240  
QY 241 QVYENILHPLQIPGRTVAACDLQSLHKQORGLSKADFLEIKNVHFFSPINWDDL 300  
Db 241 QVYENILHPLQIPGRTVAACDLQSLHKQORGLSKADFLEIKNVHFFSPINWDDL 300  
QY 301 YHKRLTPFPNPVNTGPDILKHFDEPTQBAVSKSIGCTPDTVASSSGASSAFILGFSYAPE 360  
Db 301 YHKRLTPFPNPVNTGPDILKHFDEPTQBAVSKSIGCTPDTVASSSGASSAFILGFSYAPE 360  
QY 361 DDILDC 367  
Db 361 DDILDC 367

RESULT 2  
AAU28087  
ID AAU28087 standard; protein; 367 AA.

XX AC AAU28087;

XX DT 18-DEC-2001 (first entry)

XX DE Novel human secretory protein, Seq ID No 256.

XX Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;  
KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;  
KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;  
KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;  
KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;  
KW gut protection; lung; liver fibrosis; immune deficiency; infection;  
KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;  
KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;  
KW fertility; analgesic; pain; antigen.

XX OS Homo sapiens.

XX PN WO200166689-A2.

XX PD 13-SEP-2001.

XX

PF 05-MAR-2001; 2001WO-US004942.  
XX  
PR 07-MAR-2000; 2000US-00519705.  
PR 19-MAY-2000; 2000US-00574454.  
PR 17-JUN-2000; 2000US-00596193.  
PR 14-JUL-2000; 2000US-00616847.  
PR 19-SEP-2000; 2000US-00665363.  
PR 20-OCT-2000; 2000US-00693267.  
XX (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;  
PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;  
XX  
DR WPI; 2001-589934/66.  
DR N-PSDB; AAS44987.  
XX  
PT Novel polypeptides and nucleic acids obtained from cDNA libraries  
PT prepared from various human tissues, for diagnosis and treatment of  
PT cancer, neurological, inflammatory, and autoimmune disorders.  
PS Example 4; SEQ ID NO 256; 107pp; English.

XX The invention relates to novel isolated human secreted polypeptides (I)  
CC and polynucleotides (II). (I) and (II) are useful for treating  
CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,  
CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is  
CC involved in increasing haematopoiesis, stem cell survival, bone growth  
CC and remodeling. (I), (II) and modulators of (II) are useful for  
CC prophylaxis or treatment of one or more cancers. (II) is also useful for  
CC creating transgenic animals useful for studying the in vivo activities of  
CC the polypeptide as well as for studying modulators of the polypeptides.  
CC (I) induces the proliferation of neural cells and regeneration of nerve  
CC and brain tissue and is useful for the treatment of central and  
CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,  
CC Parkinson's disease, Huntington's disease, and amyotrophic lateral  
CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic  
CC activity, regulation of haematopoiesis and is useful for treating myeloid  
CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia  
CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve  
CC tissue growth, and in tissue repair, healing of burns, incisions, ulcers,  
CC for treating osteoporosis, osteoarthritis, bone degenerative disorders,  
CC or periodontal disease. Furthermore, (I) is also useful for gut  
CC protection or regeneration and treatment of lung or liver fibrosis,  
CC reperfusion injury in various tissues, various immune deficiencies and  
CC disorders including severe combined immunodeficiency (SCID), bacterial or  
CC fungal infections, autoimmune disorders e.g. multiple sclerosis,  
CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic  
CC reactions and conditions, such as asthma or other respiratory problems.  
CC In addition, (I) affects biorhythms or circadian cycles of rhythms,  
CC fertility, metabolism, catabolism, anabolism, storage or elimination of  
CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides  
CC analgesic effects or other pain reducing effects, immunoglobulin like  
CC activity and can act as an antigen in a vaccine composition to raise an  
CC immune response. AAU28020-AAU28395 represent novel human secreted protein  
CC amino acid sequences of the invention

XX SQ Sequence 367 AA;

Query Match 100.0%; Score 1954; DB 4; Length 367;  
Best Local Similarity 100.0%; Pred. No. 1.3e-180;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSPAGTSPQPSRANGINILGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSDDGAF 60  
Db 1 MNSSPAGTSPQPSRANGINILGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSDDGAF 60

QY 61 YAVKVLQKKSILKKKEQSHIMAEVSLLKNVRHPFLVGLRYSFQTPPEKLYFVLDYVNGGE 120  
Db 61 YAVKVLQKKSILKKKEQSHIMAEVSLLKNVRHPFLVGLRYSFQTPPEKLYFVLDYVNGGE 120  
QY 121 LFFHLQRRERFLEPRARFVAEVAISGVLHSLNIIYRDLKPNILLLDCCQGHVLTDFGL 180

Db 121 LFFHLQRRERFLEPRARFYAAEVASAGVYLHSLNIIYRDLKPNILLLDCCQGHVVLTFDGL 180  
QY 181 CKEGVEPEDTTSTFCGTPYLAPEVLRKPEYDRAVDWCLGAVLYEMLHGLPPFYSDQVS 240  
Db 181 CKEGVEPEDTTSTFCGTPYLAPEVLRKPEYDRAVDWCLGAVLYEMLHGLPPFYSDQVS 240  
QY 241 QMYENILHQPLOIPGGRTVAAACDLQSLHKKDQORLGSKADFLKTNHVFSPINWDDL 300  
Db 241 QMYENILHQPLOIPGGRTVAAACDLQSLHKKDQORLGSKADFLKTNHVFSPINWDDL 300  
QY 301 YHKRLTPPNPNVTGPADLKHFDPFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360  
Db 301 YHKRLTPPNPNVTGPADLKHFDPFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360  
QY 361 DDDILDC 367  
Db 361 DDDILDC 367

RESULT 3  
AAE22765  
ID AAE22765 standard; protein; 367 AA.  
XX AAE22765;

09-AUG-2002 (first entry)

XX Human serum and glucocorticoid-induced protein kinase, SGK2-alpha.  
XX Human; cytostatic; antisense gene therapy; screening; protein kinase;  
KW cancer; liver; colon; tumour; inflammation; arthritic synovium; enzyme;  
KW serum and glucocorticoid-induced protein kinase; SGK2-alpha.  
XX Homo sapiens.

XX WO200224947-A2.

XX 28-MAR-2002.

XX 20-SEP-2001; 2001WO-1B02237.

XX 20-SEP-2000; 2000US-0233999P.

PR 02-OCT-2000; 2000US-0237419P.

PR 02-OCT-2000; 2000US-0237423P.

PR 04-OCT-2000; 2000US-0238558P.

PR 10-MAY-2001; 2001US-0290555P.

XX (KINE-) KINETEK PHARM INC.

PA (UYBR-) UNIV BRITISH COLUMBIA.

XX Yoganathan T, Delaney AD;

XX WPI; 2002-394145/42.

DR N-PSDB; AAD36141.

XX Diagnosing cancer, comprises determining the upregulation of expression

PT of a nucleic acid sequence encoding a protein kinase or upregulation of

PT expression of the protein kinase, in the cancer.

XX Claim 1; Page 66-67; 87pp; English.

XX The invention relates to a method for screening biologically active agent

CC that modulates cancer associated protein kinase function. The invention

CC also relates to a method for diagnosing cancer comprising determining the

CC upregulation of expression of a nucleic acid sequence encoding a protein

CC kinase. The method is useful for diagnosing cancer. A protein kinase is

CC such as molecular weight, amino acid and nucleotide sequences between the

CC two cells. The present sequence is human serum and glucocorticoid-induced

CC protein kinase, SGK2-alpha

XX Sequence 367 AA;

QY 1 MNSSPAGTSPSPSPPSANGNINLGPSANPNAQPTDPLKVIKGNVKGKVLAKRKSDGAF 60

Db 1 MNSSPAGTSPSPSPPSANGNINLGPSANPNAQPTDPLKVIKGNVKGKVLAKRKSDGAF 60

QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKKNVRHPFLVGLRYSFQTPKLYFVLDDYVNGGE 120

Db 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKKNVRHPFLVGLRYSFQTPKLYFVLDDYVNGGE 120

QY 121 LFFHLQRRERFLEPRARFYAAEVASAGVYLHSLNIIYRDLKPNILLLDCCQGHVVLTFDGL 180

Db 121 LFFHLQRRERFLEPRARFYAAEVASAGVYLHSLNIIYRDLKPNILLLDCCQGHVVLTFDGL 180

QY 181 CKEGVEPEDTTSTFCGTPYLAPEVLRKPEYDRAVDWCLGAVLYEMLHGLPPFYSDQVS 240

Db 181 CKEGVEPEDTTSTFCGTPYLAPEVLRKPEYDRAVDWCLGAVLYEMLHGLPPFYSDQVS 240

QY 241 QMYENILHQPLOIPGGRTVAAACDLQSLHKKDQORLGSKADFLKTNHVFSPINWDDL 300

Db 241 QMYENILHQPLOIPGGRTVAAACDLQSLHKKDQORLGSKADFLKTNHVFSPINWDDL 300

QY 301 YHKRLTPPNPNVTGPADLKHFDPFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360

Db 301 YHKRLTPPNPNVTGPADLKHFDPFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360

QY 361 DDDILDC 367

Db 361 DDDILDC 367

RESULT 4

ADD45799

ID ADD45799 standard; protein; 367 AA.

XX AC ADD45799;

XX DT 29-JAN-2004 (first entry)

XX Human Protein XP\_009494, SEQ ID NO 11468.

XX Human; pain; neuronal tissue; gene therapy;

XX spinal segmental nerve injury; chronic constriction injury; CCI;

XX spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX WO2003016475-A2.

XX PD 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEHO ) GEN HOSPITAL CORP.

XX (FARB ) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

DR GENBANK; XP\_009494.

PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
XX or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates the  
CC expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung)), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 367 AA;  
SQ  
Query Match 100.0%; Score 1954; DB 7; Length 367;  
Best Local Similarity 100.0%; Pred. No. 1.3e-180;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNSSPAGTSPQPSRANGNINLGPANPNAQPTDFDLKVGKNGYKVLAKRKSDDGAF 60  
DB 1 MNSSPAGTSPQPSRANGNINLGPANPNAQPTDFDLKVGKNGYKVLAKRKSDDGAF 60  
QY 61 YAVKVLQKKSILKKKEQSHIMAEVSLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGE 120  
DB 61 YAVKVLQKKSILKKKEQSHIMAEVSLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGE 120  
QY 121 LFFHLQRRRRFLEPRARFYAAEVAASIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180  
DB 121 LFFHLQRRRRFLEPRARFYAAEVAASIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180  
QY 181 CKEGVEPEDTTSTFCGTPEYLAPEVLKPEYDRAVDMWCLGAVLYEMHLGLPFFYSQDVS 240  
DB 181 CKEGVEPEDTTSTFCGTPEYLAPEVLKPEYDRAVDMWCLGAVLYEMHLGLPFFYSQDVS 240  
QY 241 QMYENILHQPLOIPGRTVAACDLQLSLHKDQORGLSKADFLKHNHFFSPINWDDL 300  
DB 241 QMYENILHQPLOIPGRTVAACDLQLSLHKDQORGLSKADFLKHNHFFSPINWDDL 300  
QY 301 YHKRLTPPNPNVTGPADLUKHPDFTQEAVSISGCTPDTVAASSGASSAFGLFSYAPE 360  
DB 301 YHKRLTPPNPNVTGPADLUKHPDFTQEAVSISGCTPDTVAASSGASSAFGLFSYAPE 360  
QY 361 DDDILDC 367  
DB 361 DDDILDC 367

RESULT 5  
ADI29317  
ID ADI29317 standard; protein; 367 AA.  
XX  
AC ADI29317;

XX 22-APR-2004 (first entry)  
DE Human MARK3-associated protein #87.  
XX  
XX Human; antisense gene therapy; MARK3;  
KW MAP/microtubule affinity-regulating kinase 3; cancer;  
KW Alzheimer's disease; neurodegenerative disorder;  
KW hyperproliferative disorder; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN US2003232771-A1.  
XX  
PD 18-DEC-2003.  
XX  
PF 17-JUN-2002; 2002US-00174319.  
XX  
PR 17-JUN-2002; 2002US-00174319.  
XX (ISIS-) ISIS PHARM INC.  
XX Ward DT, Freier SM, Dobie KW;  
XX  
XX WPI: 2004-052188/05.  
XX N-PSDB; ADI29435.  
XX  
XX New antisense compound targeted to a nucleic acid molecule encoding  
XX microtubule-affinity-regulating kinases (MARK3), useful for modulating  
XX expression of MARK3 or for treating cancer or Alzheimer's disease.  
XX  
XX Disclosure; SEQ ID NO 237; 233pp; English.  
XX  
XX The invention relates to a compound comprising a sequence comprising 8-80  
XX base pairs (bp) targeted to a nucleic acid encoding MARK3  
XX (MAP/microtubule affinity-regulating kinase 3), that specifically  
XX hybridizes with the nucleic acid encoding MARK3 and inhibits expression  
XX of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a  
XX composition comprising the compound and a carrier or diluent, inhibiting  
XX the expression of MARK3 in cells or tissues, treating an animal having or  
XX suspected of having a disease or condition associated with MARK3 and  
XX screening for an antisense compound. The antisense oligonucleotide is  
XX useful for preparing a composition for treating hyperproliferative  
XX disorder, particularly cancer and neurodegenerative diseases e.g.  
XX Alzheimer's disease. The present sequence is a MARK3 associated protein  
XX included in the figures but not mentioned anywhere else in the  
XX specification.  
XX  
XX Sequence 367 AA;  
SQ  
Query Match 100.0%; Score 1954; DB 8; Length 367;  
Best Local Similarity 100.0%; Pred. No. 1.3e-180;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNSSPAGTSPQPSRANGNINLGPANPNAQPTDFDLKVGKNGYKVLAKRKSDDGAF 60  
DB 1 MNSSPAGTSPQPSRANGNINLGPANPNAQPTDFDLKVGKNGYKVLAKRKSDDGAF 60  
QY 61 YAVKVLQKKSILKKKEQSHIMAEVSLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGE 120  
DB 61 YAVKVLQKKSILKKKEQSHIMAEVSLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGE 120  
QY 121 LFFHLQRRRRFLEPRARFYAAEVAASIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180  
DB 121 LFFHLQRRRRFLEPRARFYAAEVAASIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180  
QY 181 CKEGVEPEDTTSTFCGTPEYLAPEVLKPEYDRAVDMWCLGAVLYEMHLGLPFFYSQDVS 240  
DB 181 CKEGVEPEDTTSTFCGTPEYLAPEVLKPEYDRAVDMWCLGAVLYEMHLGLPFFYSQDVS 240  
QY 241 QMYENILHQPLOIPGRTVAACDLQLSLHKDQORGLSKADFLKHNHFFSPINWDDL 300  
DB 241 QMYENILHQPLOIPGRTVAACDLQLSLHKDQORGLSKADFLKHNHFFSPINWDDL 300





DR N-PSDB; AAH99535.  
XX Isolated human polynucleotides encoding polypeptides, useful for the  
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection.  
XX  
XX  
XX Claim 20; Page 227; 1217pp; English.  
XX  
XX AAH99166 to AAH99904 encode the human proteins given in AAH25225 to  
CC AAH25963. The proteins can have activities based on the tissues and cells  
CC they are expressed in, such as: antiinflammatory; antirheumatic;  
CC antarthritic; immunosuppressive; antibacterial; endocrine; cardiant;  
CC central nervous system; viricide; anti-HIV; fungicide; antimutagen;  
CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnery;  
CC antitumor; osteopathic; dermatological; antiallergic; antiasthmatic;  
CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;  
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
CC encoding them can be used in gene therapy, antisense therapy and vaccine  
CC production. The proteins and polynucleotides are useful for screening for  
CC agonists or antagonists of a protein and for the treatment and diagnosis  
CC of disorders associated with the activity of a protein e.g. inflammation,  
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal  
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,  
CC anaemia, platelet disorders, thrombocytopaenia, wounds, ulcers,  
CC osteoporosis, severe combined immunodeficiency, eczema, allergic  
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and  
CC neurological disorders  
XX  
XX Sequence 382 AA;  
Query Match 100.0%; Score 1954; DB 4; Length 382;  
Best Local Similarity 100.0%; Pred. No. 1.3e-180;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNSSPAGTSPQPSRANGNINLGPANPNAQPTDFDLKVIKGNVGVLLAKRSDGAF 60  
DB 16 MNSSPAGTSPQPSRANGNINLGPANPNAQPTDFDLKVIKGNVGVLLAKRSDGAF 75  
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPPFLVGLRYSFQTPEKLYFVLDVYNGGE 120  
DB 76 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPPFLVGLRYSFQTPEKLYFVLDVYNGGE 135  
QY 121 LFFHLQRRERFLEPPARFYAAEVAASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180  
DB 136 LFFHLQRRERFLEPPARFYAAEVAASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 195  
QY 181 CKEGVEPEDTTSTFCGTPPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYSDQVS 240  
DB 196 CKEGVEPEDTTSTFCGTPPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYSDQVS 255  
QY 241 QMYENILHQPLQIPGGRTVAAACDLLQSLHLKQDQRLGSKADFLFIKNHVFSPINWDDL 300  
DB 256 QMYENILHQPLQIPGGRTVAAACDLLQSLHLKQDQRLGSKADFLFIKNHVFSPINWDDL 315  
QY 301 YHKRLTPPNPNVTGPADLKHFDPEFTQEAHSVKSIGCTPDTVASSSGASSAFLGFSYAPE 360  
DB 316 YHKRLTPPNPNVTGPADLKHFDPEFTQEAHSVKSIGCTPDTVASSSGASSAFLGFSYAPE 375  
QY 361 DDDILDC 367  
DB 376 DDDILDC 382  
RESULT 8  
ADY37607  
ID ADY37607 standard; protein; 396 AA.  
XX  
AC ADY37607;  
XX  
DT 19-MAY-2005 (first entry)  
XX  
DE Lung cancer related protein, SEQ ID 83.

XX Cytostatic; lung tumor.  
KW  
XX Homo sapiens.  
OS  
XX  
XX US2005048589-A1.  
PN  
XX  
XX 03-MAR-2005.  
PD  
XX  
XX 25-AUG-2004; 2004US-00926543.  
PF  
XX  
XX 25-AUG-2003; 2003US-0497790P.  
PR  
XX  
XX (JEND/) JENDOUBI M.  
PA  
XX  
XX Jendoubi M;  
PI  
XX  
XX WPI; 2005-221517/23.  
DR  
XX  
XX N-PSDB; ADY37561.  
DR  
XX  
XX New antibody specific for an antigen differentially expressed between  
PT lung cancer tissue and normal tissue, useful for diagnosing, treating or  
PT preventing lung cancer.  
XX  
XX Disclosure; SEQ ID NO 83; 171pp; English.  
XX  
XX The present invention relates to an antibody (I) that binds to an antigen  
CC that is differentially expressed between lung cancer tissue and normal  
CC tissue, where the antigen is encoded by ADY37525. Also disclosed are  
CC polypeptides (ADY37573-ADY37618) encoded by lung cancer related genes  
CC (ADY37525-ADY37572), their fragments, analogs or derivatives; producing  
CC lung cancer related polypeptides; and a diagnostic kit for detection and  
CC disease management of lung cancer. (I) is useful for characterizing and  
CC analyzing biological activity and function of the lung cancer-specific  
CC gene products in relation to cellular pathways and networks in normal and  
CC disease states, purifying the cancer specific gene products, and  
CC detecting lung cancer-specific gene products and their expression levels  
CC in animal models of cancer. (I) is also useful for diagnosing, treating  
CC or preventing lung cancer, and also disorders related to abnormal  
CC cellular differentiation, proliferation or degeneration.  
XX  
XX Sequence 396 AA;  
Query Match 100.0%; Score 1954; DB 9; Length 396;  
Best Local Similarity 100.0%; Pred. No. 1.4e-180;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNSSPAGTSPQPSRANGNINLGPANPNAQPTDFDLKVIKGNVGVLLAKRSDGAF 60  
DB 30 MNSSPAGTSPQPSRANGNINLGPANPNAQPTDFDLKVIKGNVGVLLAKRSDGAF 89  
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPPFLVGLRYSFQTPEKLYFVLDVYNGGE 120  
DB 90 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPPFLVGLRYSFQTPEKLYFVLDVYNGGE 149  
QY 121 LFFHLQRRERFLEPPARFYAAEVAASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180  
DB 150 LFFHLQRRERFLEPPARFYAAEVAASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 209  
QY 181 CKEGVEPEDTTSTFCGTPPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYSDQVS 240  
DB 210 CKEGVEPEDTTSTFCGTPPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYSDQVS 269  
QY 241 QMYENILHQPLQIPGGRTVAAACDLLQSLHLKQDQRLGSKADFLFIKNHVFSPINWDDL 300  
DB 270 QMYENILHQPLQIPGGRTVAAACDLLQSLHLKQDQRLGSKADFLFIKNHVFSPINWDDL 329  
QY 301 YHKRLTPPNPNVTGPADLKHFDPEFTQEAHSVKSIGCTPDTVASSSGASSAFLGFSYAPE 360  
DB 330 YHKRLTPPNPNVTGPADLKHFDPEFTQEAHSVKSIGCTPDTVASSSGASSAFLGFSYAPE 389  
QY 361 DDDILDC 367  
|||||



XX Identifying a compound for treating a cardiovascular or thrombotic  
PT disorder by combining a compound to be tested with e.g., a 9380, 9462,  
PT 8701 or 2419 polypeptide or with a host cell expressing the polypeptide  
PT and detecting the binding.  
XX  
XX Claim 1; SEQ ID NO 126; 512pp; English.  
PS  
XX This invention relates to a novel compound that is capable of treating a  
CC cardiovascular or thrombotic disorder. Specifically, it refers to the  
CC identification of nucleic acid molecules, and the encoded proteins  
CC thereof, which are differentially expressed in cardiovascular disease  
CC states relative to their normal expression in non-diseased tissue. The  
CC present invention describes test compounds (i.e. small molecules,  
CC peptides or antibodies) that can bind to and modulate the activity of  
CC these differentially expressed membrane-bound polypeptides, where binding  
CC is detected by a competition binding assay, immunoassay or yeast two-  
CC hybrid assay. Accordingly, pharmaceutical compositions can be developed  
CC and used via gene therapy to treat aberrant vascularisation,  
CC atherosclerosis, thrombosis, coronary artery disease, hyperlipidaemia,  
CC dyslipidaemia, high blood pressure or heart failure. As such, they  
CC exhibit diuretic, thrombolytic, anticoagulant, antilipaseic, hypotensive  
CC and cardiant activities. This polypeptide sequence is a human protein  
CC that is differentially expressed in a patient with a cardiovascular  
CC disorder, given in an exemplification of the invention.  
XX  
XX Sequence 427 AA:  
SQ

[illegible]

KW	dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
KW	immune disorder; cardiovascular disease; neurodegenerative disease;
KW	cancer; autoimmune disorder; stroke; inflammatory bowel disease;
KW	inflammatory pelvic disease; multiple sclerosis; psoriasis.
XX	
OS	Homo sapiens.
XX	
PN	WO200073469-A2.
XX	
PD	07-DEC-2000.
XX	
PF	26-MAY-2000; 2000WO-US014842.
XX	
PR	28-MAY-1999; 99US-0136503P.
XX	
PA	(SUGE-) SUGEN INC.
XX	
PI	Plowman GD, Martinez R, Whyte D, Sudersanam S;
XX	
DR	WPI; 2001-032161/04.
XX	N-PSDB; AAF44737.
DR	
PT	Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT	treating immune-related diseases and disorders, cardiovascular disease,
PT	neurodegenerative diseases and/or cancers.
XX	
PS	Claim 10: Fig 1: 310pp: English.

Query Match	99.9%;	Score	1952;	DB	4;	Length	367;
Best Local Similarity	99.7%;	Pred. No.	2e-180;				
Matches	366;	Conservative	1;	Mismatches	0;	Indels	0;
Gaps	0						
Qy	1	MNSSPAGTSPQPSRANGNINLGPSANPNQAQPTDFDLKVIGKNTGKVLAKRKSDGAP	60				
Db	1	MNSSPAGTSPQPSRANGNINLGPSANPNQAQPTDFDLKVIGKNTGKVLAKRKSDGAP	60				
Qy	61	YAVKVLQKKSILKKKEQSHMAERSVLLKNVRHPFVLGLRYSFQTPEKLYFVLVDYVNGE	120				
Db	61	YAVKVLQKKSILKKKEQSHMAERSVLLKNVRHPFVLGLRYSFQTPEKLYFVLVDYVNGE	120				
Qy	121	LFPHLQRRERFLEPRARFYAAEVAASAIGYLHSLNIIVRDLPENILLLDCQGHVLLTDFGL	180				
Db	121	LFPHLQRRERFLEPRARFYAAEVAASAIGYLHSLNIIVRDLPENILLLDCQGHVLLTDFGL	180				
Qy	181	CKEGVEPEDTSTFCGTPEYLAPEVLARKPYDRAVDWMCGLGAVLYEMLHGLPPFYQDVS	240				
Db	181	CKEGVEPEDTSTFCGTPEYLAPEVLARKPYDRAVDWMCGLGAVLYEMLHGLPPFYQDVS	240				
Qy	241	QMYENILHQPLOIQGGRTVAACDLQSLHKDQQRILGSKADFLFIKNHVFPSPINWDDL	300				
Db	241	QMYENILHQPLOIQGGRTVAACDLQSLHKDQQRILGSKADFLFIKNHVFPSPINWDDL	300				
Qy	301	YHKRLTLPFPFNPNVTGPADLKHDFDPFEFTAQVSKSIGCTPDTVAASSGASAFILGFSYAPE	360				

Db 301 YHKRLTPFPNVTGPDALKHFDPEFTQEA VSKSIGCTPDTVASSGASSAFLGFSYAPE 360  
361 DDILDC 367  
361 DDILDC 367  
RESULT 12  
AAV95277  
ID AAV95277 standard; protein; 367 AA.  
XX AAV95277;  
XX 12-SEP-2000 (first entry)  
XX Mouse serum and glucocorticoid-induced protein kinase 2.  
XX Serum and glucocorticoid-induced protein kinase 2; SGK2; mouse;  
KW phosphorylation; cancer; diabetes; ischaemia; therapy.  
XX Mus musculus.  
XX WO200035946-A1.  
XX 22-JUN-2000.  
XX 14-DEC-1999; 99WO-GB004232.  
XX 14-DEC-1998; 98US-0112217P.  
PR 19-AUG-1999; 99GB-00019676.  
XX (UYDU-) UNIV DUNDEE.  
XX Cohen P, Kobayashi T, Deak M;  
PI WPI; 2000-442364/38.  
XX Modulation of serum and glucocorticoid-induced protein kinase (SGK) by  
PT phosphorylation with 3-phosphoinositide-dependent protein kinase-1 (PDK1)  
PT or dephosphorylation, useful for treatment of cancer, diabetes and  
PT ischemic diseases.  
XX Disclosure; Page 7; 127pp; English.  
XX The present sequence is that of mouse serum and glucocorticoid-induced  
XX protein kinase (SGK) isoform 2, a protein activated by phosphorylation.  
CC The invention provides methods of activating SGK (see also AAV95275-79)  
CC by phosphorylation using 3-phosphoinositide-dependent protein kinase-1  
CC (PDK1), and of reducing the activity of SGK by dephosphorylation. The  
CC invention also provides a method of identifying a compound that modulates  
CC the activity of SGK. Such compounds are useful for treating patients  
CC requiring modulation of SGK, such as patients with cancer, diabetes or  
CC ischaemic disease  
XX Sequence 367 AA;  
Query Match 94.6%; Score 1848; DB 3; Length 367;  
Best Local Similarity 94.3%; Pred. No. 2.5e-170;  
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;  
QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVLLAKRKS DGAF 60  
Db 1 MASSPVGVPQPSRANGNINLGPSANPNARTDFDLKVIKGNVGVLLAKRKS DGAF 60  
QY 61 YAVKVLQKSLKKKQSHIMAEVSLLKNVRHPLVGLRYSFQTPKLYFLVDYVNGGE 120  
Db 61 YAVKVLQKSLKKKQSHIMAEVNLLKNVRHPLVGLRYSFQTPKLYFLVDYVNGGE 120  
QY 121 LFFHLQRRERFLEPRARFYAAEVASAIQVLSHINIIYRDLKPENILLDCQGHVLTDFGL 180  
Db 121 LFFHLQRRERFLEPRARFYAAEVASAIQVLSHINIIYRDLKPENILLDCQGHVLTDFGL 180

QY 181 CKEGVEPEDTTFTFCGTPEYLAPEVLKPEPYDRAVDMWCLGAVLYEMLHGLPFPYSQDVS 240  
Db 181 CKEGVEPEDTTFTFCGTPEYLAPEVLKPEPYDRAVDMWCLGAVLYEMLHGLPFPFTDVA 240  
QY 241 QMYENILHQPLOIPGGRVTVAACDLLOSLLHKDQRLGSKADFELEIKNHVFFSPINWDDL 300  
Db 241 QMYENILHQPLOIPGGRVTVAACDLLOSLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 300  
QY 301 YHKRLTPFPNVTGPDALKHFDPEFTQEA VSKSIGCTPDTVASSGASSAFLGFSYAPE 360  
Db 301 YHKRLTPFPNVTGPDALKHFDPEFTQEA VSKSIGCTPDTVASSGASSAFLGFSYAQD 360  
QY 361 DDILDC 366  
Db 361 DDILDC 366  
RESULT 13  
ADD45797  
ID ADD45797 standard; protein; 367 AA.  
XX ADD45797;  
XX 29-JAN-2004 (first entry)  
XX Rat Protein AAF12756, SEQ ID NO 11466.  
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX Rattus norvegicus.  
XX WO2003016475-A2.  
XX 27-FEB-2003.  
XX 14-AUG-2002; 2002WO-US025765.  
XX 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX (GEO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX Woolf C, D'urso D, Befort K, Costigan M;  
XX WPI; 2003-268312/26.  
DR GENBANK; RAF12756.  
XX New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX Claim 1; Page; 1017pp; English.  
XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more



CC acid molecule may be used to diagnose, treat or prevent metabolic  
CC disorders such as diabetes or obesity, infections, cachexia, cancer,  
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's  
CC disease, immune disorders, haematopoietic disorders and various  
CC dyslipidaemias. The nucleic acids can also be used as hybridisation  
CC probes, in chromosome mapping, tissue typing, preventive medicine and  
CC pharmacogenomics. The present sequence represents a human NOVX from the  
CC present invention.  
XX  
XX

Sequence 398 AA;

Query Match 90.5%; Score 1767.5; DB 6; Length 398;  
Best Local Similarity 92.1%; Pred. No. 1.8e-162;  
Matches 338; Conservative 0; Mismatches 0; Indels 29; Gaps 1;  
QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVGKNGYGVLLAKRKS DGAF 60  
DB 61 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVGKNGYGVLLAKRKS DGAF 120  
QY 61 YAVKVLQKKSILKKKQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE 120  
DB 121 YAVKVLQKKSILKKKQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE 180  
QY 121 LPFHQRERRFLPRARFYAAEVAASAIGYLHSLNIIYRDLKPENILLDCQGHVVLTFDGL 180  
DB 181 LPFHQRERRFLPRARFYAAEVAASAIGYLHSLNIIYRDLKPENILLDCQ----- 230  
QY 181 CKGEVPEPTSTFCGTPEVLAPEVLKPSYDRAVDWVCLGAVLYEMLHGLPFPYSODYS 240  
DB 231 -----YLAPEVLKPSYDRAVDWVCLGAVLYEMLHGLPFPYSQDVS 271  
QY 241 QMVENILHQLPIPGGRTVAACDLQLLHKQORQLGSKADPLEIKNVHFFSPINWDDL 300  
DB 272 QMVENILHQLPIPGGRTVAACDLQLLHKQORQLGSKADPLEIKNVHFFSPINWDDL 331  
QY 301 YHKRLTPPNVNTGPDALKHFDPEFTQBAVSKSIGCTPDTVASSSGASSAFILGFSYAPE 360  
DB 332 YHKRLTPPNVNTGPDALKHFDPEFTQBAVSKSIGCTPDTVASSSGASSAFILGFSYAPE 391  
QY 361 DDDILDC 367  
DB 392 DDDILDC 398

RESULT 15

ADN62944

ID ADN62944 standard; protein; 398 AA.

XX AC

XX ADN62944;

XX DT 01-JUL-2004 (first entry)

XX DE Human NOV33a.

XX OS human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;

KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;

KW Alzheimer's disease; Parkinson's disease; immune disorder;

KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;

KW wasting disorder.

XX OS Homo sapiens.

XX PN US2004038223-A1.

XX XX 26-FEB-2004.

XX PF 01-OCT-2002; 2002US-00262511.

XX PR 02-OCT-2001; 2001US-0326483P.

XX PR 05-OCT-2001; 2001US-0327435P.

XX PR 09-OCT-2001; 2001US-0327449P.

XX PR 09-OCT-2001; 2001US-0327917P.

XX PR 09-OCT-2001; 2001US-0328029P.

PR 09-OCT-2001; 2001US-0328044P.  
PR 09-OCT-2001; 2001US-0328056P.  
PR 12-OCT-2001; 2001US-0328849P.  
PR 15-OCT-2001; 2001US-0329414P.  
PR 17-OCT-2001; 2001US-0330142P.  
PR 18-OCT-2001; 2001US-0330309P.  
PR 22-OCT-2001; 2001US-0341058P.  
PR 24-OCT-2001; 2001US-0339266P.  
PR 29-OCT-2001; 2001US-0343629P.  
PR 29-OCT-2001; 2001US-0349575P.  
PR 01-NOV-2001; 2001US-0346357P.  
PR 17-APR-2002; 2002US-0373260P.  
PR 19-APR-2002; 2002US-0373815P.  
PR 19-APR-2002; 2002US-0373817P.  
PR 19-APR-2002; 2002US-0373826P.  
PR 19-APR-2002; 2002US-0373884P.  
PR 22-APR-2002; 2002US-0374977P.  
PR 16-MAY-2002; 2002US-0381037P.  
PR 16-MAY-2002; 2002US-0381038P.  
PR 16-MAY-2002; 2002US-0381042P.  
PR 17-MAY-2002; 2002US-0381642P.  
PR 28-MAY-2002; 2002US-0383656P.  
PR 29-MAY-2002; 2002US-0383831P.  
PR 25-JUN-2002; 2002US-0391335P.

XX (SMIT/) SMITHSON G.

PA (MILL/) MILLET I.

PA (PEYM/) PEYMAN J A.

PA (KEKU/) KERODA R.

PA (JUJU/) JU J.

PA (LILL/) LI L.

PA (GUOX/) GUO X.

PA (PATT/) PATTURAJAN M.

PA (SPYT/) SPYTEK K A.

PA (EDIN/) EDINGER S R.

PA (ELLE/) ELLERMAN K.

PA (MALY/) MALYANKAR U M.

PA (ORTT/) ORT T.

PA (GORM/) GORMAN L.

PA (ZERH/) ZERHUSEN B D.

PA (ANDE/) ANDERSON D W.

PA (ZHON/) ZHONG M.

PA (CATT/) CATTERTON E.

PA (JIWW/) JI W.

PA (MILL/) MILLER C E.

PA (RAST/) RASTELLI L.

PA (STON/) STONE D J.

PA (PENNA/) PENNA C E A.

PA (SHEN/) SHENOY S G.

PA (SHIM/) SHIMKETS R A.

PA (ROTH/) ROTHENBERG M E.

PA (LEAC/) LEACH M D.

PA (AGBE/) AGEE M L.

PA (BERG/) BERGHS C.

PA (DIPI/) DIPIPO V A.

PA (EISE/) EISEN A.

PA (GANG/) GANGOLLI E A.

PA (RIEG/) RIEGER D K.

PA (SPAD/) SPADERNA S K.

XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;

PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;

PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;

PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoj SG;

PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;

PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;

XX WPI: 2004-213931/20.

DR N-PSDB; ADN62943.

XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,

PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.

XX



PS Claim 1; SEQ ID NO 140; 395pp; English.

XX The invention relates to isolated NOVX polypeptides and polynucleotides.  
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or  
CC treat a medical condition in human related to the aberrant expression and  
CC activity of NOVX polypeptides. For example, NOVX polypeptides and  
CC polynucleotides may be used to treat disorders associated with decreased  
CC expression or activity of NOVX by supplementing the patient our  
CC production or to rectify mutations. Conversely, antisense NA molecules  
CC may be administered to down regulate expression of NOVX polypeptides by  
CC binding with the cells own genes and preventing their expression. NOVX  
CC polynucleotides and complementary sequences may also be used as DNA  
CC probes in diagnostic assays to detect and quantitate the presence of  
CC similar sequences in samples, and so which patients may be in need of  
CC restorative therapy. NOVX polypeptides may also be used as antigens in  
CC the production of antibodies and in assays to identify modulators  
CC (agonists and antagonists) of the expression and activity of NOVX. The  
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be  
CC used to modulate NOVX polynucleotide expression and activity of NOVX  
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as  
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX  
CC polypeptides and polynucleotides may be used in this way to prevent,  
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious  
CC disorders, Alzheimer's Disease, cancer-associated cachexia, neurodegenerative  
CC haematopoietic disorders, and the various dyslipidaemias, metabolic  
CC disturbances associated with obesity, the metabolic syndrome X and  
CC wasting disorders associated with chronic diseases and various cancers.  
CC They may also be used as antibacterial agents. The present sequence  
CC represents the amino acid sequence of a human NOVX protein.

XX Sequence 398 AA;

Query Match 89.5%; Score 1748.5; DB 8; Length 398;

Best Local Similarity 91.5%; Pred. No. 1.3e-160;

Matches 335; Conservative 1; Mismatches 1; Indels 29; Gaps 1;

QY	2	NSSPAGTSPQPSRANGNINLGPSANPNAPTDFDLKVIKGNKGVLLAKRKS	61
Db	62	:     :     :     :     :     :     :     :	121
QY	62	AVKVLQKSIKKKQSHIMASRVLKNVRHPLVGLRYSFOTPEKLYFVL	121
Db	122	:     :     :     :     :     :     :     :	181
QY	122	PFHLQRRRFLPRARFYAAEVASAIYGLHSLNIYRDLKPNILLDCQ	181
Db	182	:     :     :     :     :     :     :     :	230
QY	182	KEGVPEDTTSTFCGTPEVLAPVLKPEYDRAVDWMCIGAVLYEMLHGL	241
Db	231	:     :     :     :     :     :     :     :	272
QY	242	MYENILHQPLQIPGGRTVAACDLLOSLHKDQRLGSKADFLKTNHVFFSP	301
Db	273	:     :     :     :     :     :     :     :	332
QY	302	HKRLTPFPNVTGPADLKHDPFTQEAIVSKI GCTPDTVASSSGASSAF	361
Db	333	:     :     :     :     :     :     :     :	392
QY	362	DDILDC 367	
Db	393		
		DDILDC 398	

Search completed: January 27, 2006, 23:26:36

Job time : 70.3214 secs

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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:21:11 ; Search time 17.3113 Seconds  
(without alignments)  
1752.724 Million cell updates/sec

Title: US-09-868-131A-1

Perfect score: 1954

Sequence: 1 MNSSPAGTSPQPSRANGNI.....ASSAFLGFSYAPEDDDILDC 367

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/prodata/1/iaa/5 COMB.pep.\*

2: /cgn2\_6/prodata/1/iaa/6 COMB.pep.\*

3: /cgn2\_6/prodata/1/iaa/H COMB.pep.\*

4: /cgn2\_6/prodata/1/iaa/PCUTUS COMB.pep.\*

5: /cgn2\_6/prodata/1/iaa/RE COMB.pep.\*

6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1411	72.2	407	2	US-10-067-977-4
2	1411	72.2	445	2	US-10-067-977-2
3	1407	72.0	431	2	US-09-031-295-2
4	1407	72.0	431	2	US-10-000-039-2
5	1404.5	71.9	430	1	US-08-712-709-9
6	1404.5	71.9	430	2	US-09-111-444-9
7	1404.5	71.9	430	2	US-09-541-228-9
8	1403	71.8	431	1	US-08-712-709-5
9	1403	71.8	431	2	US-09-111-444-5
10	1403	71.8	431	2	US-09-541-228-5
11	886	45.3	479	2	US-09-771-161A-246
12	886	45.3	479	2	US-09-771-161A-247
13	886	45.3	479	2	US-09-771-161A-248
14	878.5	45.0	465	2	US-09-526-043-2
15	878.5	45.0	480	2	US-09-590-740-6
16	877.5	44.9	454	2	US-09-526-043-17
17	876	44.8	480	2	US-09-526-043-13
18	876	44.8	481	2	US-09-538-092-1054
19	874.5	44.8	480	2	US-09-091-058-2
20	874.5	44.8	480	2	US-09-590-740-2
21	874.5	44.8	480	2	US-09-538-092-1053
22	874.5	44.8	480	2	US-09-526-043-14
23	874.5	44.8	480	2	US-09-771-161A-223
24	874.5	44.8	726	2	US-09-417-197-71
25	874.5	44.8	727	2	US-09-417-197-139
26	856	43.8	417	2	US-09-590-740-4
27	849.5	43.5	480	2	US-09-205-658-157

28	844.5	43.2	470	2	US-09-248-796A-18482	Sequence 18482, A
29	791	40.5	587	1	US-08-313-274-2	Sequence 2, Appli
30	791	40.5	655	2	US-09-949-016-11676	Sequence 11676, A
31	789.5	40.4	637	2	US-09-817-310-2	Sequence 2, Appli
32	789.5	40.4	637	2	US-10-355-724A-2	Sequence 2, Appli
33	788.5	40.4	482	2	US-09-430-564-2	Sequence 2, Appli
34	788.5	40.4	495	2	US-09-430-564-3	Sequence 3, Appli
35	788.5	40.4	495	2	US-09-762-258-2	Sequence 2, Appli
36	788	40.3	546	2	US-09-205-658-155	Sequence 155, App
37	783.5	40.1	541	2	US-09-205-658-154	Sequence 154, App
38	778	39.8	502	2	US-09-538-092-996	Sequence 996, App
39	778	39.8	525	1	US-08-749-902-7	Sequence 7, Appli
40	778	39.8	525	1	US-08-749-902-8	Sequence 8, Appli
41	778	39.8	525	2	US-09-430-564-16	Sequence 16, Appli
42	778	39.8	525	2	US-09-762-258-4	Sequence 4, Appli
43	769	39.4	568	2	US-09-949-016-7970	Sequence 7970, Ap
44	769	39.4	584	2	US-09-842-307-2	Sequence 2, Appli
45	765	39.2	737	2	US-09-772-647-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-10-067-977-4

; Sequence 4, Application US/10067977

; Patent No. 6830911

; GENERAL INFORMATION:

; APPLICANT: YAN, Chunhua and KE, Zhaoxi

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL001313

; CURRENT APPLICATION NUMBER: US/10/067,977

; CURRENT FILING DATE: 2002-02-08

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 407

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-067-977-4

Query Match	72.2%	Score 1411;	DB 2;	Length 407;
Best Local Similarity	71.2%	Pred. No. 2.2e-131;		
Matches 262;	Conservative 53;	Mismatches 45;	Indels 8;	Gaps 3;
QY	1	MNSSPAGTSPQPSRANGNINIGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSDGAP	60	
DB	45	MNANP--GPPSPSQ---QINLGPSNPHAKSDPHFLKVIKGSFGKVLARHKAEEVF	99	
QY	61	YAVKVLQKSLKKKEQSHMAERSVLLKNVHPFLVGLRYSPOTPEKLYFVLVYNGGE	120	
DB	100	YAVKVLQKAILKKKEKHIMSERNVLLKNVHPFLVGLRYSPOTPEKLYFVLVYNGGE	159	
QY	121	LFPHLQERRFLPRARFYAAEVAISAIGYLHSLNIYRDLKPENILLDCQGHVLTDFGL	180	
DB	160	LFYHLQRECFLEPRARFYAAEIASALGYLHSLNIYRDLKPENILLDSQGHVLTDFGL	219	
QY	181	CKGEVEPDYTTTCGTPEYLAPEVLRKEPYDRAVDMWCLGAVLYBMLHGLPPFYSDQS	240	
DB	220	CKENIEHNSVTTTCGTPEYLAPEVLRKEPYDRTVDMWCLGAVLYBMLHGLPPFYSRNTA	279	
QY	241	QMYENILHQPLOIPGRTVAACDILLQSLHKDQRLSKADPLETKNVHFPSPINWDDL	300	
DB	280	EMYDNLNKLPLKPNITNSARHLLEGQLQKDKRTKRLGAKDDFMETKSHVFFSLINWDDL	339	
QY	301	YHKRLTPPNPNVTPGADLKHFDPDPTFOEAVSKSIGCTPDTV---ASSGASSAFLGFSY	357	
DB	340	INKKLTTPPNPNVSGPNDLURHFDPTFTPEVPVNSIGKSPDSVLVTASVKEAAEALGFSY	399	
QY	358	APEDDDIL 365		

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Db 400 APPTDSFL 407

RESULT 2
US-10-067-977-2
; Sequence 2, Application US/10067977
; Patent No. 6830911
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua and KE, Zhaoxi
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001313
; CURRENT APPLICATION NUMBER: US/10/067,977
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-977-2

Query Match 72.2%; Score 1411; DB 2; Length 445;
Best Local Similarity 71.2%; Pred. No. 2.5e-131;
Matches 262; Conservative 53; Mismatches 45; Indels 8; Gaps 3;

QY 1 MNSSPAGTSPQPSRANGNINLGPANPNNAOPTDFDLKVIKGNVGVLLAKRKSDGAF 60
Db 83 MNANP--SPPPSPQ--QINLGPSSNPHAKPSDFHLKVIKGNVGVLLAKRKAEVFF 137
QY 61 YAVVLQKKSILKKKEQSHIMAERSVLLKNVHPFLVGLRYSFQTPKLYFVLDYVNGGE 120
Db 138 YAVVLQKKAAILKKKEKHIMSERVLLKNVHPFLVGLHFSFQTADKLYFVLDYINGGE 197
QY 121 LPFHLORRERFLEPPARFYAAEASAGYLHSLNIYRDLPENILLDCQGHVLTDFGL 180
Db 198 LPFHLORECFLEPPARFYAAEASAGYLHSLNIYRDLPENILLDSQGHVLTDFGL 257
QY 181 CKEGVEPEDTTFTCGTPEYLAPEVLKPEYDRAVDMWCLGAVLYEMLHGLPPFYSDQVS 240
Db 258 KENIEHNTSTTFTCGTPEYLAPEVLKPEYDRTVDMWCLGAVLYEMLYGLPPFYSRNTA 317
QY 241 QVYENILHQPQIPGRTVAACDLQSLHKKQORLQSGKADFLKIKHVFSPINWDDL 300
Db 318 EMYDNILNKPLQKPNITNSARHLLEGJLQKDRTKRLGAKDDFMEIKSHVFFSLINWDDL 377
QY 301 YHKRLTPPNPNVTGPADLKHFDPFTQBAVSKSIGCTPDTV---ASSGASSAFGLFSY 357
Db 378 INKKITPPPNPNVSGPNDLRHDPFTBEPVPNSIGKSPDSVLVTASVKEAAEAFGLFSY 437
QY 358 APEDDDIL 365
Db 438 APPTDSFL 445

RESULT 3
US-09-031-295-2
; Sequence 2, Application US/09031295
; Patent No. 6326181
; GENERAL INFORMATION:
; APPLICANT: LANG, Florian
; APPLICANT: WALDEGGER, Tubingen
; TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,295
; FILING DATE: 26-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 197-08-173.8
; FILING DATE: 28-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 058315/0123
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 431 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-031-295-2

Query Match 72.0%; Score 1407; DB 2; Length 431;
Best Local Similarity 70.9%; Pred. No. 5.8e-131;
Matches 261; Conservative 54; Mismatches 45; Indels 8; Gaps 3;

QY 1 MNSSPAGTSPQPSRANGNINLGPANPNNAOPTDFDLKVIKGNVGVLLAKRKSDGAF 60
Db 69 MNANP--SPPPSPQ--QINLGPSSNPHAKPSDFHLKVIKGNVGVLLAKRKAEVFF 123
QY 61 YAVVLQKKSILKKKEQSHIMAERSVLLKNVHPFLVGLRYSFQTPKLYFVLDYVNGGE 120
Db 124 YAVVLQKKAAILKKKEKHIMSERVLLKNVHPFLVGLHFSFQTADKLYFVLDYINGGE 183
QY 121 LPFHLORRERFLEPPARFYAAEASAGYLHSLNIYRDLPENILLDCQGHVLTDFGL 180
Db 184 LPFHLORECFLEPPARFYAAEASAGYLHSLNIYRDLPENILLDSQGHVLTDFGL 243
QY 181 CKEGVEPEDTTFTCGTPEYLAPEVLKPEYDRAVDMWCLGAVLYEMLHGLPPFYSDQVS 240
Db 244 KENIEHNTSTTFTCGTPEYLAPEVLKPEYDRTVDMWCLGAVLYEMLYGLPPFYSRNTA 303
QY 241 QVYENILHQPQIPGRTVAACDLQSLHKKQORLQSGKADFLKIKHVFSPINWDDL 300
Db 304 EMYDNILNKPLQKPNITNSARHLLEGJLQKDRTKRLGAKDDFMEIKSHVFFSLINWDDL 363
QY 301 YHKRLTPPNPNVTGPADLKHFDPFTQBAVSKSIGCTPDTV---ASSGASSAFGLFSY 357
Db 364 INKKITPPPNPNVSGPNDLRHDPFTBEPVPNSIGKSPDSVLVTASVKEAAEAFGLFSY 423
QY 358 APEDDDIL 365
Db 424 APPTDSFL 431

RESULT 4
US-10-000-039-2
; Sequence 2, Application US/10000039
; Patent No. 6855520
; GENERAL INFORMATION:
; APPLICANT: LANG, Florian
; APPLICANT: WALDEGGER, Tubingen
; TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
```



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; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,444
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/712,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 294637
;
US-09-111-444-9

Query Match 71.9%; Score 1404.5; DB 2; Length 430;
Best Local Similarity 70.9%; Pred. No. 1e-130;
Matches 261; Conservative 56; Mismatches 42; Indels 9; Gaps 4;

QY 1 MNSSPAGTSPQSPSRANGNINLGPANPNQAQPTDFDLKVGKNGYKVLAKRKSDGAF 60
DB 69 MNANP--SPPPSPSQ---QINLGPSSNPHAKPSDFHLKVGKSGFGKVLARHKAEEAF 123

QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGE 120
DB 124 YAVKVLQKKAALKKKEKHIMSERVLLKNVKHPLVGLHFSFQADKLYFVLDYINGE 183

QY 121 LFFHLQRRERFLEPPARFYAAEVAASIGYLHSLNIYYRDLKPENILLDCQGHVLTDFGL 180
DB 184 LFFHLQRRERFLEPPARFYAAEVAASIGYLHSLNIYYRDLKPENILLDCQGHVLTDFGL 243

QY 181 CKGEVEPEDTSTFCGTPYLAPVLRKEPYDRAVDWNCGLGAVLYEMHLGLPPFYSDVVS 240
DB 244 CKENIEHNGTSTTFCGTPYLAPVLRKEPYDRAVDWNCGLGAVLYEMHLGLPPFYSDVVS 303

QY 241 QMYENILHQPQIPGGRTVAAACDLQLQSLHDKQORLGSKADFLKIKHNVFFSPINWDDL 300
DB 304 EMYDNLINKPLQLK-NITNSARHLLGLELLQKDRTKRLGAKODFMEIKSHIFFSLINWDDL 362

QY 301 YHKRLTPPNPNVNTGPAHLKHPDPTQBAVSKSGTCTPDTV---ASSGASSAFLGFSY 357
DB 363 INKKTTPPNPNVNSGSDLRHFDPTTEPVPSSIGRSPDSILVTASVKEAAEAFLGFSY 422

QY 358 APEDDDIL 365
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DB 423 APPMDSFL 430

RESULT 7
US-09-541-228-9
; Sequence 9, Application US/09541228
; Patent No. 6232077
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/541,228
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/712,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 294637
;
US-09-541-228-9

Query Match 71.9%; Score 1404.5; DB 2; Length 430;
Best Local Similarity 70.9%; Pred. No. 1e-130;
Matches 261; Conservative 56; Mismatches 42; Indels 9; Gaps 4;

QY 1 MNSSPAGTSPQSPSRANGNINLGPANPNQAQPTDFDLKVGKNGYKVLAKRKSDGAF 60
DB 69 MNANP--SPPPSPSQ---QINLGPSSNPHAKPSDFHLKVGKSGFGKVLARHKAEEAF 123

QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGE 120
DB 124 YAVKVLQKKAALKKKEKHIMSERVLLKNVKHPLVGLHFSFQADKLYFVLDYINGE 183

QY 121 LFFHLQRRERFLEPPARFYAAEVAASIGYLHSLNIYYRDLKPENILLDCQGHVLTDFGL 180
DB 184 LFFHLQRRERFLEPPARFYAAEVAASIGYLHSLNIYYRDLKPENILLDCQGHVLTDFGL 243

QY 181 CKGEVEPEDTSTFCGTPYLAPVLRKEPYDRAVDWNCGLGAVLYEMHLGLPPFYSDVVS 240
DB 244 CKENIEHNGTSTTFCGTPYLAPVLRKEPYDRAVDWNCGLGAVLYEMHLGLPPFYSDVVS 303

QY 241 QMYENILHQPQIPGGRTVAAACDLQLQSLHDKQORLGSKADFLKIKHNVFFSPINWDDL 300
DB 304 EMYDNLINKPLQLK-NITNSARHLLGLELLQKDRTKRLGAKODFMEIKSHIFFSLINWDDL 362
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QY 121 LFPHLQRRERLEPRARFYAAEVAASAIGYLHSLNIYRDLPENILLDCQGHVLTDFGL 180  
Db 184 LFVHLQRRERCFLEPRARSYAAETASALGYLHSLNIYRDLPENILLDCQGHVLTDFGL 243  
QY 181 CKEGVEPEDTSTFCGTPPEYLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPPFYSDQVS 240  
Db 244 CKENIEHNSSTSTFCGTPPEYLAPEVLHKLQPYDRTVDWMCGLGAVLYEMLHGLPPFYSRNTA 303  
QY 241 QMYENILHQLQIPGGRRTVAACDLQLSLHKKQORQLGSKADFLKHNHVFSPINWDDL 300  
Db 304 EMYDNLINKPLQLKPNITNSARHLLGGLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDL 363  
QY 301 YHKRLTPPNPNVGTGADLKHDPDPEFTQEAUSKISGCTPDVT---ASSSGASAFILGFSY 357  
Db 364 INKKITPPFPNPNVSGPNDLRHDFDPEFTBEPVPNSIGKSPDSVLVTASVKEAAEAFILGFSY 423  
QY 358 APEDDDIL 365  
Db 424 APPTDSFL 431

RESULT 10  
US-09-541-228-5  
; Sequence 5, Application US/09541228  
; Patent No. 6232077  
; GENERAL INFORMATION:  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Hawkins, Phillip R.  
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/541,228  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/712,709  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0118 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 431 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE: Consensus  
US-09-541-228-5

Query Match 71.8%; Score 1403; DB 2; Length 431;  
Best Local Similarity 70.9%; Pred. No. 1.5e-130;  
Matches 261; Conservative 53; Mismatches 46; Indels 8; Gaps 3;  
QY 1 MNSSPAGTSPQPSRANGINLGPSANPNAQPTDFLKVIGKNGYKVLAKRSGDGF 60

Db 69 MNANP--SPPPSPSQ---QINLGSSPHAKPSDFHFLKVIKGSFGKVLARHKAEEVF 123  
QY 61 YAVKVLQKSKILKKKEQSHIMAERSVLLKNVRHPLVLGLRYSFQTPPEKLYFVLDYVNGGE 120  
Db 124 YAVKVLQKKAAILKKKEEKHIMSERNVLLKNVKHPFLVGLHFSFQTADKLYFVLDYINGGE 183  
QY 121 LFPHLQRRERLEPRARFYAAEVAASAIGYLHSLNIYRDLPENILLDCQGHVLTDFGL 180  
Db 184 LFVHLQRRERCFLEPRARSYAAETASALGYLHSLNIYRDLPENILLDCQGHVLTDFGL 243  
QY 181 CKEGVEPEDTSTFCGTPPEYLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPPFYSDQVS 240  
Db 244 CKENIEHNSSTSTFCGTPPEYLAPEVLHKLQPYDRTVDWMCGLGAVLYEMLHGLPPFYSRNTA 303  
QY 241 QMYENILHQLQIPGGRRTVAACDLQLSLHKKQORQLGSKADFLKHNHVFSPINWDDL 300  
Db 304 EMYDNLINKPLQLKPNITNSARHLLGGLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDL 363  
QY 301 YHKRLTPPNPNVGTGADLKHDPDPEFTQEAUSKISGCTPDVT---ASSSGASAFILGFSY 357  
Db 364 INKKITPPFPNPNVSGPNDLRHDFDPEFTBEPVPNSIGKSPDSVLVTASVKEAAEAFILGFSY 423  
QY 358 APEDDDIL 365  
Db 424 APPTDSFL 431

RESULT 11  
US-09-771-161A-246  
; Sequence 246, Application US/09771161A  
; Patent No. 6936450  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 246  
; LENGTH: 479  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-771-161A-246  
Query Match 45.3%; Score 886; DB 2; Length 479;  
Best Local Similarity 48.4%; Pred. No. 3.5e-79;  
Matches 181; Conservative 55; Mismatches 100; Indels 38; Gaps 8;  
QY 1 MNSSPAGTSPQPSRAN--GNINLGPSANPNAQPT--PDFLKVIGKNGYKVLAKRKS 56  
Db 117 MNCSPT-----SQIDNIGEBEEMDASTTHHKRTKMTWDFYLLKLLGKGTGKGVILVREKA 169  
QY 57 DGAFYAVKVLQKSKILKKKEQSHIMAERSVLLKNVRHPLVLGLRYSFQTPPEKLYFVLDVY 116  
Db 170 SGKYYAMKILKKKEVIAAKDEVAHTLITE--SRVLKNTRHHPFLTSLKYSFQTKDRLCFVMEYV 228  
QY 117 NGGELFFHLQRRERLEPRARFYAAEVAASAIGYLHSLNIYRDLPENILLDCQGHVLT 176  
Db 229 NGGELFFHLRSRVERFSEDRTRFYGAIVSALDYLSHGKIVYRDCLKLENMLDKDGHKIT 288  
QY 177 DFGLCKEGVEPEDTSTFCGTPPEYLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPPFY 236  
Db 289 DFGLCKEGITDAATMKTCGTPPEYLAPEVLEDNDYGRAVDWMCGLGAVLYEMLHGLPPFY 348  
QY 237 QDVSQMYENILHQLQIPGGRRTVAACDLQLSLHKKQORQL--GSKADFLKHNHVFSP 295



Db	349	QDHEKLFELIMEDIKFPRTTSSDAKSLISGLLIKDPNKRLLGGPDDAKEIMRHSFFSGV	408
Qy	296	NWDDLHKELTTPFPNVTGPNADLKHPDPETQAVSKSGCTPDTVASSSGASSALGCF	355
Db	409	NWQDVYDKLVPFPKQVTSETDTRYPDEET---ACTITTP-----	448

RESULT 12  
US-09-771-161A-247  
; Sequence 247, Application US/09771161A  
; Patent No. 6916450

RESULT 12  
US-09-771-161A-247  
; Sequence 247, Application US/09771161A  
; Patent No. 6916450

RESULT 12  
US-09-771-161A-247  
; Sequence 247, Application US/09771161A  
; Patent No. 6916450

RESULT 12  
US-09-771-161A-247  
; Sequence 247, Application US/09771161A  
; Patent No. 6916450

; ORGANISM: Homo sapiens  
US-09-526-043-2

Query Match 45.0%; Score 878.5; DB 2; Length 465;  
Best Local Similarity 51.0%; Pred. No. 1.9e-78;  
Matches 172; Conservative 53; Mismatches 99; Indels 13; Gaps 5;

QY 1 MNSSPAGTPSPQPSRAN--GNINLGPSANPNAOPT--DFDFLKVIGKNGYKVLAKRKS 56  
Db 117 MNCSP-----SQIDNIGEEWDASTTHHKKTWNDFYLLKLGKGTGKRVILVREKA 169  
QY 57 DGAFYAVKVLQKKSILKKKEQSHIMAEVSLLKNVRHPLVGLRYSFQTPKLYFVLVYV 116  
Db 170 SGKYAMKILKKEVIAKDEVAHTLTS-SRVLKNTRHPLFSLKYSFQIKDLRCFVMEYV 228  
QY 117 NGGELFFHLQRRRFLPRARFYAAEVAASGVLHSLNIIYRDLKPENILLDCQGHVLT 176  
Db 229 NGGELFFHLRSRERVSFSEDRTRFYGAIVSALDYHSGKIVYRDLKLENMLDKDGHKIT 288  
QY 177 DFGLCKEGVEPEDTTSTFCGTPYLAPVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYS 236  
Db 289 DFGLCKEGITDAATMTKTCGTPYLAPVLENDYGRAVDWVGLGVVYMYEMMCGRLPFYN 348  
QY 237 QVVSQMYENILHQLIPGGRTVAACDLLQSLHKKDQORL-GSKADFLEIKNHVFFSPI 295  
Db 349 QDHEKLFELLMEDIKFPRTLSSDAKSLLSGLLIKDPNKRKLGCGPDDAKEIMRHSFFSGV 408  
QY 296 NWDDLYHKRLTPFPNPNVTGPDADLKHDFDEFTQEAVS 332  
Db 409 NWQDVYDKLVPPKPKQVTSETDTRYFDEEFTAQTIT 445

RESULT 15

US-09-590-740-6  
; Sequence 6, Application US/09590740  
; Patent No. 6689807  
; GENERAL INFORMATION:

; APPLICANT: Kenneth Walsh  
; APPLICANT: St. Elizabeth's Medical Center  
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for  
; TITLE OF INVENTION: Promoting Angiogenesis  
; FILE REFERENCE: 49,784 (1417)  
; CURRENT APPLICATION NUMBER: US/09/590,740  
; CURRENT FILING DATE: 2000-06-08  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 480  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-590-740-6

Query Match 45.0%; Score 878.5; DB 2; Length 480;  
Best Local Similarity 47.8%; Pred. No. 1.9e-78;  
Matches 175; Conservative 58; Mismatches 102; Indels 31; Gaps 7;

QY 6 AGTPSPQPSRANGNINLGPSANPNAOPT--DFDFLKVIGKNGYKVLAKRKS DGAFYAV 63  
Db 122 SGSPSDNSGAEBMEVSL---AKPKHRVTWNEFEYLLKLGKTFGKVLVKEKATGRYYAM 178  
QY 64 KVLQKKSILKKKEQSHIMAEVSLLKNVRHPLVGLRYSFQTPKLYFVLVYVNGELPF 123  
Db 179 KILKKEVIVAKDEVAHTLTENRV-LQNSRHPFLTALKYSFQTHDLRCFVMEYANGELFF 237  
QY 124 HLQRRRFLPRARFYAAEVAASGVLHSLNIIYRDLKPENILLDCQGHVLTDFGLCK 182  
Db 238 HLSRERVSFSEDRARFYGAIVSALDYHSEKNVYRDLKLENMLDKDGHKITDFGLCK 297  
QY 183 EGVEPEDTTSTFCGTPYLAPVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYSQDVSM 242  
Db 298 EGKIDGATMTKTCGTPYLAPVLENDYGRAVDWVGLGVVYMYEMMCGRLPFYNQDHEKL 357  
QY 243 YENILHQLIPGGRTVAACDLLQSLHKKDQORL-GSKADFLEIKNHVFFSPINWDDLY 301

Db 358 FELLIMEEIRFPTLGPFAKSLLSGLLKKDPTQRLGGSEDAKEIMQHRFFANIVWQDVT 417  
QY 302 HKRLTPFPNPNVTGPDADLKHDFDEFTQEAVSIGCTPDVTVASSGASSAFLGFSYAPED 361  
Db 418 EKKLSPPPKPKQVTSETDTRYFDEEFTAQMIT---ITP-----PDQ 454  
QY 362 DDILDC 367  
Db 455 DDSMEC 460

Search completed: January 27, 2006, 23:33:29  
Job time : 19.3113 secs

; NUMBER OF SEQ ID NOS: 752  
; SEQ ID NO 256  
; LENGTH: 367  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-221-278-256

Query Match 100.0%; Score 1954; DB 4; Length 367;  
Best Local Similarity 100.0%; Pred. No. 1.1e-139;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLAKRKSDDGAF 60  
DB 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLAKRKSDDGAF 60  
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYNGGE 120  
DB 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYNGGE 120  
QY 121 LFFHLQRRERFLPRARFYAAEVAASAIGYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180  
DB 121 LFFHLQRRERFLPRARFYAAEVAASAIGYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180  
QY 181 CKEGVEPEDTSTFCGTPPEYLAPEVLRKEPYDRAVDWMCIGAVLYEMLHGLPPFYSDVS 240  
DB 181 CKEGVEPEDTSTFCGTPPEYLAPEVLRKEPYDRAVDWMCIGAVLYEMLHGLPPFYSDVS 240  
QY 241 QMYENILHQPLOIPGGRTVAACDLLOSLLHKDQORLGSKADFLKKNHVFSPINWDDL 300  
DB 241 QMYENILHQPLOIPGGRTVAACDLLOSLLHKDQORLGSKADFLKKNHVFSPINWDDL 300  
QY 301 YHKRLTPPNPNVTGPDALKHFDPEFTQEAIVSKSIGCTPTDVASSSGASSAFILGFSYAPE 360  
DB 301 YHKRLTPPNPNVTGPDALKHFDPEFTQEAIVSKSIGCTPTDVASSSGASSAFILGFSYAPE 360  
QY 361 DDILDC 367  
DB 361 DDILDC 367

## RESULT 5

US-10-380-235-6  
; Sequence 6, Application US/10380235  
; Publication No. US20040072184A1  
; GENERAL INFORMATION:  
; APPLICANT: Yoganathan, Thillainathan  
; APPLICANT: Delaney, Allen  
; TITLE OF INVENTION: CANCER ASSOCIATED PROTEIN KINASES AND  
; FILE REFERENCE: KINE-024CIP  
; CURRENT APPLICATION NUMBER: US/10/380,235  
; PRIOR FILING DATE: 2003-10-15  
; PRIOR APPLICATION NUMBER: IB01/02237  
; PRIOR FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/290,555  
; PRIOR FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 60/233,999  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: 60/237,419  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,423  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/238,558  
; PRIOR FILING DATE: 2000-10-04  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 367  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-380-235-6

Query Match 100.0%; Score 1954; DB 4; Length 367;

Best Local Similarity 100.0%; Pred. No. 1.1e-139;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLAKRKSDDGAF 60  
DB 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLAKRKSDDGAF 60  
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYNGGE 120  
DB 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYNGGE 120  
QY 121 LFFHLQRRERFLPRARFYAAEVAASAIGYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180  
DB 121 LFFHLQRRERFLPRARFYAAEVAASAIGYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180  
QY 181 CKEGVEPEDTSTFCGTPPEYLAPEVLRKEPYDRAVDWMCIGAVLYEMLHGLPPFYSDVS 240  
DB 181 CKEGVEPEDTSTFCGTPPEYLAPEVLRKEPYDRAVDWMCIGAVLYEMLHGLPPFYSDVS 240  
QY 241 QMYENILHQPLOIPGGRTVAACDLLOSLLHKDQORLGSKADFLKKNHVFSPINWDDL 300  
DB 241 QMYENILHQPLOIPGGRTVAACDLLOSLLHKDQORLGSKADFLKKNHVFSPINWDDL 300  
QY 301 YHKRLTPPNPNVTGPDALKHFDPEFTQEAIVSKSIGCTPTDVASSSGASSAFILGFSYAPE 360  
DB 301 YHKRLTPPNPNVTGPDALKHFDPEFTQEAIVSKSIGCTPTDVASSSGASSAFILGFSYAPE 360  
QY 361 DDILDC 367  
DB 361 DDILDC 367

## RESULT 6

US-10-296-115-1109  
; Sequence 1109, Application US/10296115  
; Publication No. US20040053248A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq Inc  
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 784PCT  
; CURRENT APPLICATION NUMBER: US/10/296,115  
; PRIOR FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: US09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: US09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 1478  
; SEQ ID NO 1109  
; LENGTH: 382  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-296-115-1109

Query Match 100.0%; Score 1954; DB 4; Length 382;  
Best Local Similarity 100.0%; Pred. No. 1.2e-139;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLAKRKSDDGAF 60  
DB 16 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLAKRKSDDGAF 75  
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYNGGE 120  
DB 76 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYNGGE 135  
QY 121 LFFHLQRRERFLPRARFYAAEVAASAIGYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180  
DB 136 LFFHLQRRERFLPRARFYAAEVAASAIGYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 195  
QY 181 CKEGVEPEDTSTFCGTPPEYLAPEVLRKEPYDRAVDWMCIGAVLYEMLHGLPPFYSDVS 240  
DB 196 CKEGVEPEDTSTFCGTPPEYLAPEVLRKEPYDRAVDWMCIGAVLYEMLHGLPPFYSDVS 255

QY 241 QMYENILHQPLOIPGGRVAAACDLSLLHKDQORLQSGKADFLKIKNHVFFSPINWDDL 300  
Db |||||||  
256 QMYENILHQPLOIPGGRVAAACDLSLLHKDQORLQSGKADFLKIKNHVFFSPINWDDL 315  
QY 301 YHKRLTPPNPNVTGPDADLKHFDPFTQBAVSKSIGCTPDTVASSSGASSAFLGFSYAPE 360  
Db |||||||  
316 YHKRLTPPNPNVTGPDADLKHFDPFTQBAVSKSIGCTPDTVASSSGASSAFLGFSYAPE 375  
QY 361 DDILDC 367  
Db |||||||  
376 DDILDC 382

## RESULT 7

US-10-926-543-83  
; Sequence 83, Application US/10926543  
; Publication No. US20050048589A1  
; GENERAL INFORMATION:  
; APPLICANT: Jendoubi, Moncef  
; TITLE OF INVENTION: LUNG CANCER SPECIFIC GENE PRODUCTS: THEIR CODING SEQUENCE, THEIR  
; TITLE OF INVENTION: ANTIBODIES AND THEIR USE IN DIAGNOSTIC, THERAPEUTIC AND DISEASE  
; TITLE OF INVENTION: MANAGEMENT OF LUNG CANCER  
; FILE REFERENCE: 705403.4004  
; CURRENT APPLICATION NUMBER: US/10/926,543  
; CURRENT FILING DATE: 2004-08-25  
; PRIOR APPLICATION NUMBER: US 60/497,790  
; PRIOR FILING DATE: 2003-08-25  
; NUMBER OF SEQ ID NOS: 94  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 83  
; LENGTH: 396  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-926-543-83

Query Match 100.0%; Score 1954; DB 5; Length 396;  
Best Local Similarity 100.0%; Pred. No. 1.2e-139;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGKVLAKRSDGAF 60  
Db |||||||  
30 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGKVLAKRSDGAF 89  
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYVNGGE 120  
Db |||||||  
90 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYVNGGE 149  
QY 121 LFFHLQRRERFLEPRARFYAAEVAASIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180  
Db |||||||  
150 LFFHLQRRERFLEPRARFYAAEVAASIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 209  
QY 181 CKEGVEPEDTTSTFCGTPEYLAPEVLKRPEDYDRAVDMWCLGAVLYEMHLGLPPFFYSQDVS 240  
Db |||||||  
210 CKEGVEPEDTTSTFCGTPEYLAPEVLKRPEDYDRAVDMWCLGAVLYEMHLGLPPFFYSQDVS 269  
QY 241 QMYENILHQPLOIPGGRVAAACDLSLLHKDQORLQSGKADFLKIKNHVFFSPINWDDL 300  
Db |||||||  
270 QMYENILHQPLOIPGGRVAAACDLSLLHKDQORLQSGKADFLKIKNHVFFSPINWDDL 329  
QY 301 YHKRLTPPNPNVTGPDADLKHFDPFTQBAVSKSIGCTPDTVASSSGASSAFLGFSYAPE 360  
Db |||||||  
330 YHKRLTPPNPNVTGPDADLKHFDPFTQBAVSKSIGCTPDTVASSSGASSAFLGFSYAPE 389  
QY 361 DDILDC 367  
Db |||||||  
390 DDILDC 396

## RESULT 8

US-10-753-267-126  
; Sequence 126, Application US/10753267  
; Publication No. US20050037946A1  
; GENERAL INFORMATION:

; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Stagliano, Nancy E.  
; APPLICANT: Healy, Aileen  
; APPLICANT: Acton, Susan L.  
; APPLICANT: Galvin, Katherine M.  
; APPLICANT: Donoghue, Mary A.  
; APPLICANT: Rodrigue-Way, Amelie  
; APPLICANT: Tomlinson, James E.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,  
; TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,  
; TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701.  
; TITLE OF INVENTION: 3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 33770,  
; TITLE OF INVENTION: 9380, 2569654, 33556, 53656, 44143, 32612, 10671, 261,  
; TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955,  
; TITLE OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408,  
; TITLE OF INVENTION: 42028, 112091, 13886, 13942, 1673, 54946 OR 2419  
; FILE REFERENCE: MPI03-003P1RNMNIM  
; CURRENT APPLICATION NUMBER: US/10/753,267  
; CURRENT FILING DATE: 2004-01-08  
; PRIOR APPLICATION NUMBER: US 60/439,683  
; PRIOR FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: US 60/445,216  
; PRIOR FILING DATE: 2003-02-05  
; PRIOR APPLICATION NUMBER: US 60/448,036  
; PRIOR FILING DATE: 2003-02-18  
; PRIOR APPLICATION NUMBER: US 60/454,189  
; PRIOR FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 60/457,541  
; PRIOR FILING DATE: 2003-03-25  
; PRIOR APPLICATION NUMBER: US 60/466,411  
; PRIOR FILING DATE: 2003-04-29  
; PRIOR APPLICATION NUMBER: US 60/469,041  
; PRIOR FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: US 60/477,414  
; PRIOR FILING DATE: 2003-06-10  
; PRIOR APPLICATION NUMBER: US 60/478,560  
; PRIOR FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: US 60/489,772  
; PRIOR FILING DATE: 2003-07-24  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: PatSeq for Windows Version 4.0  
; SEQ ID NO 126  
; LENGTH: 427  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-753-267-126

Query Match 100.0%; Score 1954; DB 5; Length 427;  
Best Local Similarity 100.0%; Pred. No. 1.3e-139;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGKVLAKRSDGAF 60  
Db |||||||  
61 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGKVLAKRSDGAF 120  
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYVNGGE 120  
Db |||||||  
121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYVNGGE 180  
QY 121 LFFHLQRRERFLEPRARFYAAEVAASIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180  
Db |||||||  
181 LFFHLQRRERFLEPRARFYAAEVAASIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 240  
QY 181 CKEGVEPEDTTSTFCGTPEYLAPEVLKRPEDYDRAVDMWCLGAVLYEMHLGLPPFFYSQDVS 240  
Db |||||||  
241 CKEGVEPEDTTSTFCGTPEYLAPEVLKRPEDYDRAVDMWCLGAVLYEMHLGLPPFFYSQDVS 300  
QY 241 QMYENILHQPLOIPGGRVAAACDLSLLHKDQORLQSGKADFLKIKNHVFFSPINWDDL 300  
Db |||||||  
301 QMYENILHQPLOIPGGRVAAACDLSLLHKDQORLQSGKADFLKIKNHVFFSPINWDDL 360

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:31:20 ; Search time 64.3981 Seconds  
(without alignments)  
2381.178 Million cell updates/sec

Title: US-09-868-131A-1

Perfect score: 1954

Sequence: 1 MNSSPAGTSPQPSRANGNI.....ASSAFGLFSGYAPEDDILDC 367

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Maximum Match 0%

Listing first 45 summaries

Database : Published Applications\_AA\_Main:\*

1: /cgn2\_6/prodata1/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/prodata1/pubpaa/US08\_PUBCOMB.pep:\*

3: /cgn2\_6/prodata1/pubpaa/US09\_PUBCOMB.pep:\*

4: /cgn2\_6/prodata1/pubpaa/US10A\_PUBCOMB.pep:\*

5: /cgn2\_6/prodata1/pubpaa/US10B\_PUBCOMB.pep:\*

6: /cgn2\_6/prodata1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1954	100.0	367	3	US-09-971-118-2
2	1954	100.0	367	4	US-10-291-172-256
3	1954	100.0	367	4	US-10-429-160-52
4	1954	100.0	367	4	US-10-221-278-256
5	1954	100.0	367	4	US-10-380-235-6
6	1954	100.0	382	4	US-10-296-115-1109
7	1954	100.0	396	5	US-10-926-543-83
8	1954	100.0	427	5	US-10-753-267-126
9	1767.5	90.5	398	4	US-10-262-511-140
10	1411	72.2	388	4	US-10-131-410-104
11	1411	72.2	407	4	US-10-067-977-4
12	1411	72.2	407	4	US-10-827-272-4
13	1411	72.2	431	3	US-09-981-353-7
14	1411	72.2	431	4	US-10-403-161-2
15	1411	72.2	431	4	US-10-403-161-4
16	1411	72.2	445	4	US-10-067-977-2
17	1411	72.2	445	4	US-10-827-272-2
18	1411	72.2	526	4	US-10-094-749-1861
19	1407	72.0	431	4	US-10-000-039-2
20	1407	72.0	431	4	US-10-353-690-12
21	1407	72.0	431	5	US-10-756-149-5279
22	1407	72.0	431	6	US-11-044-570-2
23	1404.5	71.9	430	3	US-09-810-808-9
24	1403	71.8	431	3	US-09-810-808-5
25	1392	71.2	594	5	US-10-732-923-10768
26	1390.5	71.2	433	5	US-10-732-923-10767
27	1342.5	68.7	340	4	US-10-217-574-17

28	1342.5	68.7	340	4	US-10-217-555-17	Sequence 17, Appl
29	1323.5	67.7	429	4	US-10-295-027-116	Sequence 116, App
30	1323.5	67.7	496	3	US-09-784-249-2	Sequence 2, Appli
31	1323.5	67.7	496	3	US-09-764-875-746	Sequence 746, App
32	1323.5	67.7	496	3	US-09-764-875-900	Sequence 900, App
33	1323.5	67.7	496	5	US-10-737-450-4	Sequence 4, Appli
34	1312.5	67.2	496	4	US-10-755-889-42	Sequence 42, Appl
35	1156.5	59.2	308	4	US-10-664-421-85	Sequence 85, Appl
36	1156.5	59.2	308	5	US-10-941-635-85	Sequence 85, Appl
37	983	50.3	422	4	US-10-369-493-7027	Sequence 7027, Ap
38	888.5	45.5	276	3	US-09-764-868-669	Sequence 669, App
39	888.5	45.5	276	3	US-09-764-875-1176	Sequence 1176, Ap
40	886	45.3	479	3	US-09-771-161A-246	Sequence 246, App
41	886	45.3	479	3	US-09-771-161A-247	Sequence 247, App
42	886	45.3	479	3	US-09-771-161A-248	Sequence 248, App
43	886	45.3	479	4	US-10-394-322A-3	Sequence 3, Appli
44	886	45.3	479	4	US-10-217-574-33	Sequence 33, Appl
45	886	45.3	479	4	US-10-217-555-33	Sequence 33, Appl

## ALIGNMENTS

## RESULT 1

US-09-971-118-2  
; Sequence 2, Application US/09971118  
; Patent No. US20020123056A1  
; GENERAL INFORMATION:  
; APPLICANT: DELANEY, ALLEN  
; APPLICANT: YOGANATHAN, THILLAINATHAN  
; TITLE OF INVENTION: SGK2 AND ITS USES  
; FILE REFERENCE: KINE025CIP  
; CURRENT APPLICATION NUMBER: US/09/971,118  
; CURRENT FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: PCT/US01/21479  
; PRIOR FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/237,419  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 367  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-971-118-2

Query Match	100.0%;	Score	1954;	DB	3;	Length	367;
Best Local Similarity	100.0%;	Pred. NO.	1.1e-139;				
Matches	367;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	1	MNSSPAGTSPQPSRANGNINIGPSANPNAQTD	DFLKVIGKNGYKVLAKRKS	SDGAF	60		
Db	1	MNSSPAGTSPQPSRANGNINIGPSANPNAQTD	DFLKVIGKNGYKVLAKRKS	SDGAF	60		
QY	61	YAVKVLQKSKILKKEQSHIMAEVSVLLKNVRHPLVGLRYSFQTPEKLYFVLDVYNGE	120				
Db	61	YAVKVLQKSKILKKEQSHIMAEVSVLLKNVRHPLVGLRYSFQTPEKLYFVLDVYNGE	120				
QY	121	LPFHQLRERRFLPEPRFYAAEVAISAIYGLHSLNIIYRDLKPENILLDCQGHVLTDFGL	180				
Db	121	LPFHQLRERRFLPEPRFYAAEVAISAIYGLHSLNIIYRDLKPENILLDCQGHVLTDFGL	180				
QY	181	CKEGVEPEDTSTFTCGTPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYSQDVS	240				
Db	181	CKEGVEPEDTSTFTCGTPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYSQDVS	240				
QY	241	QMYENILHQPLOIPGGRVTVAACDLQLSLHKDQORLGSKADFLEIKNHVFPSPINWDDL	300				
Db	241	QMYENILHQPLOIPGGRVTVAACDLQLSLHKDQORLGSKADFLEIKNHVFPSPINWDDL	300				
QY	301	YHKRLTPFPNPNVTGPADLKHFPDPEFTQBAVSKSGICCTPDTVASSSGASSAFGLFSGYAPE	360				
Db	301	YHKRLTPFPNPNVTGPADLKHFPDPEFTQBAVSKSGICCTPDTVASSSGASSAFGLFSGYAPE	360				

Qy 361 DDDILDC 367  
Db 361 DDDILDC 367

RESULT 2

US-10-291-172-256  
; Sequence 256, Application US/10291172  
; Publication No. US20030228584A1  
; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-045  
; CURRENT APPLICATION NUMBER: US/10/291,172  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 09/693,267  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 09/665,363  
; PRIOR FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: 09/616,847  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 09/596,193  
; PRIOR FILING DATE: 2000-06-17  
; PRIOR APPLICATION NUMBER: 09/574,454  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: 09/519,705  
; PRIOR FILING DATE: 2000-03-07  
; NUMBER OF SEQ ID NOS: 752  
; SEQ ID NO 256  
; LENGTH: 367  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-291-172-256

Query Match 100.0%; Score 1954; DB 4; Length 367;

Best Local Similarity 100.0%; Pred. No. 1.1e-139; Mismatches 0; Indels 0; Gaps 0;  
Matches 367; Conservative 0;

1 MNSSPAGTSPQPSRANGNINLGPANPNAQPTDFDLKVIKGNKGVLLAKRKS DGAF 60  
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1 MNSSPAGTSPQPSRANGNINLGPANPNAQPTDFDLKVIKGNKGVLLAKRKS DGAF 60  
61 YAVKVLQKKSILKKKQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE 120  
61 YAVKVLQKKSILKKKQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE 120  
121 LFFHLQRRERFLEPRARFYAAEVAASIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180  
121 LFFHLQRRERFLEPRARFYAAEVAASIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180  
181 CKEGVEPEDTTSTFCGTPEYLAPEVLKPEPYDRAVDWCLGAVLYEMLHGLPPFYSQDVS 240  
181 CKEGVEPEDTTSTFCGTPEYLAPEVLKPEPYDRAVDWCLGAVLYEMLHGLPPFYSQDVS 240  
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241 QMYENILHQPLOIPGGRTVAAACDLLQSLHKDQORLGSKADPLEIKNHVFFSPINWDDL 300  
301 YHKRLTPPNPNVTGPADLKHPDFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360  
301 YHKRLTPPNPNVTGPADLKHPDFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360  
361 DDDILDC 367  
361 DDDILDC 367

RESULT 3

US-10-429-160-52  
; Sequence 52, Application US/10429160  
; Publication No. US20040023276A1  
; GENERAL INFORMATION:

; APPLICANT: Ward, Teresa R  
; APPLICANT: Mac, Mac  
; APPLICANT: Linsley, Peter S  
; APPLICANT: Lund, Lund  
; TITLE OF INVENTION: LXR Ligand Induced Genes and Proteins  
; FILE REFERENCE: RS0200  
; CURRENT APPLICATION NUMBER: US/10/429,160  
; CURRENT FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: US 60/377,714  
; PRIOR FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 52  
; LENGTH: 367  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-429-160-52

Query Match 100.0%; Score 1954; DB 4; Length 367;

Best Local Similarity 100.0%; Pred. No. 1.1e-139; Mismatches 0; Indels 0; Gaps 0;  
Matches 367; Conservative 0;

Qy 1 MNSSPAGTSPQPSRANGNINLGPANPNAQPTDFDLKVIKGNKGVLLAKRKS DGAF 60  
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Db 1 MNSSPAGTSPQPSRANGNINLGPANPNAQPTDFDLKVIKGNKGVLLAKRKS DGAF 60  
Qy 61 YAVKVLQKKSILKKKQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE 120  
61 YAVKVLQKKSILKKKQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE 120  
121 LFFHLQRRERFLEPRARFYAAEVAASIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180  
121 LFFHLQRRERFLEPRARFYAAEVAASIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180  
181 CKEGVEPEDTTSTFCGTPEYLAPEVLKPEPYDRAVDWCLGAVLYEMLHGLPPFYSQDVS 240  
181 CKEGVEPEDTTSTFCGTPEYLAPEVLKPEPYDRAVDWCLGAVLYEMLHGLPPFYSQDVS 240  
241 QMYENILHQPLOIPGGRTVAAACDLLQSLHKDQORLGSKADPLEIKNHVFFSPINWDDL 300  
241 QMYENILHQPLOIPGGRTVAAACDLLQSLHKDQORLGSKADPLEIKNHVFFSPINWDDL 300  
301 YHKRLTPPNPNVTGPADLKHPDFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360  
301 YHKRLTPPNPNVTGPADLKHPDFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360  
361 DDDILDC 367  
361 DDDILDC 367

RESULT 4

US-10-221-278-256  
; Sequence 256, Application US/10221278  
; Publication No. US20040034208A1  
; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: No. US20040034208A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-045  
; CURRENT APPLICATION NUMBER: US/10/221,278  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: 09/693,267  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 09/665,363  
; PRIOR FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: 09/616,847  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 09/596,193  
; PRIOR FILING DATE: 2000-06-17  
; PRIOR APPLICATION NUMBER: 09/574,454  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: 09/519,705  
; PRIOR FILING DATE: 2000-03-07

Qy	301	YHKLRLTPPNPNVTGPADILKHEDPFTQEA	YKSGTCTPDTVA	SSGASSAF	IGFSYAPE	360
Db	361	YHKLRLTPPNPNVTGPADILKHEDPFTQEA	YKSGTCTPDTVA	SSGASSAF	IGFSYAPE	420
Qy	361	DDDLDC	367			
Db	421	DDDLDC	427			

## RESULT 9

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US-10-262-511-140
; Sequence 140, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Saasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malvankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Goiman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSeqdist version 0.1
; SEQ ID NO 140
; LENGTH: 398
; TYPE: PRT

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[illegible]

## RESULT 10

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US-10-131-410-104
; Sequence 104, Application US/10131410
; Publication No. US20030235915A1
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST
; TITLE OF INVENTION: TUMORS
; FILE REFERENCE: SCH-1763
; CURRENT APPLICATION NUMBER: US/10/131,410
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 09/646,673
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: PCT/DE99/00908
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-410-104

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Db 81 YAVKVLQKXKALKKKEKHMSERNVLLKNVHPFLVGLHFSFQTADKLYFVLVDYNGE 140  
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QY 181 CKEGVEPEDTTSTFCGTPEYLAPEVLKPEYDRAVDWCLGAVLYEMLHGLPPFYSQDVS 240  
Db 201 KENIEHNSTTSTFCGTPEYLAPEVLKPEYDRTDVMWCLGAVLYEMLYGLPPFYSRNTA 260  
QY 241 QMYENILHQLQIPGGRTVAACDLQLSLHDKQORLGSKADPLEIKNVHFFSPINWDDL 300  
Db 261 EMYDNLNKLPLQKPNITNSARHLLGLLQKDRKLGAKDDFMEIKSHVFFSLINWDDL 320  
QY 301 YHKRLTPPNPNVNTGPAULKHDFEPTQBAVSKSIGCTPDTV---ASSSGASSAFILGFSY 357  
Db 321 INKKITPPFPNPNVSGNDLRHDFEPTBPVPNSIGKSPDSVLVTASVKEAAEAFILGFSY 380  
QY 358 APEDDDIL 365  
Db 381 APPTDSFL 388

RESULT 11  
US-10-067-977-4  
; Sequence 4, Application US/10067977  
; Publication No. US20030157679A1  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Chunhua and KE, Zhaoxi  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001313  
; CURRENT APPLICATION NUMBER: US/10/067,977  
; CURRENT FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 407  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-067-977-4

Query Match 72.2%; Score 1411; DB 4; Length 407;  
Best Local Similarity 71.2%; Pred. No. 1.6e-98;  
Matches 262; Conservative 53; Mismatches 45; Indels 8; Gaps 3;  
QY 1 MNSSPAGTSPQSPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVKVLAKRKS DGAF 60  
Db 45 MNANP--SPPPSPSQ---QINLGPSNPHAKPSDFHLKVIKGSFGKVLARHKAEEVF 99  
QY 61 YAVKVLQKXKALKKKEKHMSERNVLLKNVHPFLVGLHFSFQTADKLYFVLVDYNGE 120  
Db 100 YAVKVLQKXKALKKKEKHMSERNVLLKNVHPFLVGLHFSFQTADKLYFVLVDYNGE 159  
QY 121 LFFHLQRRERFLEPRARFVAEVAASAIQVLSHLSNIIYRDLKPNENILLDCQGHVLTDFGL 180  
Db 160 LFFHLQRRERFLEPRARFVAEVAASAIQVLSHLSNIIYRDLKPNENILLDCQGHVLTDFGL 219  
QY 181 CKEGVEPEDTTSTFCGTPEYLAPEVLKPEYDRAVDWCLGAVLYEMLHGLPPFYSQDVS 240  
Db 220 KENIEHNSTTSTFCGTPEYLAPEVLKPEYDRTDVMWCLGAVLYEMLYGLPPFYSRNTA 279  
QY 241 QMYENILHQLQIPGGRTVAACDLQLSLHDKQORLGSKADPLEIKNVHFFSPINWDDL 300  
Db 280 EMYDNLNKLPLQKPNITNSARHLLGLLQKDRKLGAKDDFMEIKSHVFFSLINWDDL 339  
QY 301 YHKRLTPPNPNVNTGPAULKHDFEPTQBAVSKSIGCTPDTV---ASSSGASSAFILGFSY 357  
Db 340 INKKITPPFPNPNVSGNDLRHDFEPTBPVPNSIGKSPDSVLVTASVKEAAEAFILGFSY 399  
QY 358 APEDDDIL 365

Db 400 APPTDSFL 407  
RESULT 12  
US-10-827-272-4  
; Sequence 4, Application US/10827272  
; Publication No. US20040203127A1  
; GENERAL INFORMATION:  
; APPLICANT: KE, Zhaoxi  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001313-DIV  
; CURRENT APPLICATION NUMBER: US/10/827,272  
; CURRENT FILING DATE: 2004-04-20  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 407  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-827-272-4

Query Match 72.2%; Score 1411; DB 4; Length 407;  
Best Local Similarity 71.2%; Pred. No. 1.6e-98;  
Matches 262; Conservative 53; Mismatches 45; Indels 8; Gaps 3;  
QY 1 MNSSPAGTSPQSPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVKVLAKRKS DGAF 60  
Db 45 MNANP--SPPPSPSQ---QINLGPSNPHAKPSDFHLKVIKGSFGKVLARHKAEEVF 99  
QY 61 YAVKVLQKXKALKKKEKHMSERNVLLKNVHPFLVGLHFSFQTADKLYFVLVDYNGE 120  
Db 100 YAVKVLQKXKALKKKEKHMSERNVLLKNVHPFLVGLHFSFQTADKLYFVLVDYNGE 159  
QY 121 LFFHLQRRERFLEPRARFVAEVAASAIQVLSHLSNIIYRDLKPNENILLDCQGHVLTDFGL 180  
Db 160 LFFHLQRRERFLEPRARFVAEVAASAIQVLSHLSNIIYRDLKPNENILLDCQGHVLTDFGL 219  
QY 181 CKEGVEPEDTTSTFCGTPEYLAPEVLKPEYDRAVDWCLGAVLYEMLHGLPPFYSQDVS 240  
Db 220 KENIEHNSTTSTFCGTPEYLAPEVLKPEYDRTDVMWCLGAVLYEMLYGLPPFYSRNTA 279  
QY 241 QMYENILHQLQIPGGRTVAACDLQLSLHDKQORLGSKADPLEIKNVHFFSPINWDDL 300  
Db 280 EMYDNLNKLPLQKPNITNSARHLLGLLQKDRKLGAKDDFMEIKSHVFFSLINWDDL 339  
QY 301 YHKRLTPPNPNVNTGPAULKHDFEPTQBAVSKSIGCTPDTV---ASSSGASSAFILGFSY 357  
Db 340 INKKITPPFPNPNVSGNDLRHDFEPTBPVPNSIGKSPDSVLVTASVKEAAEAFILGFSY 399  
QY 358 APEDDDIL 365  
Db 400 APPTDSFL 407

RESULT 13  
US-09-981-353-7  
; Sequence 7, Application US/09981353  
; Patent No. US20020160382A1  
; GENERAL INFORMATION:  
; APPLICANT: Lasek, Amy W.  
; APPLICANT: Jones, David A.  
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER  
; FILE REFERENCE: PA-0038 US  
; CURRENT APPLICATION NUMBER: US/09/981,353  
; CURRENT FILING DATE: 2001-10-11  
; NUMBER OF SEQ ID NOS: 194  
; SOFTWARE: PERL Program  
; SEQ ID NO 7  
; LENGTH: 431  
; TYPE: PRT

TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-403-161-4

Query Match 72.2%; Score 1411; DB 4; Length 431;  
Best Local Similarity 71.2%; Pred. No. 1.7e-98;  
Matches 262; Conservative 53; Mismatches 45; Indels 8; Gaps 3;

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Db	69	MANP--SPPPSPQ--QINLGPSSNPHAKPSDFHFLKVIKGSFGVLLARHKAEEVF	123
QY	61	YAVKVLQKKSILKKKEQSHMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLVYNGGE	120
Db	124	YAVKVLQKKAILLKKEEKHMSERNVLLKNVHPFLVGLHFSFQTADKLYFVLVYNGGE	183
QY	121	LFPHLQRRERFLEPRARFYAAEVAISAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL	180
Db	184	LFYHLQRCRCFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTDFGL	243
QY	181	CKEGVEPEDTTSTFCGTPEYLAPEVLKPEYDRAVDWVCLGAVLYEMLHGLPPFYSDVS	240
Db	244	CKENIEHNSTTSTFCGTPEYLAPEVLHQPYDRTVDWVCLGAVLYEMLYGLPPFYSRNTA	303
QY	241	OMYENILHQPQIPGGRTVAACDLQLQSLHKKDQORQLGSKADPFLKKNHVFFSPINWDDL	300
Db	304	EMYDNILNKPLQLKPNITNSARHLEGLLQKDRTKELGAKDDFMEIKSHVFFSLINWDDL	363
QY	301	YHKRLTPPNPNVTGPAULKHFDPEFTQEAIVSKSIGCTPDTV---ASSSGASSAFILGFSY	357
Db	364	INKKITPPPNPNVSGPNLRFHFDPEFTTEPVPFVNSIGKSPDSVLVTASVKEAAEFLGFSY	423
QY	358	APEDDDIL	365
Db	424	APPTDSFL	431

Search completed: January 27, 2006, 23:57:31  
Job time : 67.3981 secs

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 3819039CD1
US-09-981-353-7

Query Match      72.2%; Score 1411; DB 3; Length 431;
Best Local Similarity 71.2%; Pred. No. 1.7e-98;
Matches 262; Conservative 53; Mismatches 45; Indels 8; Gaps 3;

Qy 1 MNSSPAGTSPQPSRANGNINLGPSANPNQAQPTDFDLKVIKGNYGKVLAKRKSDGAF 60
Db 69 MNANP--SPPPSPSQ--QINLGSSNPFAKPSDFHLKVIKGSFGKVLARHKAEEVF 123
Qy 61 YAVKVLQKSTILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYNGGE 120
Db 124 YAVKVLQKAKILKKKEKHMSERNVLLKNVRHPFLVGLHFSFQADKLYFVLDYNGGE 183
Qy 121 LFPHLQRRERFLEPRARFYAAEASAIYGLHSLNIIYRDLKPENILLDCOHHVLTDFGL 180
Db 184 LFYHLQRERCFLEPRARFYAAETASALGYLHSLNIVYRDLKPENILLDSQCHIVLTDFGL 243
Qy 181 CKEGVEPEDTTSTFCGTPYLAPEVLKPEYDRAVDMWCLGAVLYEMLHGLPPFYSDVS 240
Db 244 CKENIEHNSTTSTFCGTPYLAPEVLKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTA 303
Qy 241 QMVENILHQLPQTGGRTVAACDQLLSLLHKDQRLGSKADFLKHNHVFPPINWDDL 300
Db 304 EMYDNILNKPLQLKPNITNSARHLLGLELQKDRTRKLGAKDDFMEIKSHVFFSLINWDDL 363
Qy 301 YHKRLTPPPNPVNTGPAHLKHDFEFTQEAHSVKSIGCTPDTV--ASSSCASSAFLGFSY 357
Db 364 INKKTTPPPNPVNSGPNDRHDFEFTPEEPVPSNIGKSPDSVLVTASVKEAAEAFGLGFSY 423
Qy 358 APEDDDIL 365
Db 424 APPTDSFL 431

RESULT 14
US-10-403-161-2
; Sequence 2, Application US/10403161
; Publication No. US20040043930A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-573C
; CURRENT APPLICATION NUMBER: US/10/403,161
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/370349
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384543
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/370969
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/403748
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/372019
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/374379
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 09/779679
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181045
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 10/055877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262892
; PRIOR FILING DATE: 2001-01-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 2

; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-161-2

Query Match      72.2%; Score 1411; DB 4; Length 431;
Best Local Similarity 71.2%; Pred. No. 1.7e-98;
Matches 262; Conservative 53; Mismatches 45; Indels 8; Gaps 3;

Qy 1 MNSSPAGTSPQPSRANGNINLGPSANPNQAQPTDFDLKVIKGNYGKVLAKRKSDGAF 60
Db 69 MNANP--SPPPSPSQ--QINLGSSNPFAKPSDFHLKVIKGSFGKVLARHKAEEVF 123
Qy 61 YAVKVLQKSTILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYNGGE 120
Db 124 YAVKVLQKAKILKKKEKHMSERNVLLKNVRHPFLVGLHFSFQADKLYFVLDYNGGE 183
Qy 121 LFPHLQRRERFLEPRARFYAAEASAIYGLHSLNIIYRDLKPENILLDCOHHVLTDFGL 180
Db 184 LFYHLQRERCFLEPRARFYAAETASALGYLHSLNIVYRDLKPENILLDSQCHIVLTDFGL 243
Qy 181 CKEGVEPEDTTSTFCGTPYLAPEVLKPEYDRAVDMWCLGAVLYEMLHGLPPFYSDVS 240
Db 244 CKENIEHNSTTSTFCGTPYLAPEVLKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTA 303
Qy 241 QMVENILHQLPQTGGRTVAACDQLLSLLHKDQRLGSKADFLKHNHVFPPINWDDL 300
Db 304 EMYDNILNKPLQLKPNITNSARHLLGLELQKDRTRKLGAKDDFMEIKSHVFFSLINWDDL 363
Qy 301 YHKRLTPPPNPVNTGPAHLKHDFEFTQEAHSVKSIGCTPDTV--ASSSCASSAFLGFSY 357
Db 364 INKKTTPPPNPVNSGPNDRHDFEFTPEEPVPSNIGKSPDSVLVTASVKEAAEAFGLGFSY 423
Qy 358 APEDDDIL 365
Db 424 APPTDSFL 431

RESULT 15
US-10-403-161-4
; Sequence 4, Application US/10403161
; Publication No. US20040043930A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-573C
; CURRENT APPLICATION NUMBER: US/10/403,161
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/370349
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384543
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/370969
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/403748
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/372019
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/374379
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 09/779679
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181045
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 10/055877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262892
; PRIOR FILING DATE: 2001-01-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 4
; LENGTH: 431
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:32:16 ; Search time 9.46352 Seconds  
(without alignments)  
419.957 Million cell updates/sec

Title: US-09-868-131A-1  
Perfect score: 1954  
Sequence: 1 MNSSPAGTSPQPSRANGNI.....ASSAFLGFSYAPEDDDILDC 367

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New.\*  
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2: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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7: /cgn2\_6/prodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /cgn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1411	72.2	543	US-10-821-234-1158	Sequence 1158, Ap
2	874.5	44.8	480	US-11-109-156-18	Sequence 18, Appl
3	788.5	40.4	495	US-10-770-726-81	Sequence 81, Appl
4	761	38.9	737	US-11-152-366-28	Sequence 28, Appl
5	722.5	37.0	740	US-10-878-556A-129	Sequence 129, App
6	705.5	36.1	341	US-11-092-168-4	Sequence 4, Appli
7	701.5	35.9	942	US-10-770-726-76	Sequence 76, Appl
8	694.5	35.5	343	US-11-092-168-3	Sequence 3, Appli
9	694.5	35.5	351	US-11-132-142-13	Sequence 13, Appl
10	691.5	35.4	351	US-11-132-142-14	Sequence 14, Appl
11	690.5	35.3	462	US-11-132-142-10	Sequence 10, Appl
12	681.5	34.9	350	US-10-497-767-4	Sequence 4, Appli
13	681.5	34.9	381	US-11-132-142-9	Sequence 9, Appli
14	681	34.9	705	US-10-995-561-856	Sequence 856, App
15	681	34.9	706	US-10-995-561-855	Sequence 855, App
16	681	34.9	706	US-11-099-958-1	Sequence 1, Appli
17	679	34.7	351	US-11-099-958-2	Sequence 2, Appli
18	675	34.5	353	US-11-132-142-11	Sequence 11, Appl
19	672.5	34.4	395	US-11-132-142-12	Sequence 12, Appl
20	670	34.3	515	US-11-132-142-8	Sequence 8, Appli
21	662	33.9	398	US-11-132-142-7	Sequence 7, Appli
22	649.5	33.2	548	US-11-132-142-5	Sequence 5, Appli
23	644	33.0	480	US-11-132-142-6	Sequence 6, Appli
24	547	28.0	637	US-11-113-837-4	Sequence 4, Appli
25	541.5	27.7	1732	US-10-055-877-147	Sequence 147, App

ALIGNMENTS

RESULT 1

US-10-821-234-1158  
; Sequence 1158, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_seq\_genes Version 1.0  
; SEQ ID NO 1158  
; LENGTH: 543  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1158

Query Match 72.2%; Score 1411; DB 6; Length 543;  
Best Local Similarity 71.2%; Pred. No. 1e-121;  
Matches 262; Conservative 53; Mismatches 45; Indels 8; Gaps 3;  
QY 1 MNSSPAGTSPQPSRANGNINIGPSANPAQPTDFDLKVIKGNVGVLLAKRKS DGAF 60  
Db 181 MNANP-SPPSPSQ--QINLGPSNPHAKPSDFHLKVIKGSFGKVLARHKAEEVF 235  
QY 61 YAVKLOKSKILKKEQSHMAERSVLKNVPHFLVGLRYFQPEKLYFVLDVYNGGE 120  
Db 236 YAVKYLQKAILKKEEKHMSERNVLLKNVHFLVGLHFLVQFADKLYFVLDVYNGGE 295  
QY 121 LFFHLQRRRFLPPRARFYAAEVAISAIGVLSHLSNIYYRDLKPENILLDCQGHVLTDFGL 180  
Db 296 LFYHLQRECFLEPPRARFYAAEVAISAIGVLSHLSNIYYRDLKPENILLDSQGHVLTDFGL 355  
QY 181 CKGEVEPDTTSTFCGTPEYLAPEVLRKEPYDRAVDMWCLGAVLYEMHLGLPPFPYSQDVS 240  
Db 356 CXENIEHNTSTTFCGTPEYLAPEVLRKEPYDRTDWMCLGAVLYEMLYGLPPFYSRNTA 415  
QY 241 QMYENILHQPLOIPGRTVAACDLLOSLLHKDQORLQSKADFLKINHVFPSPINWDDL 300  
Db 416 EMYDNLNKLQKPNITNSARHLLLEGLQKDRTRLGAKDPMFBIKSHVFPFSLINWDDL 475  
QY 301 YHKRLTPPNPNVTGPADLKHDPDFTQEAVSKSGICTPDTV---ASSSGASSAFLGFSY 357





Db	83	KRI-LQAVNPFVLKLEFSFKDNSNLWNWEYVAGGEMFSLHRRIGRFAHPHAFYAAQI	141
Qy	144	ASAIYGLHSNLNIIYRDLPKPNILDDCGHVVLTDGLCKEGVBPEDTTTFCGTPPEYLAP	203
Db	142	VLTFEYLRSLDLIYRDLPKPNILLDQOQYIQVTDGFAK--RVKGRTWLTCGTPEYLAP	198
Qy	204	EVLKPEYDRADVWMCILGAVLYEMLHGLPFYSQVSQMYENILHQPLQIPGGRVAACD	263
Db	199	EILSKGYNKAVDWMALGVLIYYEAAAGYPFFADQPIQIYEKIVSGKVRFPESHFSLDKD	258
Qy	264	LLASLLHKDQORLGS-KADFLKHNHFFSPINWDDLYHKRLTTPPNPNVWTGPADLKHF	322
Db	259	LLRNLQVLTTRFNLKNGVNDIKNHKFWATTDWIAIYQKVEAPIPKFKGPGDTSNP	318
Qy	323	DPEFTQEAWSKI 335	
Db	319	D-DYEEEEIRVSI 330	
RESULT 7			
US-10-770-726-76			
; Sequence 76, Application US/10770726			
; Publication No. US20050266409A1			
; GENERAL INFORMATION:			
; APPLICANT: Wyeth			
; APPLICANT: Brown, Eugene			
; APPLICANT: Liu, Wei			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING			
; TITLE OF INVENTION: CANCERS			
; FILE REFERENCE: AM101079 (031896-010000)			
; CURRENT APPLICATION NUMBER: US/10/770,726			
; CURRENT FILING DATE: 2004-02-04			
; NUMBER OF SEQ ID NOS: 48640			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 76			
; LENGTH: 942			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-770-726-76			
Query Match 35.9%; Score 701.5; DB 6; Length 942;			
Best Local Similarity 40.7%; Pred. No. 2.4e-56;			
Matches 154; Conservative 65; Mismatches 124; Indels 35; Gaps 8;			
Qy	3	SSPAGTSP-QPSRANGINILGPSANPAOFT-----PELPSQTQETPCPALSPLRKSPLTLEDFKFLAVLGRG	624
Db	572	SPSSLSSPIQESTA-----PELPSQTQETPCPALSPLRKSPLTLEDFKFLAVLGRG	624
Qy	45	NYGKVLAKKSDGAFYAVKVLQKKSLKKKQSHMAERSVL--LKNVRHPFLVGLRYS	102
Db	625	HFGKVLILSEFRPSGELFAIKALKGDIVARDEVESLMCEKRIILAAVTSAGHPFLVNLFGC	684
Qy	103	FQTPKLYFLVDYNGGELFFHLQRRERFLEPRARFYAAEVASAIGYLHSLNIIYRDLKP	162
Db	685	FQTPHEVCFVMEYSAGGDLMLHISD-VFSEPRAIIFYSACVVLGQLFHEHKIYRDLKL	743
Qy	163	ENILDDCGHVLTDFGLCKEGVEPEDTTTCGTPPEYLAPVLRKPEPYDRAVDWNCIGA	222
Db	744	DNLLDTEGYVKIADFGLCKEGMGYGRDTSTFCGTPPEFLAPEVLTDTSTYAVDWMGLGV	803
Qy	223	VLYEMLHGLPPFYSQVSQMYENILHQPLQIPGGRVAACDLLQSLHKDQORLQ-SKA	281
Db	804	LLXEMLVGESPPFGDDEEYFVSIVNDEVYRPFRLSAEAIIGMRLLRRNPERLGSER	863
Qy	282	DFLEIKNHVFPSPINWDDLHKRLTPFPFNPNVWTGPADLKHFDPDEFTQEA--VSKSIGCTP	339
Db	864	DAEDVKKQPFRTLCWALLARLLPPEFVTLTSGRDVSFNDFEFTGEAFTLSPPRDAP	923
Qy	340	DTVASSSGASSAFLGSY 357	
Db	924	LTAEE-----QAADFDFD 937	



```
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: CYCLIC-AMP-DEPENDENT ORF3 IN SARS-CORONAVIRUS IS A
; TITLE OF INVENTION: CYCLIC-AMP-DEPENDENT KINASE AND A TARGET FOR SARS THERAPY
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Xenopus sp.
US-11-132-142-13
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Query Match 35.5%; Score 694.5; DB 7; Length 351;
Best Local Similarity 43.1%; Pred. No. 2.7e-56;
Matches 135; Conservative 65; Mismatches 106; Indels 7; Gaps 5;
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QY 24 PSANPNAQPTDFDLKVIKGNKGVLLAKRKSDGAFYAVKVLQKKSILKKKEQSHIMAE 83
DB 34 PPNQ-TASLDDFDPMKTLGTGSGRVMVVKHGAEQIYAMKILDKQKVKLQKIEHTLNE 92
QY 84 RSVLLKNVRHPPFLVGLRYSQTPEKLYFVLDYVNGGELFFHLQRRRFLPRARFYAAEV 143
DB 93 KRI-LQAVNPPFLVRLSEYFKDNSNLYMVEYVPGGEMFSLHRRIGRFSPEHARFYAAQI 151
QY 144 ASAIGYLSNIIYRDLKPENILLDCQGHVLTDFGLCKEGVEPEDTTSTFCGTPPYLAP 203
DB 152 VLTFEYLHSLDLIYRDLKPENILLDQGGYIQVTDGFAK---RVKGRWTWLCGTPPYLAP 208
QY 204 EVLRKEPYDRAVDMWCLGAVLYEMHLGLPPFYSDQVSQMYENILHQLPQIPGRTVAACD 263
DB 209 EILSKGYNKAVDWMALGVLYEMAGYPPFPADQPIQIYEKIVSGKVRFPFSFSDLDK 268
QY 264 LQOSLLHKDQORLGS-KADFLKIKNHVFPSPINWDDLYHKRLTPFPNPNVTGPDALKHF 322
DB 269 LLRNLLQVLDLTRKFGNLKGVNDIKNHKWFATTDWIAIYQKVEAPFIPKCRPGDTSNF 328
QY 323 DPEFTQEAIVSKSI 335
DB 329 D-DYEEEDIRVSL 340
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RESULT 10
US-11-132-142-14
; Sequence 14, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; TITLE OF INVENTION: CYCLIC-AMP-DEPENDENT KINASE AND A TARGET FOR SARS THERAPY
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-132-142-14
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Query Match 35.4%; Score 691.5; DB 7; Length 351;
Best Local Similarity 43.1%; Pred. No. 5.1e-56;
Matches 135; Conservative 65; Mismatches 106; Indels 7; Gaps 5;
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QY 24 PSANPNAQPTDFDLKVIKGNKGVLLAKRKSDGAFYAVKVLQKKSILKKKEQSHIMAE 83
DB 34 PAQN-TAHLDDQPERIKTLGTGSGRVMVVKHGETGNHYAMKILDKQKVKLQKIEHTLNE 92
QY 84 RSVLLKNVRHPPFLVGLRYSQTPEKLYFVLDYVNGGELFFHLQRRRFLPRARFYAAEV 143
DB 93 KRI-LQAVNPPFLVRLSEYFKDNSNLYMVEYVPGGEMFSLHRRIGRFSPEHARFYAAQI 151
QY 144 ASAIGYLSNIIYRDLKPENILLDCQGHVLTDFGLCKEGVEPEDTTSTFCGTPPYLAP 203
DB 152 VLTFEYLHSLDLIYRDLKPENILLDQGGYIQVTDGFAK---RVKGRWTWLCGTPPYLAP 208
QY 204 EVLRKEPYDRAVDMWCLGAVLYEMHLGLPPFYSDQVSQMYENILHQLPQIPGRTVAACD 263
DB 209 EILSKGYNKAVDWMALGVLYEMAGYPPFPADQPIQIYEKIVSGKVRFPFSFSDLDK 268
QY 264 LQOSLLHKDQORLGS-KADFLKIKNHVFPSPINWDDLYHKRLTPFPNPNVTGPDALKHF 322
DB 269 LLRNLLQVLDLTRKFGNLKGVNDIKNHKWFATTDWIAIYQKVEAPFIPKCRPGDTSNF 328
QY 323 DPEFTQEAIVSKSI 335
DB 329 D-DYEEEDIRVSI 340
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RESULT 11
US-11-132-142-10
; Sequence 10, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; TITLE OF INVENTION: CYCLIC-AMP-DEPENDENT KINASE AND A TARGET FOR SARS THERAPY
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Amblyomma
US-11-132-142-10
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Query Match 35.3%; Score 690.5; DB 7; Length 462;
Best Local Similarity 44.0%; Pred. No. 9.2e-56;
Matches 136; Conservative 61; Mismatches 105; Indels 7; Gaps 5;
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QY 24 PSANPNAQPTDFDLKVIKGNKGVLLAKRKSDGAFYAVKVLQKKSILKKKEQSHIMAE 83
DB 145 PSSN-TASLDDFDRIKTLGTGSGRVMVQHKQKDYFAMKILDKQKVKLQKIEHTLNE 203
QY 84 RSVLLKNVRHPPFLVGLRYSQTPEKLYFVLDYVNGGELFFHLQRRRFLPRARFYAAEV 143
DB 204 KRI-LQAVEFPFLVRLSEYFKDNSNLYMVEYVPGGEMFSLHRRIGRFSPEHARFYAAQI 262
QY 144 ASAIGYLSNIIYRDLKPENILLDCQGHVLTDFGLCKEGVEPEDTTSTFCGTPPYLAP 203
DB 263 VLAFOYLHSLDLIYRDLKPENILLDHTGYIKVTDGFAK---RVKGRWTWLCGTPPYLAP 319
QY 204 EVLRKEPYDRAVDMWCLGAVLYEMHLGLPPFYSDQVSQMYENILHQLPQIPGRTVAACD 263
DB 320 EILSKGYNKAVDWMALGVLYEMAGYPPFPADQPIQIYEKIVSGKVRFPFSFSDLDK 379
QY 264 LQOSLLHKDQORLGS-KADFLKIKNHVFPSPINWDDLYHKRLTPFPNPNVTGPDALKHF 322
DB 380 LLRNLLQVLDLTRKFGNLKGVNDIKNHKWFATTDWIAIYKVEAPFIPKCRPGDTSNF 439
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QY 323 DPEFTQEA 331
Db 440 D-EYEEAL 447

RESULT 12
US-10-497-767-4
; Sequence 4, Application US/10497767
; Publication No. US20050261836A1
; GENERAL INFORMATION:
; APPLICANT: VERTEX PHARMACEUTICALS INCORPORATED
; APPLICANT: MENG, WUYI
; APPLICANT: SWENSON, LOVORKA
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF MITOGEN-ACTIVATED PROTEIN
; TITLE OF INVENTION: KINASE-ACTIVATED PROTEIN KINASE 2 AND BINDING POCKETS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: VPI/01-13 PCT
; CURRENT APPLICATION NUMBER: US/10/497,767
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/337,513
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (10)
; OTHER INFORMATION: Variable amino acid
; NAME/KEY: MOD RES
; LOCATION: (338)
; OTHER INFORMATION: Variable amino acid
US-10-497-767-4

Query Match 34.9%; Score 681.5; DB 6; Length 350;
Best Local Similarity 42.5%; Pred. No. 4.2e-55;
Matches 133; Conservative 65; Mismatches 108; Indels 7; Gaps 5;

QY 24 PSANPAQDPDFLKVIGKNGYKVLAKRSDGAFYAVKLOKKSILKKKEQSHIMAE 83
Db 33 PAQN-TAHLDOPEIRIKTLGTGSGRVMVKHMETGNHYAMKILDKQKVKLQIEHTLNE 91

QY 84 RSVLLKNVRHPLVGLRYSGFTPEKLYFVLDYVNGGELPFHLQRRRFLPEPRARFYAAEV 143
Db 92 KRI-LQAVNPFVFLKLEFSKONSPLYMVMYVPGGEMFSLRRIGRFSEPHARFYAAQI 150

QY 144 ASAIGYLHSLNIYRDLKPENTLLDCQGHVLTDFGLCKEGVEPEDTTTFCGTPEYLAP 203
Db 151 VLTFEYLHSLDLIYRDLKPENTLLDQGGYIQVTDGFAK---RVKRTWTLCGTPEYLAP 207

QY 204 EVLRKEPYDRADVWMCGLGAVLYEMLHGLPPYSQDVSMYENILHQLPIPGGRTVAACD 263
Db 208 EILSGYKNAVDWALGVLIYEMAGYPPFPADQPIQYKIVSKVRFSPHFSDDLKD 267

QY 264 LQSLHDKQORQLGS-KADFLKIKNHVFFSPINWDDLYHKRLTPFPNPNVTGPADLKH 322
Db 268 LLRNLLQVLDLTKRFGNLKGVNDIKNKKWFATTDIAIYQKVEAFPIPKFGPGDTSNF 327

QY 323 DPEFTQEA 335
Db 328 D-DYEEERXVI 339

RESULT 13
US-11-132-142-9
; Sequence 9, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey

; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 9
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Leishmania sp.
US-11-132-142-9

Query Match 34.9%; Score 681.5; DB 7; Length 381;
Best Local Similarity 42.0%; Pred. No. 4.7e-55;
Matches 136; Conservative 62; Mismatches 113; Indels 13; Gaps 5;

QY 33 TDFDLKVIGKNGYKVLAKRSDGAFYAVKLOKKSILKKKEQSHIMAEKRSVLLKNVR 92
Db 70 SDFELKNTLGTGSGRVRIAHRKGTGEYYAIKRLKREIIMKQOQHVAQEGILME-LC 128

QY 93 HPFLVGLRYSFOTPEKLYFVLDYVNGGELPFHLQRRRFLPEPRARFYAAEASAILYLS 152
Db 129 HPFIVMMCSPODEKKVIFLLEFVNGGEMFTHLRTAGFPNDVAKFYHAEIVLAPEYLS 188

QY 153 LNIYRDLKPENTLLDCQGHVLTDFGLCKEGVEPEDTTTFCGTPEYLAPVLRKPYD 212
Db 189 LDVIYRDLKPENTLLDNKGHVKTDFGPAK---KVPDRTFTLCGTPEYLAPVIOKSGHG 245

QY 213 RAVDWMCGLGAVLYEMLHGLPPYSQDVSMYENILHQLPIPGGRTVAACDLQSLHDK 272
Db 246 KAVDWMTMGVLLYEFYAGYPPFYDTPPRIYEKILAGRLKFPNWFGRARDLVKGLLQTD 305

QY 273 QRORLGS-KADFLKIKNHVFRSPINWDDLYHKRLTPFPNPNVTGPADLKHDFPEFTQEA 331
Db 306 HTKRLGTUUGPADVKNHPYFHGANWDKLYARYYPAPIVRVKSPGDSNFE-KYPDSPV 364

QY 332 SKSIGCTPDTVASSSGASSAFLGF 355
Db 365 DR-----TPALTSAQAELKGF 381

RESULT 14
US-10-995-561-856
; Sequence 856, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 856
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-856

Query Match 34.9%; Score 681; DB 6; Length 705;
Best Local Similarity 39.8%; Pred. No. 1.2e-54;
Matches 139; Conservative 60; Mismatches 138; Indels 12; Gaps 3;

QY 9 PSPQPSRANGNINLGPSANPNNAQPTDFDLKVIGKNGYKVLAKRSDGAFYAVKLOK 68
Db 359 PEPENLKER-----PSLQIKLKIEDFILHKLMLKGSFGKVLAFBPKTKTNQFPAIKALKK 412
```

Qy	69	KSILKKQSQSHMAERSVULLKNVRHPLVLGLRYSFQTPPEKLVDPVLDYVNGBELFFHLQRE	128
Db	413	DVWLMDDDVECTWSEKRVLSLAWBHPFTLHMCTFTQKENLFFVMEYLLNGGDLIMVHIQSC	472
Qy	129	RRFLEPRARFYAAAVASAIYGLSHLSNIIYRDLKPENILLDCQHVVLTPDGLCKEGVEPE	188
Db	473	HKFDLSRATFYAAEIIQLGFLHSGIVYRDLKLNILLDKDGHIKIADFGCKENMLGD	532
Qy	189	DTTSTFCCTPEVLAPEVLRKEBYDRAVDWVCIGAVLYEMLHGLPPYSDVSQMYENILH	248
Db	533	AKTNTFCGTPDYIAPEILLGQKYNHSDVMWSFGVLLYEMLIQSPHPGQDEELFHSIRM	592
Qy	249	QPLQIPGGRTVAACDLLOSLLHKQORLGSKADFLIEIKNHVFSPINWDDLHYHKELTPP	308
Db	593	DNPFVPRWLEAKDOLLVKLVFREPEKRLGVRGD---IRQHLPLFREINWEELEKEIDPP	649
Qy	309	FNPVNTGPAIDLKHPDEFTQEAUVKSIGCTPDTVASSGASSAFLGFSY	357
Db	650	FRPKVKSFPDCSNFDKEPNLEKPLRSLFA---DRALINSMDONWFRNFSP	695

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RESULT 15
US-10-995-561-855
; Sequence 855, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 855
; LENGTH: 706
; TYPE: FRT
; ORGANISM: Homo sapiens
US-10-995-561-855

```

Query Match	34.9%;	Score 681;	DB 6;	Length 706;
Best Local Similarity	39.8%;	Pred. NO. 1.2e-54;		
Matches	139;	Conservative 60;	Mismatches 138;	Indels 12; Gaps 3
QY	9	PSRQPSRANGINLGPSANPAQPTDFDLKVIKGNKYKVLAKKSDGAPYAVKVLQK	58	
DB	360	PEPELNKER-----PSLQIKLKIEDFLHKMLGKSGFKVPLABFKTKNQFATKALK	413	
QY	69	KSILKKKEQSHIMAEERSVLLKNVRHPPVLGLRYSQTPTEKLYFVLVDYVNGSGELPFHLORE	128	
DB	414	DVVLMDDDVECTWVEKRVLSLAWHEPFLTHMFCFTQTKENLFFVMEYINGGDLMYTHIQSC	473	
QY	129	RRFLPEPRARFVAEASVAGYLHSUNIIYRDLKPNILLDCQGHVVLTFGLCKEGVPE	188	
DB	474	HKFDLSRATFYAABIILGLQFLSHKGIYVRDLKLDNILLDKDGHIKIADFGMCKENMLGD	533	
QY	189	DTTSTFCGTPYLAPEVLKPEYDRAVDWMCLGAVLYEMLHCLPFPYSQDYSQMYENILH	248	
DB	534	AKTNWFCGTPDYIAPEILLGQYHNHSDVMWSFGVLLYEMLIQCSFPHQDEBELFHSIRM	593	
QY	249	QPLQIPGGRTVAACDLQLSLHKDQORQLSGSKADPLEIKNHVFFSPINWDDLYHKRLTTP	308	
DB	594	DNPPYPRWLEKEANDLLVKLVFVPEKEKLVGRGD---IRQHPLEINWHEELERKEIDPP	650	
QY	309	FNEVNTGADLKHDPDPTQBAVSKSIGCTPDTVASSGSASAFIGFSY	357	
DB	651	FRPKVSPFDCSNFDKPFLENKPLRSFA---DRALINSDMONMFENFSF	596	

Search completed: January 27, 2006, 23:58:23  
Job time : 11.4635 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:12:00 ; Search time 10.8484 Seconds  
(without alignments)  
3254.993 Million cell updates/sec

Title: US-09-868-131a-1  
Perfect score: 1954  
Sequence: 1 MNSSPAGTSPQPSRANGNI.....ASSAFLGFSYAPEDDDILDC 367

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1413	72.3	431	2 A48094	serum and glucocor
2	983	50.3	422	2 T23334	hypothetical prote
3	886	45.3	479	1 A59380	protein kinase (EC
4	878.5	45.0	462	1 T17287	protein kinase (EC
5	878.5	45.0	480	1 S33364	protein kinase (EC
6	878.5	45.0	763	1 A40831	gag-akt polyprotai
7	877.5	44.9	454	1 JC4345	protein kinase (EC
8	876	44.8	481	1 A48288	protein kinase (EC
9	875.5	44.8	480	1 JC2437	protein kinase (EC
10	874.5	44.8	480	1 A39360	protein kinase (EC
11	866	44.3	680	2 S37955	protein kinase YPK
12	863.5	44.2	480	1 S62117	protein kinase (EC
13	862	44.1	481	1 JC2438	protein kinase (EC
14	852	43.6	479	2 A38578	protein kinase 2 (
15	846	43.3	677	2 JS0178	protein kinase YKR
16	835.5	42.8	611	1 A59888	protein kinase (EC
17	803	41.1	569	2 T50414	probable prolifera
18	791	40.5	586	2 A53758	protein kinase C (
19	791	40.5	587	2 A49509	protein kinase C (
20	789.5	40.4	646	2 T38171	probable serine/ch
21	789	40.4	481	2 JE0377	p70 S6 kinase (EC
22	788	40.3	546	1 T43233	protein kinase (EC
23	787	40.3	1016	1 A46079	protein kinase (EC
24	783.5	40.1	541	1 T43232	protein kinase (EC
25	778	39.8	525	1 A41687	ribosomal protein
26	778	39.8	525	1 S12906	probable ribosomal
27	776	39.7	634	1 B32392	protein kinase C (
28	769.5	39.4	696	2 S55694	protein kinase (EC
29	769	39.4	525	1 TVRTK6	ribosomal protein

RESULT 1

A48094

serum and glucocorticoid-regulated kinase - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 31-Dec-2004

C:Accession: A48094

R:Webster, M.K.; Goya, L.; Ge, Y.; Maiyar, A.C.; Firestone, G.L.

Mol. Cell. Biol. 13, 2031-2040, 1993

A:Title: Characterization of sgk, a novel member of the serine/threonine protein kinase

A:Reference number: A48094; MUID:93204949; PMID:8455596

A:Accession: A48094

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-431 <WEB>

A:Cross-references: UNIPARC:UPI000017AJE8

A:Experimental source: Con8.hd6 mammary epithelial tumor cells

A:Note: sequence extracted from NCBI backbone (NCBIN:127618, NCBIPI:127619)

C:Keywords: ATP

F:96-355/Domain: protein kinase homology <KIN>

F:104-112/Region: protein kinase ATP-binding motif

Query Match	72.3%	Score 1413;	DB 2;	Length 431;
Best Local Similarity	70.9%	Pred. No. 8.5e-60;		
Matches	261;	Conservative	56;	Mismatches 43; Indels 8; Gaps 3;
QY	1	MNSSPAGTSPQPSRANGNINIGPSANPNQAQPTDFDKVIGKNGYKVLAKRKSDGAF	60	
Db	69	MNANP--SPPSPSQ---QINLGPSNPHAKPSDFHLKVIKGSFGKVLARHKAEEAF	123	
QY	61	YAVKVLQKKSILKKKEQSHMAERSVLLKNVRHPPFLVGLRYSFQTPKLYFVLVYVNGGE	120	
Db	124	YAVKVLQKKAALKKKEKHMSERNVLLKNVRHPPFLVGLRYSFQADKLYFVLVYINGGE	183	
QY	121	LFPHLQRRRRFLPRARFYAAEVAISAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL	180	
Db	184	LFYHLQRECFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHVLTDFGL	243	
QY	181	CKGEVEPDDTSTFCGTPPEYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLPPFYSDVS	240	
Db	244	CKENIEHNGTSTFCGTPPEYLAPEVLRKEPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTA	303	
QY	241	QYENILHQPLOIIPGRTVAACDLQLSLHKDQORQLGSKADPLETKNHFVSPINWDDL	300	
Db	304	EMYDNLNKLPLQKNITNSARHLEGLLQKDKRTKRLGAKDDFMETKSHIFFSLINWDDL	363	
QY	301	YHKRLTPFPNPNVTGPADLKHPDPEFTQEAHSVKSIGCTPDTV---ASSSGASSAFLGFSY	357	
Db	364	INKKLTTPFPNPNVSGPSDLRHPDFTPEVPSSIGRSPDSILVTASVKAEAEALFGFSY	423	
QY	358	APEDDIL 365		
Db	424	APPMDSFL 431		

RESULT 2  
T26334  
hypothetical protein W10G6.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 05-Oct-2004  
C:Accession: T26334  
R:McMurray, A.  
submitted to the EMBL Data Library, October 1996  
A:Reference number: Z20201  
A:Accession: T26334  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-422 <WIL>  
A:Cross-references: UNIPROT:Q94365; UNIPARC:UPI000007852E; EMBL:Z81140; PIDN:CAB03485.1;  
A:Experimental source: clone W10G6  
C:Genetics:  
A:Gene: CBSP:W10G6.2  
A:Map position: X  
A:Introns: 14/3; 60/2; 88/2; 135/3; 179/3; 217/2; 290/3; 393/1  
Query Match 50.3%; Score 983; DB 2; Length 422;  
Best Local Similarity 54.7%; Pred. No. 1.2e-39;  
Matches 176; Conservative 57; Mismatches 89; Indels 0; Gaps 0;  
QY 13 PSRANGINILGPSANPNAQTPDFLKVITGKNGYKVLAKRSGAFYAVKVLQKKSIL 72  
DB 72 PDDDENNVDLGPSERKTATANDPYLTITGKSGFGRVYQVRHKETKKIYAMKILSKHEHR 131  
QY 73 KKKEQSHIAERSVLLKNVRHPLVGLRYSFQTPEKLYEVLVDVNGGELFFHLQERRRL 132  
DB 132 KQNEVHVWAEARNVLLNNFKHPLVSLHFSFQNKELYFVLHNGGELFFSHLQREKHPFS 191  
QY 133 EPRARFYAAEVAISAIGYLHSLMIYRDLPENILLDCQGHVVLTFGLCKEGVEPEDTTS 192  
DB 192 ESRSRFYAAEACALGYLHEKNIYRDLPENILLDDKGYLVLTDFGLCKEDMQGSKTTS 251  
QY 193 TFCGTPEYLAPEVLKPEYDRAVDWVWCLGAVLYEMHLGPPYSDVQSVQMYENILHQPLO 252  
DB 252 TFCGTPEYLAPEILKPKYDKTVDWVWCLGSLVYEMIFGLPPFYSDHNMEDYKIINQPLR 311  
QY 253 IFCGRTVAACDLQSLHKDQRLGSKADFLYELKHNHVFSPINWDDLHYHKBLTPFPNPN 312  
DB 312 LKHINISVPCSELITGLLQKDRSKRLHRNDFRDRHPFPLPVDWDLNRELKAPFIPK 371  
QY 313 VTGPAADLKHFDPEFTQEAIVSKS 334  
DB 372 VKNAMDTSNISKEFVEIQIDPS 393  
RESULT 3  
A59380  
protein kinase (EC 2.7.1.37) akt3 long splice form [similarity] - human  
N:Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific prote  
C:Species: Homo sapiens (man)  
C>Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C:Accession: A59380; A59379  
R:Brodebeck, D.; Cron, P.; Hemmings, B.A.  
J. Biol. Chem. 274, 9133-9136, 1999  
A:Title: A human protein kinase Bgamma with regulatory phosphorylation sites in the acti  
A:Reference number: A59380; MUID:99194749; PMID:10092583  
A:Accession: A59380  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-479 <BRO>  
A:Cross-references: UNIPROT:Q9Y243; UNIPARC:UPI00000335E8; GB:AAD29089; NID:94757579; PI  
R:Maure, S.; Haefner, B.; Wesselinck, J.J.; Hoefnagel, E.; Mortier, E.; Verhasselt, P.;  
Eur. J. Biochem. 265, 353-360, 1999  
A:Title: Molecular cloning, expression and characterization of the human serine/threonin  
A:Reference number: A59379; MUID:99421751; PMID:10491192  
A:Accession: A59379  
A>Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-479 <MAS>  
A:Cross-references: UNIPARC:UPI00000335E8; GB:CAB53537; NID:95804886; PIDN:CAB53537.1  
C:Genetics:  
A:Gene: GDB:AKT3; PKBG; PRKBG; RAC-gamma  
A:Cross-references: GDB:9954867  
A:Map position: 1q44-1q44  
C:Function:  
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonil  
A:Pathway: signal transduction pathways regulating various processes  
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen  
F:7-108/Domain: pleckstrin repeat homology <PLK>  
F:149-408/Domain: protein kinase homology <KIN>  
F:157-165/Region: protein kinase ATP-binding motif  
F:177/Active site: Lys #status predicted  
F:305/Binding site: phosphate (Thr) (covalent) #status predicted  
F:474/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predict  
Query Match 45.3%; Score 886; DB 1; Length 479;  
Best Local Similarity 48.4%; Pred. No. 4.7e-35;  
Matches 181; Conservative 55; Mismatches 100; Indels 38; Gaps 8;  
QY 1 MNSSPAGTPSPQPSRAN--GNINLGPSANPNAQPT--DFDLKLVIGKNGYKVLAKRKS 56  
DB 117 MNCSTP-----SOLDNIGBEEMDASTTHHKKRTMNDPFDYDLKLGKGTFGKVLIVREKA 169  
QY 57 DGAFYAVKVLQKKSILKKKEQSHIAERSVLLKNVRHPLVGLRYSFQTPEKLYFVLVDYV 116  
DB 170 SGKYYAMKILKEVIIIAKDEVAHTLTE--SRVLKNTRHFPFLTSLKYSFQTKDRLCFVMEV 228  
QY 117 NGGELFFHLQERRRLEPRARFYAAEVAISAIGYLHSLMIYRDLPENILLDCQGHVLT 176  
DB 229 NGGELFFHLRERVSERTRFYGAIEIVSALDYLSHGKIVYRDLEKLEMLDKDGHKIT 288  
QY 177 DFLCKEGVEPEDTTSFCGTPEYLAPEVLKPEYDRAVDWVWCLGAVLYEMHLGPPFYS 236  
DB 289 DFLCKEGITDAATWMTFCGTPEYLAPEVLDEDNDYGRAVDWVWGLGVYEMMCGRLPFFYN 348  
QY 237 QVDSQMYENILHQPLOIFGRTVAACDLQSLHLLHDKQRL--GSKADFLYELKHNHVFSP 295  
DB 349 QDHEKLFELLMEDIKFPRTLSSDAKSLSLGLLIKDPNKLGGGPDDAKEIMRHSFFSGV 408  
QY 236 NWDDLYHKRLTPFPNPNVTGPAADLKHFDPEFTQEAIVSKSIGCTPDTVASSSGASSAFGLF 355  
DB 409 NMQDYVDKLVPPPKPQVTSETDTRYFDEET---AQTTITTP----- 448  
QY 356 SVAPE--DDDILDC 367  
DB 449 ---PEKYDEDDGMD 459  
RESULT 4  
T17287  
protein kinase (EC 2.7.1.37) akt3 short splice form - human  
N:Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific prote  
C:Species: Homo sapiens (man)  
C>Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C:Accession: T17287  
R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, September 1999  
A:Reference number: Z18723  
A:Accession: T17287  
A:Molecule type: mRNA  
A:Residues: 1-462 <POU>  
A:Cross-references: UNIPARC:UPI000016AC77; EMBL:AL117525; GB:CAB55977; NID:95912043; PI  
A:Experimental source: adult testis; clone DKFZp434N0250  
R:Nakatani, K.; Thompson, D.A.; Barthel, A.; Sakaue, H.; Liu, W.; Weigel, R.J.; Roth, R.  
J. Biol. Chem. 274, 21528-21532, 1999  
A:Title: Up-regulation of Akt3 in estrogen receptor-deficient breast cancers and amdrpg  
A:Reference number: A64199; PMID:10419456  
A:Contents: annotation  
C:Comment: This protein is increased in estrogen receptor-negative breast cancers and ar



Db 405 SGSPSDNSGAEEVSL---AKPKHRTVMNEFEYLKLLGKGTGKVLVKEKATGRYYAM 461

QY 64 KVLQKSLKKKEQSHMAERSVLLKNVRHPPFLVGLRYSFOTPEKLYFVLVDYVNGGELEFF 123

Db 462 KILKKEVIVAKDVAHTLTENRV-LQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELEFF 520

QY 124 HLQRRRFLPEPRARFYAAAEVASAIGVLHS-LNIYRDLKPENILLDCQGHVLTDFGLCK 182

Db 521 HLSRERFVEDRARFYGAIVSALDYLHSEKNVVYRDLKLENMLDKDGHIKITDFGLCK 580

QY 183 EGVEPEDTTSTFCGTPPEYLAPEVLKPEYDRAVDMWCLGAVLYEMLHGLPPFYSDVSQM 242

Db 581 EGIKDGAATMKTFCGTPPEYLAPEVLEDNDYGRAVDMWGLGVWYVMWCGRLPFYNQDHEKL 640

QY 243 YENILHQIPIGGRVVAACDLLOSLHLKQDQORQL-GSKADFLFIKNHVFSPINWDDLY 301

Db 641 FELILMEEIRFRTLPEAKSLLSGLLKKDPTQRLGGSEDAAKEIMQHRFFANIVMQDYY 700

QY 302 HKRLTPFPNPNVTGPADLKHFDPEFTQEAUVSKSIGCTPDTVASSSGASSAFLGFSYAPED 361

Db 701 EKKLSPPFPQVITSETDTRYFDEEFTAQMIT-----ITP-----PDQ 737

QY 362 DDILDC 367

Db 738 DDSMEC 743

RESULT 7

JC4345

protein kinase (EC 2.7.1.37) akt3 [validated] - rat

N:Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific prote

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004

C:Accession: JC4345

R:Konishi, H.; Kuroda, S.; Tanaka, M.; Matsuzaki, H.; Ono, Y.; Kameyama, K.; Haga, T.; K

Biochem. Biophys. Res. Commun. 216, 526-534, 1995

A:Title: Molecular cloning and characterization of a new member of the RAC protein kinase

e C subspecies and beta gamma subunits of G proteins.

A:Reference number: JC4345; MUID:96063640; PMID:7488143

A:Accession: JC4345

A:Molecule type: mRNA

A:Residues: 1-454 <KON>

A:Cross-references: UNIPROT:Q63484; UNIPARC:UPI000012577F; DDBJ:D49836; NID:g1136777; PI

A:Experimental source: brain

C:Function:

A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin

A:Pathway: signal transduction pathways regulating various processes

C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat

C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k

F:4-105/Domain: pleckstrin repeat homology <PLK>

F:146-405/Domain: protein kinase homology <KIN>

F:154-162/Region: protein kinase ATP-binding motif

F:177/Active site: Lys #status predicted

Query Match 44.9%; Score 877.5; DB 1; Length 454;

Best Local Similarity 51.0%; Pred. No. 1.1e-34; Mismatches 99; Indels 13; Gaps 5;

Matches 172; Conservative 53

QY 1 MNSSPAGTSPSPSRAN--GNINLGPSANPNAQPT--DFDFLKVIKGNVGVLLAKRKS 56

Db 117 MNCSP-----SQIDNIGEEEMDASTTHHKRTMNDFDYLLKLGKGTFGKVLVREKA 169

QY 57 DGAFYAVKVLQKSLKKKEQSHMAERSVLLKNVRHPPFLVGLRYSFQTEKLYFVLVDYV 116

Db 170 SGKYYAMKILKKKEVITAKDEVAHTLTS-SRVLKNTRHPFLTSLKYSFQTKDRLCFVMEYV 228

QY 117 NGSELFFHLQRRRRFLPEPRARFYAAAEVASAIGVLHSNLIYRDLKPENILLDCQGHVLT 176

Db 229 NGSELFFHLSRRRVFSDRTFRFYGAIVSALDYLHSEKNVVYRDLKLENMLDKDGHIKIT 288

QY 177 DFGLCKEGVEPEDTTSTFCGTPPEYLAPEVLKPEYDRAVDMWCLGAVLYEMLHGLPPFFYS 236

Db 289 DFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDNDYGRAVDMWGLGVWYVMWCGRLPFYN 348

QY 237 QDVQSMYENILHQIPIGGRVVAACDLLOSLHLKQDQORQLGSKADF-LEIKNHVFFSP 295

Db 349 QDHEKLFELIMEDIKFRTLSSDAKSLLSGLLIDPNKRLGGGDDPKBEIMRHSFFSGV 408

QY 296 NWDDLYHKRLTPFPNPNVTGPADLKHFDPEFTQEAUVS 332

Db 409 NWQDYYDKLVPPFPQVITSETDTRYFDEEFTAQIT 445

RESULT 8

A46288

protein kinase (EC 2.7.1.37) akt2 - human

N:Alternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific protei

C:Species: Homo sapiens (man)

C:Date: 22-Sep-1993 #sequence\_revision 12-May-1994 #text\_change 16-Aug-2004

C:Accession: A46288

R:Cheng, J.O.; Godwin, A.K.; Bellacosa, A.; Taguchi, T.; Franke, T.F.; Hamilton, T.C.; J

Proc. Natl. Acad. Sci. U.S.A. 89, 9267-9271, 1992

A:Title: AKT2, a putative oncogene encoding a member of a subfamily of protein-serine/th

A:Reference number: A46288; MUID:93028445; PMID:1409633

A:Accession: A46288

A:Molecule type: mRNA

A:Residues: 1-481 <CHE>

A:Cross-references: UNIPROT:P31751; UNIPARC:UPI000049EDB; GB:M95936; NID:g178325; PIDN

A>Note: sequence extracted from NCBI backbone (NCBIP:115859)

C:Comment: This protein is amplified in some pancreatic, ovarian, and other carcinomas.

C:Genetics:

A:Gene: GDB:AKT2

A:Cross-references: GDB:135660; OMIM:164731

A:Map position: 19q13.2-19q13.2

C:Function:

A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin

A:Pathway: signal transduction pathways regulating various processes

C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat

C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k

F:4-106/Domain: pleckstrin repeat homology <PLK>

F:150-409/Domain: protein kinase homology <KIN>

F:158-166/Region: protein kinase ATP-binding motif

F:181/Active site: Lys #status predicted

Query Match 44.8%; Score 876; DB 1; Length 481;

Best Local Similarity 48.9%; Pred. No. 1.4e-34;

Matches 174; Conservative 57; Mismatches 113; Indels 12; Gaps 5;

QY 10 SPQSPRANGINLGPS-ANPNAQPTDFDFLKVIKGNVGVLLAKRKS DGAFYAVKVLQK 68

Db 126 SPDSSTTEMEVAVSKARAKVTMNDFDYLLKLGKGTGKVLVREKATGRYYAMKILRK 185

QY 69 KSILKKKQSHMAERSVLLKNVRHPPFLVGLRYSFQTEKLYFVLVDYVNGGELFFHLQRE 128

Db 186 EVIIAKDEVAHTVTS-SRVLQNTRHPPFLTALKYAFQTHDRLCFVMEYANGGSLFFHLSRE 244

QY 129 RFLPEPRARFYAAAEVASAIGVLHSNLIYRDLKPENILLDCQGHVLTDFGLCKEGVEPE 188

Db 245 RVFTTEARFYGAIVSALDYLHSEKNVVYRDLKLENMLDKDGHIKITDFGLCKEGISDG 304

QY 189 DTTSTFCGTPPEYLAPEVLKPEYDRAVDMWCLGAVLYEMLHGLPPFYSDVSQMYENILH 248

Db 305 ATMTFCGTPPEYLAPEVLEDNDYGRAVDMWGLGVWYVMWCGRLPFYNQDHERLPELILM 364

QY 249 QPLQIPGGRVVAACDLLOSLHLKQDQORQL-GSKADFLFIKNHVFSPINWDDLYHKRLTP 307

Db 365 EEIRFRTLSPKASLLAGLKKDKPQRLGGGSDAKBEVMEHRFFLSINWQDVQVKLLP 424

QY 308 PNPNTGPADLKHFDPEFTQEAUVSKSIGCTPDTVASSSG-----ASSAFLGFSYA 358

Db 425 FPKPQVTVSEVTRYFDDEFT-----AQSTITTPDRYDSLGLLELDQRTHPQFSYS 476

RESULT 9

JC2437

protein kinase (EC 2.7.1.37) akt1 [validated] - rat



N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific protein kinase  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C;Accession: J02437  
R;Konishi, H.; Shinomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.  
Biochem. Biophys. Res. Commun. 205, 817-825, 1994  
A;Title: Molecular cloning of rat RAC protein kinase alpha and beta and their association  
A;Reference number: J02437; MUID:95091823; PMID:7999118  
A;Accession: J02437  
A;Molecule type: mRNA  
A;Residues: 1-480 <KON>  
A;Cross-references: UNIPROT:P47196; UNIPARC:UPI000012E044; DDBJ:D30040; NID:g485402; PDB:1Y88  
A;Experimental source: testis  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate  
A;Pathway: signal transduction pathways regulating various processes  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein kinase  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene  
F;4-106/Domain: pleckstrin repeat homology <PLK>  
F;148-408/Domain: protein kinase homology <KIN>  
F;156-164/Region: protein kinase ATP-binding motif  
F;179/Active site: Lys #status predicted  
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein kinase)  
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted  
Query Match 44.8%; Score 875.5; DB 1; Length 480;  
Best Local Similarity 47.8%; Pred. No. 1.5e-34;  
Matches 175; Conservative 57; Mismatches 103; Indels 31; Gaps 7;  
QY 6 AGTPSPQSRANGNINLGSANPNNAOPT--DFDFLKVIKGVNGYKVLAKRSDGAFYAV 63  
Db 122 SGSPSDNSGAEMEVAL---AKPKHRVTWNEPEYKLLGKGTGKVLKKEATGRYAM 178  
QY 64 KVLQKSKILKKKEQSHIMAEVSLLKKNVHPELVGLRYSFQPEKLYFVLDYNGGELEFP 123  
Db 179 KILKKEIVAKDEVAHTLTENRV-LQNSRHPFLTALKYSFQTHRLCFVMEYANGGELFP 237  
QY 124 HLQERRRFLPRARFYAAEVAASAIGLYHS-LNIIYRDLKPNILLDCQGHVLTDFGLCK 182  
Db 238 HLSRERVFSDRARFYGAIVSALDYLHSEKNVYRDLKLENMLDKDGHKITDFGLCK 297  
QY 183 EGVEPEDTTSTFCGTPPEYLAPEVLRKEPYDRAVDWMCGLGAVLYEMLHGLPFYSDVQSM 242  
Db 298 EGKKGATMKTFCGTPPEYLAPEVLENDYGRAVDWMCGLGAVLYEMLHGLPFYSDVQSM 357  
QY 243 YENILHQLPIQGRVTVACDILQLSLHKKQORL-GSKADFLKIKNVHFFSPINWDDLY 301  
Db 358 FELILMEIRFRTLGPPEAKSLSLGKLLKDDPTQRLGGSGEDAKETMQRFFANIVMQDYV 417  
QY 302 HKRLTPFPNVTGPDADLKHDFPEFTQEAIVSKSIGCTPTDVASSSGASSAFLGFSVAPED 361  
Db 418 EKLSPPFPQVTSFDTYFDEEFTAQMIT----ITP-----PDQ 454  
QY 362 DDILDC 367  
Db 455 DDSMEC 460  
RESULT 10  
A39360  
N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific protein kinase  
C;Species: Homo sapiens (man)  
C;Date: 20-Mar-1992 #sequence\_revision 12-May-1994 #text\_change 16-Aug-2004  
A;Accession: A39360; S36389; S18000; S20836  
R;Jones, P.F.; Jakubowicz, T.; Pitosoi, F.J.; Maurer, F.; Hemmings, B.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 4171-4175, 1991  
A;Title: Molecular cloning and identification of a serine/threonine protein kinase of the  
A;Reference number: A39360; MUID:91239529; PMID:1851997  
A;Accession: A39360  
A;Molecule type: mRNA  
A;Residues: 1-480 <JON>  
A;Cross-references: UNIPROT:P31749; UNIPARC:UPI000002E75B; GB:M63167; NID:g190827; PIDN:

R;Coffer, P.J.; Woodgett, J.R.  
Eur. J. Biochem. 205, 1217, 1992  
A;Reference number: S24423; MUID:92249329; PMID:1533586  
A;Contents: erratum  
A;Accession: S36389  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 63-172, 'A', 175-201, 'Q', 203-211, 'R', 213-245, 'A', 247-408, 'T', 410-475, 'P', 477,  
A;Cross-references: UNIPARC:UPI000016AEB1; EMBL:X61037; NID:g35480; PIDN:CAA43372.1; P1;  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1991  
A;Note: this a revision to the sequence from reference S17999  
R;Coffer, P.J.; Woodgett, J.R.  
Eur. J. Biochem. 201, 475-481, 1991  
A;Title: Molecular cloning and characterisation of a novel putative protein-serine kinase  
A;Reference number: S17999; MUID:92037600; PMID:1718748  
A;Accession: S18000  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 63-70, 'TPSSSAACSGPLSSNAPSMWRLRSGVDNRHPCGRRPQ', 'EAGGGDGLPVGLTORQLRGRDRDGG  
A;Cross-references: UNIPARC:UPI00001725AB; EMBL:X61037  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1991  
A;Note: this sequence has been revised in reference S24423  
R;Coffer, P.  
submitted to the EMBL Data Library, July 1991  
A;Reference number: S20836  
A;Accession: S20836  
A;Molecule type: mRNA  
A;Residues: 63-70, 'TPSSSAACSGPLSSNAPSMWRLRSGVDNRHPCGRRPQ', 'EAGGGDGLPVGLTORQLRGRDRDGG  
A;Cross-references: UNIPARC:UPI00001725AC; EMBL:X61037  
A;Note: this sequence has been revised in reference S24423  
R;Aleski, D.R.; Andjelkovic, M.; Caudwell, B.; Cron, P.; Morrice, N.; Cohen, P.; Hemmin  
EMBO J. 15, 6541-6551, 1996  
A;Title: Mechanism of activation of protein kinase B by insulin and IGF-1.  
A;Reference number: A64193; MUID:97133284; PMID:8978681  
A;Contents: annotation; phosphorylation sites  
R;Toker, A.; Newton, A.C.  
J. Biol. Chem. 275, 8271-8274, 2000  
A;Title: Akt/protein kinase B is regulated by autophosphorylation at the hypothetical P  
A;Reference number: A64193; MUID:20187529; PMID:10722653  
A;Contents: annotation; autophosphorylation site  
C;Comment: Akt1 is ubiquitous as an inactive multimeric complex. It binds phosphatidyl-  
nt protein kinase 1 complex. Akt1 can then autophosphorylate and become fully active.  
C;Genetics:  
A;Gene: GDB:AKT1; RAC: PKB  
A;Cross-references: GDB:118989; OMIM:164730  
A;Map position: 14q32.32-14q32.32  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-  
e production  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen  
F;4-106/Domain: pleckstrin repeat homology <PLK>  
F;148-408/Domain: protein kinase homology <KIN>  
F;156-164/Region: protein kinase ATP-binding motif  
F;179/Active site: Lys #status predicted  
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein kinase)  
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status experim  
Query Match 44.8%; Score 874.5; DB 1; Length 480;  
Best Local Similarity 47.5%; Pred. No. 1.6e-34;  
Matches 174; Conservative 59; Mismatches 102; Indels 31; Gaps 7;  
QY 6 AGTPSPQSRANGNINLGSANPNNAOPT--DFDFLKVIKGVNGYKVLAKRSDGAFYAV 63  
Db 122 SGSPSDNSGAEMEVSLL---AKPKHRVTWNEPEYKLLGKGTGKVLKKEATGRYAM 178  
QY 64 KVLQKSKILKKKEQSHIMAEVSLLKKNVHPELVGLRYSFQPEKLYFVLDYNGGELEFP 123  
Db 179 KILKKEIVAKDEVAHTLTENRV-LQNSRHPFLTALKYSFQTHRLCFVMEYANGGELFP 237  
QY 124 HLQERRRFLPRARFYAAEVAASAIGLYHS-LNIIYRDLKPNILLDCQGHVLTDFGLCK 182

Db 238 HLSRERFVSDRARFYGAIEVSALDYHSEKNVYVRDLKLENMLDKDGHKIKITDGLCK 297  
QY 183 EGVEPEDTSTTCGTPPYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLUPPYQSQVSQM 242  
Db 298 EGIKDGAATWKTCGTPPYLAPEVLENDYGRAVDMWGLGVWVYEMWCGRLPFYNQDHEKL 357  
QY 243 YENILHQPLOIGCGRTVAACDLLOSLLLHKDQORLG--GSKADFLKIKHVFSPINWDDLY 301  
Db 358 FELILMEEIRFRTLGPKEAKSLSLGLLKKDPKORLGGGSEDAKEIMQHRFFAGIVQHVY 417  
QY 302 HKRLTPFPNVTGTPADLKHFOPEFTQEAUVSKSIGCTPDTVASSSGASSAFLGFSVAPED 361  
Db 418 EKKLSPPFKPQVTSIDTRYFDEEFTAQMIT----ITP-----PDQ 454  
QY 362 DILDC 367  
Db 455 DDSMEC 460

RESULT 11  
S37955  
protein kinase YPK1 (EC 2.7.1.1) - yeast (Saccharomyces cerevisiae)  
N:Alternate names: protein YKL126w  
C:Species: Saccharomyces cerevisiae  
C:Date: 03-May-1994 #sequence revision 03-May-1994 #text\_change 05-Oct-2004  
C:Accession: S37955; A31248; S30903  
R:Ramazani Rad, M.; Xu, G.; Kirchrath, L.; Fritz, C.; Keuchel, H.; Hollenberg, C.P.  
submitted to the Protein Sequence Database, March 1994  
A:Reference number: S37953  
A:Accession: S37955  
A:Molecule type: DNA  
A:Residues: 1-680 <RAM>  
A:Cross-references: UNIPROT:P12698; UNIPARC:UPI000013BDPE; EMBL:Z28126; PID  
A:Experimental source: strain S288C  
R:Maurer, R.A.  
DNA 7, 469-474, 1988  
A:Title: Isolation of a yeast protein kinase gene by screening with a mammalian protein  
A:Reference number: A31248; MUID:89090805; PMID:2850145  
A:Accession: A31248  
A:Molecule type: DNA  
A:Residues: 1-200, 'L', 202-552, 'I', 554-680 <MAU>  
A:Cross-references: UNIPARC:UPI0000168D89; EMBL:M21307; NID:G172180; PIDN:AAA34880.1; PI  
R:Chen, P.; Lee, K.S.; Levin, D.E.  
Mol. Gen. Genet. 236, 443-447, 1993  
A:Title: A pair of putative protein kinase genes (YPK1 and YPK2) is required for cell gr  
A:Reference number: S30903; MUID:93173125; PMID:8437590  
A:Accession: S30903  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-200, 'L', 202-226, 'T', 228-552, 'I', 554-680 <CHE>  
A:Cross-references: UNIPARC:UPI000017A451  
C:Genetics:  
A:Gene: SGD:YPK1  
A:Cross-references: SGD:S0001609; MIPS:YKL126w  
A:Map position: 11L  
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase  
F:345-602/Domain: protein kinase homology <KIN>  
F:353-361/Region: protein kinase ATP-binding motif  
F:470/Active site: Asp #status predicted

Query Match 44.3%; Score 866; DB 2; Length 680;  
Best Local Similarity 51.5%; Pred. No. 5.5e-34;  
Matches 177; Conservative 53; Mismatches 106; Indels 8; Gaps 5;  
QY 15 RANGINLGPSPANPNAQPTDFDLKVIKGNKGVLLAKRKSDBGAPYAVKVLQKKSILKK 74  
Db 327 KINISIDYPSRNKPLSIDDFLLKVIKGSFGKVMQVRKKDTQKYALKARKSYIVSK 386  
QY 75 EQSHIMAERSVLLKNVRHFFLVGLRYSFQTPKLYFVLDDYVNGGELFFHLQRRFLRP 134  
Db 387 SEVTHTLAERTVLAR-VDCPFIVPLKFSFQSPKLYFVLAFLNGGELFFHLQKGRFDLS 445  
QY 135 RARFYAAEVAISAIGYLHSLNIYRDLKPNILLDCQGHVVLDFGLCKGVEPEDTTSTF 194

Db 446 RARFYATALLCALDNLHKLDDVYRDLKPEINILLDYQGHIALCDFGLCKLNMKDDKTDTF 505  
QY 195 CQTPEYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLPPFYQSQVSQMYENILHQPLOIP 254  
Db 506 CQTPEYLAPELLGLGYTKAVDWMWTLGVLLYEMLTGLPPYDDEVPKMYKKILQBELVFP 565  
QY 255 GGRVVAACDLLOSLLLHKDQORLG--SKADFLKIKHVFSPINWDDLYHKRLTPFPNPNV 313  
Db 566 DQFDRADKDLGLSLRDPTRRLGYNGAD--EIRNHPFSQLSWKRLLMKGYIPPYKPAV 623  
QY 314 TGPADLKHFDPEFTQEAUVSKSIGCTPDTVASSSGASSAFLGPSY 357  
Db 624 SNSMDTSNFDEFTRE---KPIDSVVDEYLSSES-VQKQFGGWTY 663

RESULT 12  
S62117  
protein kinase (EC 2.7.1.37) akt1 [similarity] - bovine  
N:Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prot  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 16-Aug-2004  
C:Accession: S62117; S24423; S17999; S15714; S36388  
R:Coffer, P.J.; Woodgett, J.R.  
submitted to the EMBL Data Library, December 1991  
A:Reference number: S62117  
A:Accession: S62117  
A:Molecule type: mRNA  
A:Residues: 1-480 <COF>  
A:Cross-references: UNIPROT:Q01314; UNIPARC:UPI000012E042; EMBL:X61036; NID:G630; PIDN:  
A:Note: this is a revision to the sequence from reference S17999  
R:Coffer, P.J.; Woodgett, J.R.  
Eur. J. Biochem. 205, 1217, 1992  
A:Reference number: S24423; MUID:92249329; PMID:1533586  
A:Contents: exratum  
A:Accession: S24423  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 70-78, 'N', 80-145 <COM>  
A:Cross-references: UNIPARC:UPI00001725AD; EMBL:X61036  
A:Note: this is a revision to the sequence from reference S17999  
R:Coffer, P.J.; Woodgett, J.R.  
Eur. J. Biochem. 201, 475-481, 1991  
A:Title: Molecular cloning and characterisation of a novel putative protein-serine kinas  
A:Reference number: S17999; MUID:92037600; PMID:1718748  
A:Accession: S17999  
A:Molecule type: mRNA  
A:Residues: 1-70, 'TPSSSAACSGPRSSASRTWRRPRSGVDHRRPDGRRRAQAGGGDGLPVGLTRRELGRDGGVAGQ  
A:Cross-references: UNIPARC:UPI00001725AE; EMBL:X61036  
A:Note: this sequence has been revised in references S62117 and S24423  
C:Function:  
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A:Pathway: signal transduction pathways regulating various processes  
A:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen  
F:4-106/Domain: pleckstrin repeat homology <PK>  
F:148-408/Domain: protein kinase homology <KIN>  
F:156-164/Region: protein kinase ATP-binding motif  
F:179/Active site: Lys #status predicted  
F:308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki  
F:473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predict

Query Match 44.2%; Score 863.5; DB 1; Length 480;  
Best Local Similarity 48.2%; Pred. No. 5.4e-34;  
Matches 174; Conservative 60; Mismatches 112; Indels 15; Gaps 7;  
QY 6 ACTPSPQSRANGINLGPSPANPNAQPT--DFDLKVIKGNKGVLLAKRKSDBGAFYAV 63  
Db 122 SGSPENSGAEMEVSLS---AKPKHRVTMNEFEYKLLKGGTFGKLVLYKKAATAAYAM 178  
QY 64 KVLQKKSILKKKQSHIMAERSVLLKNVRHPPVLGLRYSFQTPKLYFVLDDYVNGGELFF 123  
Db 179 KILKEVIVAKDEVAHTLTENRV-LQNSRHSLTALKYSFQTHDRLCFVMEVANGELFF 237





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:08:15 ; Search time 59.7818 Seconds  
(without alignments)  
4331.236 Million cell updates/sec

Title: US-09-868-131A-1

Perfect score: 1954

Sequence: 1 MNSPPAGTSPQPSRANGNI.....ASSAFLGFSYAPDDDDILDC 367

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1954	100.0	427	1	SGK2 HUMAN
2	1954	100.0	427	2	Q5H8Y6 HUMAN
3	1947	99.6	367	2	Q5T2R3_HUMAN
4	1943	99.4	393	2	Q52PK5_HUMAN
5	1938.5	99.2	366	2	Q5H8Z1_HUMAN
6	1932	98.9	367	2	Q5RDZ9_PONPY
7	1848	94.6	367	1	SGK2 MOUSE
8	1540	78.8	302	1	SGK2 RAT
9	1497	76.6	285	2	Q5H8Y4_HUMAN
10	1450.5	74.2	350	2	Q4SY9Y_TETNG
11	1436	73.5	433	2	Q7ZTW4_BRARE
12	1432	73.3	431	2	Q5Q0U5_FUNHE
13	1419	72.6	432	2	Q6ULI9_CHICK
14	1418	72.6	434	2	Q93524_XENLA
15	1416	72.5	431	1	SGK1 RABIT
16	1415	72.4	434	2	Q6GFN6_XENLA
17	1413	72.3	431	2	Q68G05_RAT
18	1411	72.2	418	2	Q5BKK4_XENTR
19	1411	72.2	421	2	Q5TCN4_HUMAN
20	1411	72.2	431	2	Q5TCN3_HUMAN
21	1411	72.2	445	2	Q5TCN2_HUMAN
22	1411	72.2	526	2	Q5VY65_HUMAN
23	1409	72.1	431	1	SGK1 MOUSE
24	1409	72.1	519	2	Q6NS85_MOUSE
25	1407	72.0	431	1	SGK1 HUMAN
26	1406	72.0	431	2	Q4R633_MACFA
27	1404.5	71.9	430	1	SGK3 RAT
28	1394.5	71.4	490	2	Q4RR91_TETNG
29	1394	71.3	434	2	Q6GLY8_XENLA
30	1392	71.2	594	2	Q73927_SQUAC
31	1390.5	71.2	433	2	Q73926_squalus aca

32	1331.5	68.1	429	2	Q8VEK1_MOUSE
33	1331.5	68.1	496	1	SGK3_MOUSE
34	1323.5	67.7	429	2	Q6FHV7_HUMAN
35	1323.5	67.7	496	1	SGK3_HUMAN
36	1323.5	67.7	496	2	Q53EW6_HUMAN
37	1323.5	67.7	496	2	Q5R7A7_PONPY
38	1320.5	67.6	518	2	Q4SFC2_TETNG
39	1318.5	67.5	496	2	Q5H9Q5_HUMAN
40	1314.5	67.3	490	2	Q5ZJQ4_CHICK
41	1213	62.1	1114	2	Q4SYX7_TETNG
42	1063	54.4	316	2	Q4RI65_TETNG
43	1035	53.0	1550	2	Q4SYI0_TETNG
44	1025.5	52.5	198	2	Q5H8Y5_HUMAN
45	984	50.4	423	2	Q613H2_CAEBR

#### ALIGNMENTS

RESULT 1	SGK2_HUMAN	STANDARD;	PRT;	427 AA.
ID	SGK2_HUMAN	STANDARD;	PRT;	427 AA.
AC	Q9HBY8; Q9UKG6;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Serine/threonine-protein kinase Sgk2 (EC 2.7.1.37)			
DE	(Serum/glucocorticoid regulated kinase 2).			
GN	Name=SGK2;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2), PHOSPHORYLATION SITE THR-253, AND MUTAGENESIS OF SER-416.			
RX	MEDLINE=20018032; PubMed=10548550; DOI=10.1042/0264-6021:3440189;			
RA	Kobayashi T., Deak M., Morrice N., Cohen P.,			
RT	"Characterization of the structure and regulation of two novel isoforms of serum- and glucocorticoid-induced protein kinase."			
RL	Biochem. J. 344:189-197(1999).			
RN	[2]			
RN	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] (ISOFORM 1).			
RX	MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;			
RA	Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,			
RA	Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,			
RA	Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,			
RA	Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,			
RA	Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,			
RA	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,			
RA	Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,			
RA	Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,			
RA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,			
RA	Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,			
RA	Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,			
RA	Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,			
RA	Kay M.P., Kimberling A.M., King A., Knights A., Laird G.K., Lawlor S.,			
RA	Lehvaeslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,			
RA	Marsh V.L., Martin S.L., McConnachie L.J., McKay K., McKerray A.A.,			
RA	Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,			
RA	Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,			
RA	Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,			
RA	Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,			
RA	Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,			
RA	Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,			
RA	Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,			
RA	Whithead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,			
RA	Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,			
RA	Rogers J.;			
RL	"The DNA sequence and comparative analysis of human chromosome 20.";			
RL	Nature 414:865-871(2001).			
RN	[3]			

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
RC TISSUE=Brain, and Colon;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Heiton E., Kretzman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
RT "generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [4]  
RP FUNCTION  
RX MEDLINE=22284526; PubMed=12397388; DOI=10.1007/s00424-002-0873-2;  
RA Gamber N., Fillon S., Feng Y., Friedrich B., Lang P.A., Henke G.,  
RA Huber S.M., Kobayashi T., Cohen P., Lang F.;  
RT "K(+) channel activation by all three isoforms of serum- and  
RT glucocorticoid-dependent protein kinase SGK.";  
RL Pflugers Arch. 445:60-66(2002)  
CC -!- FUNCTION: Involved in the activation of potassium channels.  
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=2; Synonyms=beta;  
CC IsoId=Q9HBY8-1; Sequence=displayed;  
CC Name=1; Synonyms=alpha;  
CC IsoId=Q9HBY8-2; Sequence=VSP\_004932;  
CC -!- TISSUE SPECIFICITY: Highly expressed in liver, kidney and  
CC pancreas, and at lower levels in brain.  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
CC -!- CAUTION: Not regulated by serum or glucocorticoids.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
DR EMBL; AF186470; AAG17012.1; -; mRNA.  
DR EMBL; AF169034; AAF12757.2; -; mRNA.  
DR EMBL; Z98752; CAC18509.1; -; Genomic DNA.  
DR EMBL; BC014037; AAH14037.2; ALT SEQ; mRNA.  
DR EMBL; BC065511; AAH65511.1; -; mRNA.  
DR HSSP; P31751; IGZK.  
DR Ensembl; ENSG00000101049; Homo sapiens.  
DR HGNC; HGNC:13900; SGK2.  
DR MIM; 607589; -.  
DR GO; GO:0015459; F:potassium channel regulator activity; IDA.  
DR GO; GO:0004682; F:protein kinase CK2 activity; NAS.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.  
DR GO; GO:0017080; F:sodium channel regulator activity; NAS.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.  
DR GO; GO:0007243; P:protein kinase cascade; TAS.  
DR GO; GO:0006979; P:response to oxidative stress; TAS.  
DR InterPro; IPR00961; Pkinase\_C.  
DR InterPro; IPR008271; Ser\_thr\_pkin.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR Pfam; PF00069; Pkinase; 1.  
DR Pfam; PF00433; Pkinase C; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.

DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TKC; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW Alternative splicing; ATP-binding; Kinase; Nucleotide-binding;  
KW Phosphorylation; Serine/threonine-protein kinase; Transferase.  
FT DOMAIN 95 352 Protein kinase.  
FT NP\_BIND 101 109 ATP (by similarity).  
FT MOTIF 128 138 Nuclear localization signal (By  
FT similarity).  
FT ACT\_SITE 219 219 Proton acceptor (By similarity).  
FT BINDING 124 124 ATP (By similarity).  
FT MOD\_RES 253 253 Phosphothreonine (by PDPK1).  
FT VARSPPLIC 1 60 Missing (in isoform 1).  
FT FTID=VSP\_004932.  
FT MUTAGEN 416 416 S->D: Increased activation.  
FT SEQUENCE 427 AA; 47604 MW; D8F0FA6DF54B1370 CRC64;  
Query Match 100.0%; Score 1954; DB 1; Length 427;  
Best Local Similarity 100.0%; Pred. No. 4.4e-125;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNSSPAGTSPQPSRANGNINIGPSANPNAQPTDFELKVIKGNVGVLLAKRKSDGAF 60  
DB 61 MNSSPAGTSPQPSRANGNINIGPSANPNAQPTDFELKVIKGNVGVLLAKRKSDGAF 120  
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGE 120  
DB 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGE 180  
QY 121 LFFHLQRRERFLEPRARFYAAEVAISAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180  
DB 181 LFFHLQRRERFLEPRARFYAAEVAISAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 240  
QY 181 CKEGVEPEDTSTFCGTPPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYSDVYS 240  
DB 241 CKEGVEPEDTSTFCGTPPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYSDVYS 300  
QY 241 QMYENILHQPLQIPGGRVTVACDLQLSLHKDQRLGSKADFLKKNHVFSPINWDDL 300  
DB 301 QMYENILHQPLQIPGGRVTVACDLQLSLHKDQRLGSKADFLKKNHVFSPINWDDL 360  
QY 301 YHKRLTPFPNPVNTGPADLKHPDPEFTQEAHSVSKSGCTPDTVASSSGASSAFGLGFSYAPE 360  
DB 361 YHKRLTPFPNPVNTGPADLKHPDPEFTQEAHSVSKSGCTPDTVASSSGASSAFGLGFSYAPE 420  
QY 361 DDDILDC 367  
DB 421 DDDILDC 427  
RESULT 2  
QSH8Y6 HUMAN  
ID QSH8Y6\_HUMAN PRELIMINARY; PRT; 427 AA.  
AC QSH8Y6;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE OTTHUMP00000031703.  
GN Name=SGK2; ORFNames=RP1-138B7.2-002;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1] NUCLEOTIDE SEQUENCE.  
RP Beasley H.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z98752; CAI42312.1; -; Genomic DNA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR	GO: 0004674; F:protein serine/threonine kinase activity; IEA.
DR	GO: 0004713; F:protein-tyrosine kinase activity; IEA.
DR	GO: 0006468; P:protein amino acid phosphorylation; IEA.
DR	InterPro: IPR000961; Pkinase C.
DR	InterPro: IPR000719; Prot_kinase.
DR	InterPro: IPR008271; Ser_Thr_pkin_AS.
DR	InterPro: IPR002290; Ser_Thr_pkinase.
DR	InterPro: IPR001245; Tyr_pkinase.
DR	Pfam: PF00069; Pkinase; 1.
DR	Pfam: PF00433; Pkinase C; 1.
DR	ProDom: PD000001; Prot_kinase; 1.
DR	SMART: SM00133; S_TK_X; 1.
DR	SMART: SM00220; S_TKC; 1.
DR	SMART: SM00219; TyrK; 1.
DR	PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR	PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW	Kinase.
SQ	SEQUENCE 367 AA; 41233 MW; C91DD892C4C2486B CRC64;
Query Match 99.6%; Score 1947; DB 2; Length 367;	
Best Local Similarity 99.7%; Pred. No. 1.1e-124;	
Matches 366; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 MNSSPAGTSPQSPSRANGNINLGPSANPNNAQPTDFDKVIGKNGYGVLLAKRKSQDAF 60
Db	1 MNSSPAGTSPQSPSRANGNINLGPSANPNNAQPTDFDKVIGKNGYGVLLAKRKSQDAF 60
Qy	61 YAVKVLQKSLILKKQESHIMWERSVLLIKNVRHPPFLGLRYSFQTPKLYPVLVDVNGGE 120
Db	61 YAVKVLQKSLILKKQESHIMWERSVLLIKNVRHPPFLGLRYSFQTPKLYPVLVDVNGGE 120
Qy	121 LFFHLQRRERFLPRARFYAAEVASAIQYLHLSNIIYRDLKPNELLDCQGHVVLTDFFGL 180
Db	121 LFFHLQRRERFLPRARFYAAEVASAIQYLHLSNIIYRDLKPNELLDCQGHVVLTDFFGL 180
Qy	181 CKGVEPEDTTSFCGTPEYLAPEVLRKBPYDRAVDWMCIGAVLYEMHLGLPPFYSQDVS 240
Db	181 CKGVEPEDTTSFCGTPEYLAPEVLRKBPYDRAVDWMCIGAVLYEMHLGLPPFYSQDVS 240
Qy	241 QMYENILHQLPQIPGGRTVAACDLQSLHLHKDQORLGSKADFLIEIKNHVFFSPINVDDL 300
Db	241 QMYENILHQLPQIPGGRTVAACDLQSLHLHKDQORLGSKADFLIEIKNHVFFSPINVDDL 300
Qy	301 YHKRLTPFPNPVNTGADLKHDFPEFTQEAVSKSIGCTPDTVAASSGASSAFLGFSYAPE 360
Db	301 YHKRLTPFPNPVNTGADLKHDFPEFTQEAVSKSIGCTPDTVAASSGASSAFLGFSYAPE 360
Qy	361 DDILDC 367
Db	361 DDILDC 367

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RESULT 4
Q52PK5_HUMAN
ID      Q52PK5_HUMAN PRELIMINARY;      PRT;   393 AA.
AC      Q52PK5;
DT      13-SEP-2005 (TrEMBLrel. 31, Created)
DT      13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT      13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE      Serum/glucocorticoid regulated kinase 2.
GN      Name=SGK2;
OS      Homo sapiens (human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC      Homo.
OC      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RA      Li H., Nong W., Zhou G., Ke R., Shen C., Zhong Z., Liang M.,
RA      Xiao W., Lin L., Yang S.;
RT      "Direct Submission.";
RL      Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.

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EMBL; AY987010; AAX88805.1; -; mRNA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0004668; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000961; Pkinase C.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR008271; Ser Thr pkin AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase C; 1.  
 DR ProDom; PD000001; Prot kinase; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR SMART; SM00219; TyrKC; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW Kinase.  
 SQ SEQUENCE 393 AA; 43962 MW; B9931E71A8B998D6 CRC64;  
 Query Match 99.4%; Score 1943; DB 2; Length 393;  
 Best Local Similarity 99.5%; Pred. No. 2.3e-124;  
 Matches 365; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVLLAKRKS DGAF 60  
 DB 27 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVLLAKRKS DGAF 86  
 QY 61 YAVKVLQKSLILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFOTPEKLYFVLDVYNGGE 120  
 DB 87 YAVKVLQKSLILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFOTPEKLYFVLDVYNGGE 146  
 QY 121 LFFHLQRRERFLEPPARFYAAEVAASAI GYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180  
 DB 147 LFFHLQRRERFLEPPARFYAAEVAASAI GYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 206  
 QY 181 CKEGVEPEDTTSTFCGTPEYLAPEVLKRPYDRAVDWVCLGAVLYEMLHGLPPFSQDV 240  
 DB 207 CKEGVEPEDTTSTFCGTPEYLAPEVLKRPYDRAVDWVCLGAVLYEMLHGLPPFSQDV 266  
 QY 241 QMYENILHQPLOIPGRTVAACDLQLSLHKQORQLGSKADFLEIKNHVFFSPINWDDL 300  
 DB 267 QMYENILHQPLOIPGRTVAACDLQLSLHKQORQLGSKADFLEIKNHVFFSPINWDDL 326  
 QY 301 YHKRLTPPNVNTGPDALKHFDPEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360  
 DB 327 YHKRLTPPNVNTGPDALKHFDPEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 386  
 QY 361 DDDILDC 367  
 DB 387 DDDILDC 393

RESULT 5  
 QSH8Z1 HUMAN  
 ID QSH8Z1 HUMAN PRELIMINARY; PRT; 366 AA.  
 AC QSH8Z1;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE OTTHUMP00000031706.  
 GN Name=SGK2; ORFNames=RP1-13887.2-006;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Beasley H.;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

EMBL; Z98752; CAI42315.1; -; Genomic\_DNA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0004668; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000961; Pkinase C.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR008271; Ser Thr pkin AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase C; 1.  
 DR ProDom; PD000001; Prot kinase; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR SMART; SM00219; TyrKC; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 SQ SEQUENCE 366 AA; 41047 MW; 8B8546894C23571F CRC64;  
 Query Match 99.2%; Score 1938.5; DB 2; Length 366;  
 Best Local Similarity 99.7%; Pred. No. 4.2e-124;  
 Matches 366; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVLLAKRKS DGAF 60  
 DB 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVLLAKRKS DGAF 60  
 QY 61 YAVKVLQKSLILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFOTPEKLYFVLDVYNGGE 120  
 DB 61 YAVKVLQKSLILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFOTPEKLYFVLDVYNGGE 119  
 QY 121 LFFHLQRRERFLEPPARFYAAEVAASAI GYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180  
 DB 120 LFFHLQRRERFLEPPARFYAAEVAASAI GYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 179  
 QY 181 CKEGVEPEDTTSTFCGTPEYLAPEVLKRPYDRAVDWVCLGAVLYEMLHGLPPFSQDV 240  
 DB 180 CKEGVEPEDTTSTFCGTPEYLAPEVLKRPYDRAVDWVCLGAVLYEMLHGLPPFSQDV 239  
 QY 241 QMYENILHQPLOIPGRTVAACDLQLSLHKQORQLGSKADFLEIKNHVFFSPINWDDL 300  
 DB 240 QMYENILHQPLOIPGRTVAACDLQLSLHKQORQLGSKADFLEIKNHVFFSPINWDDL 299  
 QY 301 YHKRLTPPNVNTGPDALKHFDPEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360  
 DB 300 YHKRLTPPNVNTGPDALKHFDPEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 359  
 QY 361 DDDILDC 367  
 DB 360 DDDILDC 366

RESULT 6  
 QSRDZ9 PONPY  
 ID QSRDZ9 PONPY PRELIMINARY; PRT; 367 AA.  
 AC QSRDZ9;  
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
 DE Hypothetical protein DKFZp469N2435.  
 GN Name=DKFZp469N2435;  
 OS Pongo pygmaeus (Orangutan).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Pongo.  
 OC NCBI\_TaxID=9600;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Kidney;  
 RG The German cDNA Consortium;  
 RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,



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RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR857741; CAH90008.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein-serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser Thr pkin AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase C.
DR Pfam; PF00433; Pkinase C; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein.
SQ SEQUENCE 367 AA; 41218 MW; 61128B6CC0519B73 CRC64;

Query Match          98.9%; Score 1932; DB 2; Length 367;
Best Local Similarity 98.6%; Pred. No. 1.2e-123;
Matches 362; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNSSPAGTSPQPSRANGNINLGSANPNNAOPTDFDLKVGKNGYKVLAKRKSDGAF 60
DB 1 MNSSPAGTSPQPSRANGNINLGSANPNNAOPTDFDLKVGKNGYKVLAKRKSDGTF 60

QY 61 YAVKVLQKSLKAKKQSHIMASRVLLKNVRPELVGLRYSFQTEKLYFVLVDYNGE 120
DB 61 YAVKVLQKSLKAKKQSHIMASRVLLKNVRPELVGLRYSFQTEKLYFVLVDYDGE 120

QY 121 LFFHLQRRERFLPRARFYAAEVAASAIQYLHSLNIYRDLKPNILLDCQGHVVLDFGL 180
DB 121 LFFHLQRRERFLPRARFYAAEVAASAIQYLHSLNIYRDLKPNILLDCQGHVVLDFGL 180

QY 181 CKEGVPEPTTSTFCGTPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYSDVS 240
DB 181 CKEGVPEPTTSTFCGTPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYSDVS 240

QY 241 QMYENILHOPLOPGRTVAACDLLOSLHKQORQLGSKADFLKKNHVFSPINWDDL 300
DB 241 QMYENILHOPLOPGRTVAACDLLOSLHKQORQLGSKADFLKKNHVFSPINWDDL 300

QY 301 YHKRLTPFPNPNVTGTPADLKHFDPEFTQEA VSKSIGCTPDTVA SSGASSAFGLGFSYAPE 360
DB 301 YHKRLTPFPNPNVAGPADLKHFDPEFTQEA VSKSIGCTPDTVA SSGASSAFGLGFSYAPE 360

QY 361 DDILDC 367
DB 361 DDILDC 367

RESULT 7
SGK2_MOUSE
AC Q9QZS5; Q8R0P6; STANDARD; PRT; 367 AA.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine-protein kinase Sgk2 (EC 2.7.1.37)
DE (Serum/glucocorticoid regulated kinase 2).
GN Name=Sgk2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=20018032; PubMed=10548550; DOI=10.1042/0264-6021:3440189;
RA Kobayashi T., Deak M., Morrice N., Cohen P.;
RT "Characterization of the structure and regulation of two novel
RT isoforms of serum- and glucocorticoid-induced protein kinase.";
RL Biochem. J. 344:189-197(1999).
RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
RC SPRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojohori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tonita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Involved in the activation of potassium channels (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- ALTERNATIVE PRODUCTS.
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoID=Q9QZS5-1; Sequence=Displayed;
CC Name=2;
CC IsoID=Q9QZS5-2; Sequence=VSP_004933;
CC Note=No experimental confirmation available;

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CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -!- CAUTION: Not regulated by serum or glucocorticoids.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF169033; AAF12756.1; -; mRNA.
CC EMBL; AK050009; BAC34031.1; -; mRNA.
CC EMBL; BC026549; AAH26549.1; -; mRNA.
CC HSSP; P31751; 1GZK.
CC Ensembl; ENSMUSG0000017868; Mus musculus.
CC MGI; MGI:1351318; Sgk2.
CC DR GO; GO:0015459; F:potassium channel regulator activity; ISS.
CC DR GO; GO:0004682; F:protein kinase CK2 activity; ISS.
CC DR GO; GO:0017080; F:sodium channel regulator activity; ISS.
CC DR GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
CC DR InterPro; IPR000961; Pkinase_C.
CC DR InterPro; IPR000719; Prot_kinase.
CC DR InterPro; IPR008271; Ser_thr_pkin_AS.
CC DR InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; Pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00133; S_TK_X; 1.
CC SMART; SM00220; S_TK; 1.
CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC Alternative splicing; ATP-binding; Kinase; Nucleotide-binding;
KW Phosphorylation; Serine/threonine-protein kinase; Transferase.
FT DOMAIN 35 292 Protein kinase.
FT NP_BIND 41 49 ATP (By similarity).
FT MOTIF 68 78 Nuclear localization signal (By
FT similarity).
FT ACT_SITE 159 159 Proton acceptor (By similarity).
FT BINDING 64 64 ATP (By similarity).
FT MOD_RES 193 193 Phosphothreonine (by PDPK1) (By
FT similarity).
FT VARSPLIC 171 199 Missing (in isoform 2).
FT CONFLICT 77 77 /FTId=VSP_004933.
FT SEQUENCE 367 AA; 41359 MW; 668C04B1AE9E33A CRC64;

Query Match 94.6%; Score 1848; DB 1; Length 367;
Best Local Similarity 94.3%; Pred. No. 6.3e-118;
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNVYGVLLAKRKSQDGF 60
DB 1 MASSPVGVSPQPSRANGNINLGPSANPNARPTDFDLKVIKGNVYGVLLAKRKSQDGF 60

QY 61 YAVKVLQKSLKXKQSHMAERSVLLKNVRHPLVGLRYSFOTPEKLYFVLVDYNGGE 120
DB 61 YAVKVLQKSLKXKQSHMAERNVLLKNVRHPLVGLRYSFOTPEKLYFVLVDYNGGE 120

QY 121 LPFHLOQRERFLPEPRARFYAAEASVAGYLHLSNIIYRDLKPENILLDCQGHVLTDFGL 180
DB 121 LPFHLOQRERFLPEPRARFYAAEASVAGYLHLSNIIYRDLKPENILLDCQGHVLTDFGL 180

QY 181 CKGEVPEPTTSTFCTPYLAPEVLRLKEFPYDRAVDWCLGAVLYBMLHGLPPFYSDVYS 240
DB 181 CKCEVPEPTTSTFCTPEYLAPEVLRLKEFPYDRAVDWCLGAVLYBMLHGLPPFYNTDVA 240

QY 241 QMYENTLHPLOIPIGGRVTAACDILLOSLHKQORQLGSKADFELEIKNVHFFSPINWDDL 300
DB 241 QMYENTLHPLOIPIGGRVTAACDILLOSLHKQORQLGSKEDFLDIKNHFFSPINWDDL 300

QY 301 YHKRLTPPPNPNVTGADLKHDFEPTQBAVSKSIGCTPDTVASSSGASSAFILGFSYAPE 360
DB 301 YHKRLTPPPNPNVEGADLKHDFEPTQBAVSKSIGCTPDTVASSSGASSAFILGFSYAQD 360

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QY 361 DDDILD 366
DB 361 DDDILD 366

RESULT 8
ID SGK2 RAT STANDARD; PRT; 302 AA.
AC Q8RAU9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine-protein kinase Sgk2 (EC 2.7.1.37)
DE (Serum/glucocorticoid regulated kinase 2) (Fragment).
GN Name=Sgk2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Murioidea; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RA Feng Y.X., Huber S.M., Waerntges S., Lang F.;
RT "SGK2 and SGK3 mRNA expression in rat kidney.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DDJ databases.
CC -!- FUNCTION: Involved in the activation of potassium channels (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF361756; AAL91351.1; -; mRNA.
CC HSSP; P31751; 1GZK.
CC Ensembl; ENSRNOG00000033573; Rattus norvegicus.
CC RGD; 620232; Sgk2.
CC DR GO; GO:0015459; F:potassium channel regulator activity; ISS.
CC DR GO; GO:0004682; F:protein kinase CK2 activity; ISS.
CC DR GO; GO:0017080; F:sodium channel regulator activity; ISS.
CC DR GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
CC DR InterPro; IPR000719; Prot_kinase.
CC DR InterPro; IPR008271; Ser_thr_pkin_AS.
CC DR InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; Pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00220; S_TK; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 18 275 Protein kinase.
FT NP_BIND 24 32 ATP (By similarity).
FT MOTIF 51 61 Nuclear localization signal (By
FT similarity).
FT ACT_SITE 142 142 Proton acceptor (By similarity).
FT BINDING 47 47 ATP (By similarity).
FT MOD_RES 176 176 Phosphothreonine (by PDPK1) (By
FT similarity).
FT NON_TER 1 1
FT NON_TER 302 302
FT SEQUENCE 302 AA; 34622 MW; A74EB3F424283D66 CRC64;

Query Match 78.8%; Score 1540; DB 1; Length 302;
Best Local Similarity 94.7%; Pred. No. 5e-97;
Matches 286; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

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QY 18 GNINLGPSANPNAQPTDFDLKVLGKNGYKVKLLAKRKSOGAFYAVKVLQKKSILKKKEQ 77  
 Db 1 GNINLGPSANPNAQPTDFDLKVLGKNGYKVKLLAKRKSOGAFYAVKVLQKKSILKKKEQ 60  
 QY 78 SHIMASERSVLLKNVRHPLVGLRYSFQTEPKLYFVLDYVNGGELFPHLOREERPLPRAR 137  
 Db 61 SHIMASERNVLLKNVRHPLVGLRYSFQTEPKLYFVLDYVNGGELFPHLOREERPLPRAR 120  
 QY 138 FYAAEVASAIYGLHSLNIIYRDLPENILLLDCQGHVVLTDFTGLCKEKGVEPEDTTSFQGT 197  
 Db 121 FYTAEVASAIYGLHSLNIIYRDLPENILLLDCQGHVVLTDFTGLCKEKGVEPEDTTSFQGT 180  
 QY 198 PEYLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPPFYSDVSQMTENILHQLQIPGGR 257  
 Db 181 PEYLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPPFYSDVSQMTENILHQLQIPGGR 240  
 QY 258 TAAACDLLOGLLHKDQORLQSGKADFLKIKNVHFFSPINWDDLYHKLTPPENPNVTGPA 317  
 Db 241 TAAACDLLOGLLHKDQORLQSGKEDFLDIKNHFFSPINWDDLYHKLTPPENPNVEGPA 300  
 QY 318 DL 319  
 Db 301 DL 302  
 RESULT 9  
 Q5H8Y4 HUMAN  
 ID Q5H8Y4 HUMAN PRELIMINARY; PRT; 285 AA.  
 AC Q5H8Y4  
 DT 10-MAY-2005 (TEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TEMBLrel. 30, Last sequence update)  
 DE OTTHUMP0000031704.  
 GN Name=SGK2; ORFNames=RP1-138B7.2-004;  
 OS Homo sapiens, (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Beasley H.;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL; Z98752; CAI42314.1; -; Genomic\_DNA.  
 DR GO; GO:000524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR008271; Ser\_Thr\_kinase.  
 DR InterPro; IPR002290; Ser\_Thr\_kinase.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR ProDom; PD000001; Prot kinase; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR SMART; SM00219; TYRCK; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Nucleotide-binding;  
 KW Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 285 AA; 32130 MW; A3493A701ABB4542 CRC64;  
 Query Match 76.6%; Score 1497; DB 2; Length 285;  
 Best Local Similarity 99.6%; Pred. NO. 4e-94;  
 Matches 283; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNSSPAGTSPQPSRANGINILGPSANPNAQPTDFDLKVLGKNGYKVKLLAKRKSOGAF 60  
 Db 1 MNSSPAGTSPQPSRANGINILGPSANPNAQPTDFDLKVLGKNGYKVKLLAKRKSOGAF 60

# RESULT 10 Q4S7Y9 TETNG

ID Q4S7Y9 TETNG PRELIMINARY; PRT; 350 AA.  
 AC Q4S7Y9;  
 DT 13-SEP-2005 (TEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)  
 DE Chromosome 9 SCAF14710, whole genome shotgun sequence.  
 DE (Fragment).  
 GN ORFNames=GSTENG0002577001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 RA Mauceli E., Bounneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,  
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
 RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.;  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 the early vertebrate proto-karyotype.";  
 RL Nature 431:946-957 (2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Genoscope, Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC -!- FUNCTION: Plays a key role in the control of the eukaryotic cell  
 cycle. It is required in higher cells for entry into S-phase and  
 mitosis. Component of the kinase complex that phosphorylates the  
 repetitive C-terminus of RNA polymerase II. Catalytic component of  
 MPF (By similarity).  
 CC -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in  
 mature oocytes (By similarity).  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL; CAEE01014710; CAG03243.1; -; Genomic\_DNA.  
 DR InterPro; IPR000961; Pkinase C.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR008271; Ser\_Thr\_kinase.  
 DR InterPro; IPR002290; Ser\_Thr\_kinase.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase\_C; 1.

DR ProDom: PD000001; Prot kinase; 1.  
DR SMART: SM00133; S\_TK\_X; 1.  
DR SMART: SM00220; S\_TKC; 1.  
DR SMART: SM00219; TyrKC; 1.  
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.  
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.  
KW ATP-binding; Kinase; Nucleotide-binding;  
KW Serine/threonine-protein kinase; Transferase.  
FT NON\_TER 1  
SQ SEQUENCE 350 AA; 39571 MW; 56BF9C5C2889D924 CRC64;  
  
Query Match 74.2%; Score 1450.5; DB 2; Length 350;  
Best Local Similarity 77.1%; Pred. No. 7.6e-91;  
Matches 270; Conservative 36; Mismatches 43; Indels 1; Gaps 1;  
  
QY 16 ANGINLGSANPNAOPTDFDLKVIKGNKGYKVLAKRKS DCAFYAVKVLQKKSILKKK 75  
DB 2 SHDDVNLGSANPHARTDFDLAVIGKGTFGKVLAKHKTDSSFYAVKVLQKVKILKKK 61  
  
QY 76 EQSHIMAERSVLLKVRHPLVGLRYSFOTPEKLYFVLDYVNGGELFFHLQRRERFLPR 135  
DB 62 EQKNIMAERNVLLKSLKPLFVLRHLSYFQAEKLYFVLDYVNGGELFFHLQRRERCFSEPR 121  
  
QY 136 ARFYAAEVAISAIGYLHSLNIYRDLPENILLDCQGHVLTDFGLCKEGVEPDTTSTFC 195  
DB 122 ARFYAAEVAISAIGYLHSLNIYRDLPENILLDSQGHVLTDFGLCKEGVEPDTTSTFC 181  
  
QY 196 GTPEYLAPEVLRKEPYDRADVWMCGLGAVLYEMHLGLPPFYSQDVSWYENILHQPILQIPG 255  
DB 182 GTPEYLAPEVLRKEPYDRTVWMCGLGAVLYEMIYSLPPFYSRVDGVWYDGLHKPLQLPP 241  
  
QY 256 GRTVAACDLQLSLHKKDQRLKSGADFLKINHNHVFSPINWDDLKHLKLTTPFPNPNVTG 315  
DB 242 GKSDAVCSLLVGLLQDKHRLGAIADFLKINHNHVFETPINWDDLKHLKLTTPFPNPNVRG 301  
  
QY 316 PADLKHDFDEFTOEAVSKSGTCTPDTVASSSGASSAFLGFSYAPEDDDIL 365  
DB 302 PADTQHIDPFTREMVSSVSQTPEFTASAS-ASNAFNGFSFVATEDSFL 350

## RESULT 11

Q7ZTW4 BRARE  
ID Q7ZTW4\_BRARE PRELIMINARY; PRT; 433 AA.  
AC Q7ZTW4;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Serum/glucocorticoid regulated kinase.  
GN Name=sgk;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Kidney, and Whole body;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.W.,  
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Whole body;  
RG NIH MGC Project;  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Kidney;  
RG NIH MGC Project;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (inactive holoenzyme and  
monomeric catalytic subunit). Translocates into the nucleus  
(By similarity).  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
DR EMBL; BC052134; AAH52134.1; -; mRNA.  
DR EMBL; BC067618; AAH67618.1; -; mRNA.  
DR HSP; P31751; 1MRX.  
DR Ensembl; ENSDARG0000025522; Danio rerio.  
DR ZFIN; ZDB-GENE-030131-2860; sgk.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000961; Pkinase C.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR Pfam; PF00069; Pkinase; 1.  
DR Pfam; PF00433; Pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TKC; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;  
KW Serine/threonine-protein kinase; Transferase; cAMP.  
SQ SEQUENCE 433 AA; 48983 MW; F2AA4771E245FF56 CRC64;  
  
Query Match 73.5%; Score 1436; DB 2; Length 433;  
Best Local Similarity 72.6%; Pred. No. 9.6e-90;  
Matches 267; Conservative 46; Mismatches 47; Indels 8; Gaps 3;  
  
QY 1 MNSSPAGTSPSPSANGNINILGSPANPNNAOPTDFDLKVIKGNKGYKVLAKRKS DCA 60  
DB 71 MNSNP--SPPPSPSQ--QINIGPSNPTAKPSDFDLKVIKGNKGYKVLAKRHSDEKP 125  
  
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKVRHPLVGLRYSFOTPEKLYFVLDYVNGG 120  
DB 126 YAVKVLQKAILKKKEKHINSEKINSEKINSEKINSEKINSEKINSEKINSEKINSE 195  
  
QY 121 LFFHLQRRERFLPRFYAAEVAISAIGYLHSLNIYRDLPENILLDCQGHVLTDFGL 180  
DB 186 LFFHLQRRERFLPRFYAAEVAISAIGYLHSLNIYRDLPENILLDSQGHVLTDFGL 245  
  
QY 181 CKEGVEPDTTSTFCGTPEYLAPEVLRKEPYDRADVWMCGLGAVLYEMHLGLPPFYSQDV 240  
DB 246 CKENIEPNGTSTFTCGTPEYLAPEVLRKEPYDRADVWMCGLGAVLYEMHLGLPPFYSRNTA 305  
  
QY 241 QMYENILHQPILQIPGRTVAAACDLQLSLHKKDQRLKSGADFLKINHNHVFSPINWDDL 300  
DB 306 EMYDNLINKPLQLKPNISNAARHLEGLLQKDKTRELGTDDFTTEIKHNHVFSPINWDDL 365  
  
QY 301 YHKRLTTPFPNPNVTGPADLKHDFDEFTOEAVSKSGTCTPDT---VASSSGASSAFLGFSY 357  
DB 366 NAKLTLTPFPNPNVTGPNDLKHDFDEFTOEAVSKSGTCTPDT---VASSSGASSAFLGFSY 425

QY 358 APEDDDIL 365  
DB 426 APAMDYL 433

## RESULT 12

Q5Q0U5\_FUNHE PRELIMINARY; PRT; 431 AA.  
ID Q5Q0U5\_FUNHE  
AC Q5Q0U5;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Serum and glucocorticoid-regulated kinase.  
GN Name=SGK;  
OS Fundulus heteroclitus (Killifish) (Mummichog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;  
OC Cyprinodontiformes; Fundulidae; Fundulus.  
OC NCBI\_TaxID=8078;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Liver;  
RA Sato J.D., Clarke C.C., Stanton B.A.;  
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY800243; AAV80429.1; -; mRNA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000961; Pkinase C.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; Pkinase C.  
DR Pfam; PF00433; Pkinase C; 1.  
DR ProDom; PD000001; Prot kinase; 1.  
DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TKC; 1.  
DR SMART; SM00219; Ty\_KC; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW Kinase.  
SQ SEQUENCE 431 AA; 48870 MW; 91C80821F64B454D CRC64;

Query Match 73.3%; Score 1432; DB 2; Length 431;  
Best Local Similarity 72.0%; Pred. No. 1.8e-89;  
Matches 265; Conservative 47; Mismatches 48; Indels 8; Gaps 3;  
QY 1 MNSSPAGTSPQPSRANGNINILGPSANPNAQTDFFLKVIGKNGYKVLAKRKSDGAF 60  
DB 69 MNSNP--SPPPSPSQ---QINLGPSSNPSPAKSDPHFLKVIKGSFGKVLARHRTDDQF 123  
QY 61 YAVKVLQKSIKKKEQSHMAERSVLLKNVRHPLVGLRYSFOTPEKLYFVLDYNGGE 120  
DB 124 YAVKVLQKAILKKKEKHMSERNVLLKNVHPLVGLHYSFQTADKLYFVLDYNGGE 183  
QY 121 LFPHLQRRERFLPRARFYAAEVAASAIYGLHLSNIIYRDLKPNENILLDCQGHVLTDFGL 180  
DB 184 LFPHLQRRERFLPRARFYAAEVAASAIYGLHLSNIIYRDLKPNENILLDCQGHVLTDFGL 243  
QY 181 CKGEVPEPTTSTFCGTPEYLAPEVLKPEYDRAVDWVWCLGAVLYEMLHGLPPFYSDVS 240  
DB 244 CKENIEHNGTSTFCGTPEYLAPEVLHQPYDRTVDWVWCLGAVLYEMLYGLPPFYSRNTA 303  
QY 241 QMVENILHQPLOIPGGRTVAACDLQSLHKKQORLQSKADFLKKNHVFSPINWDDL 300  
DB 304 EMDNINLKPLQKPNISNARHLLGGLQKQRTKRGCKDDFTKKNHVFSPINWDDL 363  
QY 301 YHKRLTTPPNVNTGPDALKHFDPEFTQEAVSXSGTCTPDV---TVASSSGASSAFILGFSY 357

DB 364 NAKKMTPPPNVNTGPNDLRHFDPETDEVPSSIGCSPDCALATASIKEAAEAFVGSY 423  
QY 358 APEDDDIL 365  
DB 424 APSMDSYL 431  
RESULT 13  
Q6U119\_CHICK PRELIMINARY; PRT; 432 AA.  
ID Q6U119;  
AC Q6U119;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Serum- and glucocorticoid-induced kinase.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OC NCBI\_TaxID=9031;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Malkiewicz S.A., Porter T.E.;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY380825; AAQ88435.1; -; mRNA.  
DR HSP; P05132; IATP.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000961; Pkinase C.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; Pkinase C; 1.  
DR ProDom; PD000001; Prot kinase; 1.  
DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TKC; 1.  
DR SMART; SM00219; Ty\_KC; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW Kinase.  
SQ SEQUENCE 432 AA; 48890 MW; 83AB52AFF2609953 CRC64;

Query Match 72.6%; Score 1419; DB 2; Length 432;  
Best Local Similarity 71.2%; Pred. No. 1.4e-88;  
Matches 262; Conservative 53; Mismatches 45; Indels 8; Gaps 3;  
QY 1 MNSSPAGTSPQPSRANGNINILGPSANPNAQTDFFLKVIGKNGYKVLAKRKSDGAF 60  
DB 70 MNSNP--SPPPSPSQ---QINLGPSSNPSPAKSDPHFLKVIKGSFGKVLARHKAEOE 124  
QY 61 YAVKVLQKSIKKKEQSHMAERSVLLKNVRHPLVGLRYSFOTPEKLYFVLDYNGGE 120  
DB 125 YAVKVLQKAILKKKEKHMSERNVLLKNVHPLVGLHYSFQTADKLYFVLDYNGGE 184  
QY 121 LFPHLQRRERFLPRARFYAAEVAASAIYGLHLSNIIYRDLKPNENILLDCQGHVLTDFGL 180  
DB 185 LFPHLQRRERFLPRARFYAAEVAASAIYGLHLSNIIYRDLKPNENILLDCQGHVLTDFGL 244  
QY 181 CKGEVPEPTTSTFCGTPEYLAPEVLKPEYDRAVDWVWCLGAVLYEMLHGLPPFYSDVS 240  
DB 245 CKENIEHNGTSTFCGTPEYLAPEVLHQPYDRTVDWVWCLGAVLYEMLYGLPPFYSRNTA 304  
QY 241 QMVENILHQPLOIPGGRTVAACDLQSLHKKQORLQSKADFLKKNHVFSPINWDDL 300  
DB 305 EMDNINLKPLQKPNISNARHLLGGLQKQRTKRGAKEDFTKKNHVFSPINWDDL 364  
QY 301 YHKRLTTPPNVNTGPDALKHFDPEFTQEAVSXSGTCTPDV---ASSSGASSAFILGFSY 357

Db 365 INKKTTPPNVNSGSDLRHFDPEFTDPEVNSIGQSPDSILITASVKEAAEFLGFSY 424  
 Qy 358 APEDDDIL 365  
 Db 425 APVDSFL 432

## RESULT 14

O93524 XENLA  
 ID O93524 XENLA PRELIMINARY; PRT; 434 AA.  
 AC O93524;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Renal tubule;  
 RX MEDLINE=99162637; PubMed=10051674; DOI=10.1073/pnas.96.5.2514;  
 RA Chen S.-Y., Bhargava A., Mastroberardino L., Meijer O.C., Wang J.,  
 Buse P., Firestone G.L., Verrey F., Pearce D.;  
 RT "Epithelial sodium channel regulated by aldosterone-induced protein  
 sgk.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:2514-2519(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Renal tubule;  
 RA Chen S.-Y., Pearce D.;  
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (inactive holoenzyme and  
 monomeric catalytic subunit). Translocates into the nucleus  
 (monomeric catalytic subunit) (By similarity).  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL; AF057138; AAC62398.1; -; mRNA.  
 DR HSSP; P31751; 1MRV.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004668; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000961; Pkinase C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase C; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Cell cycle; Cell division; Hypothetical protein; Kinase;  
 KW Nuclear protein; Nucleotide-binding; Serine/threonine-protein kinase;  
 KW Transferase; CAMP.  
 SQ SEQUENCE 434 AA; 49130 MW; 4A061E38B6AA6F61 CRC64;

Query Match 72.6%; Score 1418; DB 2; Length 434;  
 Best Local Similarity 70.3%; Pred. No. 1.6e-88;  
 Matches 258; Conservative 57; Mismatches 42; Indels 10; Gaps 2;

Qy 2 NSSPACTPSPPSRANGNTNLGSPANPNAQPTDFDLKVIKGNVGVLLAKRKSGAFY 61  
 Db 75 NSSPPSPSQ-----INLGSSNPFAKPSDFQLKIIGKSGFGKVLARHQSDKEY 127  
 Qy 62 AVKVLQKGIKKKEQSHMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYNGGEL 121  
 Db 128 AVKVLQKAILKKKEKHIMSERVLLKNVHPFLVGLHFSQTTSRLYFILDYNGGEL 187

Qy 122 PHLQREFFLEPRARFYAAEVAASIGYLHSLNIITYRDLKPNILLDCOGHVLTDFGLC 181  
 Db 188 FYHLQRERCFLEPRARFYAAETASALGYLHSLNIITYRDLKPNILLDSQGHVLTDFGLC 247  
 Qy 182 KEGVEPEDTSTFCGTPPEYLAPVLRKEPYDRAVDWCLGAVLYEMLHGLPPFPYSODVSQ 241  
 Db 248 KENIEPNGTSTFCGTPPEYLAPVLRKEPYDRTVDWCLGAVLYEMLYGLPFPYSSENTAE 307  
 Qy 242 MYENILHQPLOIPGGRTVAACDLLQSLHKKOQRLGSKADFLKHNHVFFSPINWDDLY 301  
 Db 308 MYDNLNKPLQLKPNITNSARNLLGLLQKDRTKRIGAKNDFMEIKNHIFFSPINWDDLI 367  
 Qy 302 HKRLTPPNPNVTGPADLKHPDPEETOAVSISGCTEDTV--ASSSGASAFGLGFSYA 358  
 Db 368 NKKITPPPNVNSGSDLRHFDPEFTDPEVNSIGQSPDSILITASVKEAAEFLGFSYA 427  
 Qy 359 PEDDDIL 365  
 Db 428 PPMESYL 434

RESULT 15  
 SGK1 RABIT  
 ID SGK1 RABIT STANDARD; PRT; 431 AA.  
 AC Q9XTI8;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Serine/threonine-protein kinase Sgk1 (EC 2.7.1.37)  
 DE (Serum/glucocorticoid-regulated kinase 1).  
 GN Name=Sgk; Synonyms=SGK1;  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;  
 OC Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=New Zealand white;  
 RX MEDLINE=99287894; PubMed=10358046; DOI=10.1074/jbc.274.24.16973;  
 RA Naray-Fejes-Toth A., Canessa C., Cleaveland E.S., Aldrich G.,  
 Fejes-Toth G.;  
 RT "sgk is an aldosterone-induced kinase in the renal collecting duct.  
 Effects on epithelial Na+ channels.";  
 RL J. Biol. Chem. 274:16973-16978(1999).  
 CC -1- FUNCTION: Protein kinase that plays an important role in  
 activating certain potassium, sodium, and chloride channels,  
 suggesting an involvement in the regulation of processes such as  
 cell survival, neuronal excitability, and renal sodium excretion.  
 CC May be a key component of cellular stress response. Phosphorylates  
 NEBD4L, which leads to its inactivation and to the subsequent  
 activation of various channels and transporters such as ENAC,  
 Kv1.3, or EAAT1 (By similarity).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -1- SUBUNIT: Interacts with NEBD4 and NEBD4L (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear, upon  
 phosphorylation (By similarity).  
 CC -1- PTM: Regulated by phosphorylation. Phosphoinositide 3-kinase (PI3-  
 kinase) pathway promotes phosphorylation at Ser-422 which in turn  
 increases the phosphorylation of Thr-256 by PDPK1 (By similarity).  
 CC -1- PTM: Ubiquitinated by NEBD4L; which promotes proteasomal  
 degradation (By similarity).  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC EMBL; AF139639; AAD43303.1; -; mRNA.  
 DR HSSP; P31751; 1GZK.  
 DR InterPro; IPR000961; Pkinase\_C.



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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:06:05 ; Search time 65.3214 Seconds  
(without alignments)  
2468.595 Million cell updates/sec

Title: US-09-868-131A-3  
Perfect score: 1959  
Sequence: 1 MASSPVGVSPQPSRANGNI.....ASSAFLGFSYAQDDDDILDS 367

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A\_Geneseq\_21.\*
- 1: Geneseqp1980s.\*
  - 2: Geneseqp1990s.\*
  - 3: Geneseqp2000s.\*
  - 4: Geneseqp2001s.\*
  - 5: Geneseqp2002s.\*
  - 6: Geneseqp2003as.\*
  - 7: Geneseqp2003bs.\*
  - 8: Geneseqp2004s.\*
  - 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1959	100.0	367	3	AAY95277 Mouse ser
2	1959	100.0	367	7	ADD45797 Rat Prote
3	1848	94.3	367	3	AAY95275 Human ser
4	1848	94.3	367	4	AAY95275 Human ser
5	1848	94.3	367	5	AAD28087 Novel hum
6	1848	94.3	367	5	AAD28087 Human ser
7	1848	94.3	367	7	ADD45799 Human pro
8	1848	94.3	367	8	ADI29317 Human MAR
9	1848	94.3	367	8	ADI29317 LXR-ligan
10	1848	94.3	382	4	AAM25594 Human pro
11	1848	94.3	396	9	ADY37607 Lung canc
12	1848	94.3	427	3	AAY95276 Human ser
13	1846	94.2	427	8	ADQ88284 Human 549
14	1674.5	85.5	367	4	AAB65708 Novel pro
15	1660.5	84.8	398	6	ADA05780 Human NOV
16	1615	82.4	319	8	ADN62944 Human NOV
17	1615	82.4	319	8	AAB99838 AGC prote
18	1606	82.0	335	8	ADJ38886 SGK2 amin
19	1583	80.8	330	8	ADP29822 Human sec
20	1389	70.9	431	3	ADN61463 Human KPP
21	1389	70.9	431	3	AAB24116 Rat serum
22	1387	70.8	407	7	AAY95530 A rat ser
23	1387	70.8	431	2	ADC69794 Human ser
24	1387	70.8	431	6	AAW90139 Human sgk
					ADA10889 Human cdn

25	1387	70.8	431	7	ADG31708	Adg31708 Human pro
26	1387	70.8	431	7	ADK50982	Adk50982 Human NOV
27	1387	70.8	431	7	ADK50984	Adk50984 Human NOV
28	1387	70.8	431	8	ADOS5118	Ados5118 Protein #
29	1387	70.8	431	9	ADY14632	Ady14632 PRO polyp
30	1387	70.8	431	9	ADY19878	Ady19878 PRO polyp
31	1387	70.8	431	9	AEA04529	Aea04529 Human pro
32	1387	70.8	431	7	ADG31706	Adg31706 Human pro
33	1387	70.8	445	7	ADC69792	Adc69792 Human pro
34	1387	70.8	526	6	ADA54293	Ada54293 Human pro
35	1387	70.8	526	7	ADG31710	Adg31710 Human pro
36	1387	70.8	788	7	ADD93289	Add93289 p53-SGK16
37	1385	70.7	431	8	ADO60030	Ado60030 CRH signa
38	1385	70.7	431	8	ADO44573	Ado44573 Serum/glu
39	1383	70.6	373	4	AAB99815	Aab99815 AGC prote
40	1383	70.6	430	7	ADN95921	Adn95921 Human BEC
41	1383	70.6	431	2	AAW77217	Aaw77217 Human cel
42	1383	70.6	431	3	AAY95279	Aay95279 Human ser
43	1383	70.6	431	3	AAB24115	Aab24115 Human ser
44	1383	70.6	431	4	AAB65613	Aab65613 Novel pro
45	1383	70.6	431	7	ADD14174	Add14174 Human src

ALIGNMENTS

RESULT 1

AAY95277  
ID AAY95277 standard; protein; 367 AA.

AC AAY95277;

DT 12-SRP-2000 (first entry)

DE Mouse serum and glucocorticoid-induced protein kinase 2.

XX Seram and glucocorticoid-induced protein kinase 2; SGK2; mouse; phosphorylation; cancer; diabetes; ischaemia; therapy.

OS Mus musculus.

XX WO200035946-A1.

XX 22-JUN-2000.

XX 14-DEC-1999; 99WO-GB004232.

XX 14-DEC-1998; 98US-0112217P.

XX 19-AUG-1999; 99GB-00019676.

XX (UYDU-) UNIV DUNDEE.

XX Cohen P, Kobayashi T, Deak M;

XX WPI; 2000-442364/38.

XX Modulation of serum and glucocorticoid-induced protein kinase (SGK) by phosphorylation with 3-phosphoinositide-dependent protein kinase-1 (PDK1) or dephosphorylation, useful for treatment of cancer, diabetes and ischemic diseases.

XX Disclosure; Page 7; 127pp; English.

XX The present sequence is that of mouse serum and glucocorticoid-induced protein kinase (SGK) isoform 2, a protein activated by phosphorylation. The invention provides methods of activating SGK (see also AAY95275-79) by phosphorylation using 3-phosphoinositide-dependent protein kinase-1 (PDK1), and of reducing the activity of SGK by dephosphorylation. The invention also provides a method of identifying a compound that modulates the activity of SGK. Such compounds are useful for treating patients requiring modulation of SGK, such as patients with cancer, diabetes or ischaemic disease

SQ	Sequence 367 AA;	CC	The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
	Query Match 100.0%; Score 1959; DB 3; Length 367;	CC	
	Best Local Similarity 100.0%; Pred. No. 1.5e-188;	CC	
	Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	
QY	1 MASSPVGVPSQPSRANGNINLGPSANPNARPTDFDLKVIKGNKGKVLAKRKS DGAF 60	CC	
Db	1 MASSPVGVPSQPSRANGNINLGPSANPNARPTDFDLKVIKGNKGKVLAKRKS DGAF 60	CC	
QY	61 YAVKVLQKKSILKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGE 120	CC	
Db	61 YAVKVLQKKSILKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGE 120	CC	
QY	121 LFFHLQRRERFLPRARFYTAEVASAI GYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180	CC	
Db	121 LFFHLQRRERFLPRARFYTAEVASAI GYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180	CC	
QY	181 CKECVEPEETTSFCGTPEYLAPEVLKRPYDRAVDWCLGAVLYEMLHGLPPFNTDVA 240	CC	
Db	181 CKECVEPEETTSFCGTPEYLAPEVLKRPYDRAVDWCLGAVLYEMLHGLPPFNTDVA 240	CC	
QY	241 QMYENILHQPILQIPGGRTVAACDLQLGLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 300	CC	
Db	241 QMYENILHQPILQIPGGRTVAACDLQLGLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 300	CC	
QY	301 YHKRLTPPNPNVEGPADLKHFDPEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAQD 360	CC	
Db	301 YHKRLTPPNPNVEGPADLKHFDPEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAQD 360	CC	
QY	361 DDDILDS 367	CC	
Db	361 DDDILDS 367	CC	
	Query Match 100.0%; Score 1959; DB 7; Length 367;	CC	
	Best Local Similarity 100.0%; Pred. No. 1.5e-188;	CC	
	Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	
QY	1 MASSPVGVPSQPSRANGNINLGPSANPNARPTDFDLKVIKGNKGKVLAKRKS DGAF 60	QY	1 MASSPVGVPSQPSRANGNINLGPSANPNARPTDFDLKVIKGNKGKVLAKRKS DGAF 60
Db	1 MASSPVGVPSQPSRANGNINLGPSANPNARPTDFDLKVIKGNKGKVLAKRKS DGAF 60	Db	1 MASSPVGVPSQPSRANGNINLGPSANPNARPTDFDLKVIKGNKGKVLAKRKS DGAF 60
QY	61 YAVKVLQKKSILKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGE 120	QY	61 YAVKVLQKKSILKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGE 120
Db	61 YAVKVLQKKSILKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGE 120	Db	61 YAVKVLQKKSILKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGE 120
QY	121 LFFHLQRRERFLPRARFYTAEVASAI GYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180	QY	121 LFFHLQRRERFLPRARFYTAEVASAI GYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180
Db	121 LFFHLQRRERFLPRARFYTAEVASAI GYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180	Db	121 LFFHLQRRERFLPRARFYTAEVASAI GYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180
QY	181 CKECVEPEETTSFCGTPEYLAPEVLKRPYDRAVDWCLGAVLYEMLHGLPPFNTDVA 240	QY	181 CKECVEPEETTSFCGTPEYLAPEVLKRPYDRAVDWCLGAVLYEMLHGLPPFNTDVA 240
Db	181 CKECVEPEETTSFCGTPEYLAPEVLKRPYDRAVDWCLGAVLYEMLHGLPPFNTDVA 240	Db	181 CKECVEPEETTSFCGTPEYLAPEVLKRPYDRAVDWCLGAVLYEMLHGLPPFNTDVA 240
QY	241 QMYENILHQPILQIPGGRTVAACDLQLGLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 300	QY	241 QMYENILHQPILQIPGGRTVAACDLQLGLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 300
Db	241 QMYENILHQPILQIPGGRTVAACDLQLGLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 300	Db	241 QMYENILHQPILQIPGGRTVAACDLQLGLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 300
QY	301 YHKRLTPPNPNVEGPADLKHFDPEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAQD 360	QY	301 YHKRLTPPNPNVEGPADLKHFDPEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAQD 360
Db	301 YHKRLTPPNPNVEGPADLKHFDPEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAQD 360	Db	301 YHKRLTPPNPNVEGPADLKHFDPEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAQD 360
QY	361 DDDILDS 367	QY	361 DDDILDS 367
Db	361 DDDILDS 367	Db	361 DDDILDS 367
	Query Match 100.0%; Score 1959; DB 7; Length 367;	QY	1 MASSPVGVPSQPSRANGNINLGPSANPNARPTDFDLKVIKGNKGKVLAKRKS DGAF 60
	Best Local Similarity 100.0%; Pred. No. 1.5e-188;	Db	1 MASSPVGVPSQPSRANGNINLGPSANPNARPTDFDLKVIKGNKGKVLAKRKS DGAF 60
	Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY	61 YAVKVLQKKSILKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGE 120
	Query Match 100.0%; Score 1959; DB 7; Length 367;	Db	61 YAVKVLQKKSILKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGE 120
	Best Local Similarity 100.0%; Pred. No. 1.5e-188;	QY	121 LFFHLQRRERFLPRARFYTAEVASAI GYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180
	Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	121 LFFHLQRRERFLPRARFYTAEVASAI GYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180
	Query Match 100.0%; Score 1959; DB 7; Length 367;	QY	181 CKECVEPEETTSFCGTPEYLAPEVLKRPYDRAVDWCLGAVLYEMLHGLPPFNTDVA 240
	Best Local Similarity 100.0%; Pred. No. 1.5e-188;	Db	181 CKECVEPEETTSFCGTPEYLAPEVLKRPYDRAVDWCLGAVLYEMLHGLPPFNTDVA 240
	Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY	241 QMYENILHQPILQIPGGRTVAACDLQLGLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 300
	Query Match 100.0%; Score 1959; DB 7; Length 367;	Db	241 QMYENILHQPILQIPGGRTVAACDLQLGLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 300
	Best Local Similarity 100.0%; Pred. No. 1.5e-188;	QY	301 YHKRLTPPNPNVEGPADLKHFDPEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAQD 360
	Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	301 YHKRLTPPNPNVEGPADLKHFDPEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAQD 360
	Query Match 100.0%; Score 1959; DB 7; Length 367;	QY	361 DDDILDS 367
	Best Local Similarity 100.0%; Pred. No. 1.5e-188;	Db	361 DDDILDS 367
	Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
RESULT 2			
ADD45797			
ID	ADD45797 standard; protein; 367 AA.		
XX	ADD45797;		
AC			
XX			
DT	29-JAN-2004 (first entry)		
XX			
DE	Rat Protein AAF12756, SEQ ID NO 11466.		
XX			
KW	Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;		
XX	chronic constriction injury; CCI; spared nerve injury; SNI; Chung.		
OS	Rattus norvegicus.		
XX			
PN	WO2003016475-A2.		
XX			
PD	27-FEB-2003.		
XX			
PF	14-AUG-2002; 2002WO-US025765.		
XX			
PR	14-AUG-2001; 2001US-0312147P.		
PR	01-NOV-2001; 2001US-0346382P.		
PR	26-NOV-2001; 2001US-0333347P.		
XX			
PA	(GEHO ) GEN HOSPITAL CORP.		
PA	(FARB ) BAYER AG.		
XX			
PI	Woolf C, D'urso D, Befort K, Costigan M;		
XX			
DR	WPI; 2003-268312/26.		
DR	GENBANK; AAF12756.		
XX			
PT	New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.		
XX			
PS	Claim 1; Page; 1017pp; English.		
XX			
XX			



CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic  
CC activity, regulation of haematopoiesis and is useful for treating myeloid  
CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia  
CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve  
CC tissue growth, and in tissue repair, healing of burns, incisions, ulcers,  
CC for treating osteoporosis, osteoarthritis, bone degenerative disorders,  
CC or periodontal disease. Furthermore, (I) is also useful for gut  
CC protection or regeneration and treatment of lung or liver fibrosis,  
CC reperfusion injury in various tissues, various immune deficiencies and  
CC disorders including severe combined immunodeficiency (SCID), bacterial or  
CC fungal infections, autoimmune disorders e.g. multiple sclerosis,  
CC rheumatoid arthritis, diabetes mellitus, myaesthesia gravis, allergic  
CC reactions and conditions, such as asthma or other respiratory problems.  
CC In addition, (I) affects biorhythms or circadian cycles of rhythms,  
CC fertility, metabolism, catabolism, anabolism, storage or elimination of  
CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides  
CC analgesic effects or other pain reducing effects, immunoglobulin like  
CC activity and can act as an antigen in a vaccine composition to raise an  
CC immune response. AAU28020-AAU28395 represent novel human secreted protein  
CC amino acid sequences of the invention  
XX  
SQ Sequence 367 AA;

Query Match 94.3%; Score 1848; DB 4; Length 367;  
Best Local Similarity 94.3%; Pred. No. 2.5e-177;  
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;  
QY 1 MASSPVGVPSQPSRANGNINLGPSANPNARPTDFDLKVIKGNVGVLLAKRKS DGAF 60  
Db 1 MNSSPAGTSPQPSRANGNINLGPSANPNARPTDFDLKVIKGNVGVLLAKRKS DGAF 60  
QY 61 YAVKVLQKKSILKKEQHMAERNVLLKNVRHPELVGLRYSFQTPKLYFVLDYVNGE 120  
Db 61 YAVKVLQKKSILKKEQHMAERSVLLKNVRHPELVGLRYSFQTPKLYFVLDYVNGE 120  
QY 121 LFFHLQRRERFLEPRARFYTAEVASAI GYLHSLNIIYRDLPENILLDCQGHVLTDFGL 180  
Db 121 LFFHLQRRERFLEPRARFYTAEVASAI GYLHSLNIIYRDLPENILLDCQGHVLTDFGL 180  
QY 181 KCEGVEPETTTSTFCGTPPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFFNTDVA 240  
Db 181 KCEGVEPETTTSTFCGTPPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFFNTDVA 240  
QY 241 QMYENILHQPLOIPGGRVTAACDLLOGLLHKDQRLGSKEDFLDIKNHFFSPINWDDL 300  
Db 241 QMYENILHQPLOIPGGRVTAACDLLOGLLHKDQRLGSKEDFLDIKNHFFSPINWDDL 300  
QY 301 YHKRLTPPNPNVVEGPADLKHPDPEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAQD 360  
Db 301 YHKRLTPPNPNVVEGPADLKHPDPEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360  
QY 361 DDILD 366  
Db 361 DDILD 366

## RESULT 5

AAE22765  
ID AAE22765 standard; protein; 367 AA.  
XX  
AC AAE22765;  
XX  
XX 09-AUG-2002 (first entry)  
DT Human serum and glucocorticoid-induced protein kinase, SGK2-alpha.  
DE Human; cytostatic; antisense gene therapy; screening; protein kinase;  
XX cancer; liver; colon; tumour; inflammation; arthritic synovium; enzyme;  
KW serum and glucocorticoid-induced protein kinase; SGK2-alpha.  
XX  
OS Homo sapiens.  
XX  
PN WO200224947-A2.

XX 28-MAR-2002.  
PD  
XX 20-SEP-2001; 2001WO-IB002237.  
PF  
XX 20-SEP-2000; 2000US-0233999P.  
XX 02-OCT-2000; 2000US-0237419P.  
PR 02-OCT-2000; 2000US-0237423P.  
PR 04-OCT-2000; 2000US-0238558P.  
PR 10-MAY-2001; 2001US-0290555P.  
XX (KINE-) KINETEK PHARM INC.  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
XX  
XX Yoganathan T, Delaney AD;  
PI WPI; 2002-394145/42.  
XX N-PSDB; AAD36141.  
DR  
XX  
PT Diagnosing cancer, comprises determining the upregulation of expression  
PT of a nucleic acid sequence encoding a protein kinase or upregulation of  
PT expression of the protein kinase, in the cancer.  
XX  
PS Claim 1; Page 66-67; 87pp; English.  
XX  
CC The invention relates to a method for screening biologically active agent  
CC that modulates cancer associated protein kinase function. The invention  
CC also relates to a method for diagnosing cancer comprising determining the  
CC upregulation of expression of a nucleic acid sequence encoding a protein  
CC kinase. The method is useful for diagnosing cancer. A protein kinase is  
CC useful for screening biological agents that modulate cancer associated  
CC protein kinase function. Downregulating the activity of protein kinase is  
CC useful for inhibiting the growth of a cancer cell, e.g. liver or colon  
CC cancer. A nucleic acid encoding protein kinase is useful to screen biopsy  
CC derived tumours and inflammatory samples such as arthritic synovium, for  
CC amplified DNA in the cell or increased expression of corresponding mRNA  
CC or protein and is also useful to detect differences in expression levels  
CC such as molecular weight, amino acid and nucleotide sequences between the  
CC two cells. The present sequence is human serum and glucocorticoid-induced  
CC protein kinase, SGK2-alpha  
XX  
SQ Sequence 367 AA;

Query Match 94.3%; Score 1848; DB 5; Length 367;  
Best Local Similarity 94.3%; Pred. No. 2.5e-177;  
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;  
QY 1 MASSPVGVPSQPSRANGNINLGPSANPNARPTDFDLKVIKGNVGVLLAKRKS DGAF 60  
Db 1 MNSSPAGTSPQPSRANGNINLGPSANPNARPTDFDLKVIKGNVGVLLAKRKS DGAF 60  
QY 61 YAVKVLQKKSILKKEQHMAERNVLLKNVRHPELVGLRYSFQTPKLYFVLDYVNGE 120  
Db 61 YAVKVLQKKSILKKEQHMAERSVLLKNVRHPELVGLRYSFQTPKLYFVLDYVNGE 120  
QY 121 LFFHLQRRERFLEPRARFYTAEVASAI GYLHSLNIIYRDLPENILLDCQGHVLTDFGL 180  
Db 121 LFFHLQRRERFLEPRARFYTAEVASAI GYLHSLNIIYRDLPENILLDCQGHVLTDFGL 180  
QY 181 KCEGVEPETTTSTFCGTPPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFFNTDVA 240  
Db 181 KCEGVEPETTTSTFCGTPPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFFNTDVA 240  
QY 241 QMYENILHQPLOIPGGRVTAACDLLOGLLHKDQRLGSKEDFLDIKNHFFSPINWDDL 300  
Db 241 QMYENILHQPLOIPGGRVTAACDLLOGLLHKDQRLGSKEDFLDIKNHFFSPINWDDL 300  
QY 301 YHKRLTPPNPNVVEGPADLKHPDPEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAQD 360  
Db 301 YHKRLTPPNPNVVEGPADLKHPDPEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360  
QY 361 DDILD 366  
Db 361 DDILD 366

Db 361 DDDILD 366

RESULT 6  
ADD45799  
ID ADD45799 standard; protein; 367 AA.  
XX  
AC ADD45799;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human Protein XP\_009494, SEQ ID NO 11468.  
XX  
KW Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
OS Homo sapiens.  
XX  
PN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX  
DR WPI; 2003-268312/26.  
DR GENBANK; XP\_009494.  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
PS Claim 1; Page; 1017pp; English.  
XX  
CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also,  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 367 AA;

Query Match 94.3%; Score 1848; DB 7; Length 367;

Best Local Similarity 94.3%; Pred. No. 2.5e-177;  
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MASSPVGPSPPSPRANGNINLGPSANPNRPTDPLKVIKGNKGKVLAKRKSDGAF 60  
DB 1 MNSSPAGTSPSPRANGNINLGPSANPNRPTDPLKVIKGNKGKVLAKRKSDGAF 60  
QY 61 YAVKVLQKKSILKNKEQNHIAMERNVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYNGGE 120  
DB 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYNGGE 120  
QY 121 LFFHLQRRERFLEPRARFYTAEVASAIYGLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180  
DB 121 LFFHLQRRERFLEPRARFYAAEVASAIYGLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180  
QY 181 CKECVEPEETSTFCGTPEVLAPVLRKEPYDRAVDWMCILGAVLYEMLHGLPPEFNTDVA 240  
DB 181 CKEGVEPEETSTFCGTPEVLAPVLRKEPYDRAVDWMCILGAVLYEMLHGLPPEFNTDVA 240  
QY 241 QMYENILHQPLOIPGGRITVAACDQLLQGLLHKDQORLGSKEDEFLDKNHNHFFSPINWDDL 300  
DB 241 QMYENILHQPLOIPGGRITVAACDQLLQGLLHKDQORLGSKEDEFLDKNHNHFFSPINWDDL 300  
QY 301 YHKRLTPFPNPNVEGPADLKHFDPEFTQBAVSKSICCTPDTVASSGASSAFLGFSYAQD 360  
DB 301 YHKRLTPFPNPNVTGPADLKHFDPEFTQBAVSKSICCTPDTVASSGASSAFLGFSYAPE 360  
QY 361 DDDILD 366  
DB 361 DDDILD 366

RESULT 7  
ADI29317  
ID ADI29317 standard; protein; 367 AA.  
XX  
AC ADI29317;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Human MARK3-associated protein #87.  
XX  
KW Human; antisense gene therapy; MARK3;  
KW MAP/microtubule affinity-regulating kinase 3; cancer;  
KW Alzheimer's disease; neurodegenerative disorder;  
KW hyperproliferative disorder; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN US2003232771-A1.  
XX  
PD 18-DEC-2003.  
XX  
PF 17-JUN-2002; 2002US-00174319.  
XX  
PR 17-JUN-2002; 2002US-00174319.  
XX (ISIS-) ISIS PHARM INC.  
XX  
PI Ward DT, Freier SM, Dobie KW;  
XX  
DR WPI; 2004-052188/05.  
DR N-PSDB; ADI29435.  
XX  
PT New antisense compound targeted to a nucleic acid molecule encoding  
PT microtubule-affinity-regulating kinases (MARK3), useful for modulating  
PT expression of MARK3 or for treating cancer or Alzheimer's disease.  
XX  
PS Disclosure; SEQ ID NO 237; 233pp; English.  
XX  
CC The invention relates to a compound comprising a sequence comprising 8-80  
CC base pairs (bp) targeted to a nucleic acid encoding MARK3  
CC (MAP/microtubule affinity-regulating kinase 3), that specifically

CC hybridises with the nucleic acid encoding MARK3 and inhibits expression  
 CC of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a  
 CC composition comprising the compound and a carrier or diluent, inhibiting  
 CC the expression of MARK3 in cells or tissues, treating an animal having or  
 CC suspected of having a disease or condition associated with MARK3 and  
 CC screening for an antisense compound. The antisense oligonucleotide is  
 CC useful for preparing a composition for treating hyperproliferative  
 CC disorder, particularly cancer and neurodegenerative diseases e.g.  
 CC Alzheimer's disease. The present sequence is a MARK3 associated protein  
 CC included in the figures but not mentioned anywhere else in the  
 CC specification.  
 XX  
 XX  
 SQ Sequence 367 AA;

Query Match 94.3%; Score 1848; DB 8; Length 367;  
 Best Local Similarity 94.3%; Pred. No. 2.5e-177;  
 Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 MASSPVGVSPQPSRANGNINLGPSANPNARPTDFDLKVGKNGYKVLAKRKS DGAF 60  
 Db 1 MNSSPAGTSPQPSRANGNINLGPSANPNARPTDFDLKVGKNGYKVLAKRKS DGAF 60  
 QY 61 YAVKVLQKKSILKNKEQNHMAERNVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE 120  
 Db 61 YAVKVLQKKSILKKKEQSHMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE 120  
 QY 121 LFFHLQRRRRFLEPRARFYTAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180  
 Db 121 LFFHLQRRRRFLEPRARFYTAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180  
 QY 181 CKECVEPEETSTFCGTPEYLAPEVLKRPYDRAVDWVCLGAVLYEMLHGLPPFTNDVA 240  
 Db 181 CKECVEPEETSTFCGTPEYLAPEVLKRPYDRAVDWVCLGAVLYEMLHGLPPFTNDVA 240  
 QY 241 QMYENILHQLQIPGGRTVAAACDLQLLHKDQORQLGSKEDFLDIKNHMFSPINWDDL 300  
 Db 241 QMYENILHQLQIPGGRTVAAACDLQLLHKDQORQLGSKADFLDIKNHVFSPINWDDL 300  
 QY 301 YHKRLTPFPNPNVEGPADLKHFDPEFTQBAVSKSIGCTPDTVASSSGASSAFLGFSYAQD 360  
 Db 301 YHKRLTPFPNPNVTGPADLKHFDPEFTQBAVSKSIGCTPDTVASSSGASSAFLGFSYAPE 360  
 QY 361 DDDILD 366  
 Db 361 DDDILD 366

RESULT 8  
 ID ADJ45521  
 XX ADJ45521 standard; protein; 367 AA.  
 AC ADJ45521;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE LXR-ligand induced transcript seq id 52.  
 XX  
 KW LXR; liver X receptor; cholesterol; gallstone; atherosclerosis;  
 KW lipid storage disease; obesity; diabetes; hypercholesterolaemia;  
 KW LXR-ligand induced 1; LXRL1; human; LXR-ligand induced transcript;  
 KW LXR regulated gene.  
 XX

OS Homo sapiens.  
 XX  
 XX US2004023276-A1.  
 XX  
 PD 05-FEB-2004.  
 XX  
 XX  
 PF 02-MAY-2003; 2003US-00429160.  
 XX  
 PR 03-MAY-2002; 2002US-0377714P.  
 XX  
 XX (WARD/) WARD T R.

PA (MAOM/) MAO M.  
 PA (LINS/) LINSLEY P S.  
 PA (LUND/) LUND E.  
 XX  
 XX Ward TR, Mao M, Linsley PS, Lund E;  
 PI  
 DR WPI; 2004-224687/21.  
 DR N-PSDB; ADJ45520.  
 XX  
 PT New purified liver X receptor (LXR) nucleic acids, useful for diagnosing  
 PT a disease involving LXR activity, such as cholesterol gallstones,  
 PT atherosclerosis, lipid storage diseases, obesity, diabetes, or  
 PT hypercholesterolemia.  
 XX  
 XX Example 1; SEQ ID NO 52; 141pp; English.  
 XX  
 CC The invention describes a purified nucleic acid comprising a fully  
 CC defined sequence of 1586 bp (SEQ ID NO: 1) as given in the specification,  
 CC or its complement. The methods and compositions are useful for diagnosing  
 CC a disease or disorder involving LXR (liver X receptor) activity in a  
 CC sample by detecting an increase or decrease in the transcript level  
 CC relative to the amount present in an analogous sample from a subject not  
 CC having the disease or disorder or not subjected to therapy, wherein the  
 CC disease or disorder is cholesterol gallstones, atherosclerosis, lipid  
 CC storage diseases, obesity, diabetes, or hypercholesterolaemia. They are  
 CC also used to identify a compound that changes LXR activity, wherein the  
 CC compound changes the estimated level of LXR activity in a sample from the  
 CC subject contacted with the compound relative to the estimated level of  
 CC LXR activity in an analogous sample from the subject not contacted with  
 CC the compound. This is the amino acid sequence of an LXR regulated  
 CC protein.  
 XX  
 SQ Sequence 367 AA;

Query Match 94.3%; Score 1848; DB 8; Length 367;  
 Best Local Similarity 94.3%; Pred. No. 2.5e-177;  
 Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 MASSPVGVSPQPSRANGNINLGPSANPNARPTDFDLKVGKNGYKVLAKRKS DGAF 60  
 Db 1 MNSSPAGTSPQPSRANGNINLGPSANPNARPTDFDLKVGKNGYKVLAKRKS DGAF 60  
 QY 61 YAVKVLQKKSILKNKEQNHMAERNVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE 120  
 Db 61 YAVKVLQKKSILKKKEQSHMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE 120  
 QY 121 LFFHLQRRRRFLEPRARFYTAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180  
 Db 121 LFFHLQRRRRFLEPRARFYTAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180  
 QY 181 CKECVEPEETSTFCGTPEYLAPEVLKRPYDRAVDWVCLGAVLYEMLHGLPPFTNDVA 240  
 Db 181 CKECVEPEETSTFCGTPEYLAPEVLKRPYDRAVDWVCLGAVLYEMLHGLPPFSQDVS 240  
 QY 241 QMYENILHQLQIPGGRTVAAACDLQLLHKDQORQLGSKEDFLDIKNHMFSPINWDDL 300  
 Db 241 QMYENILHQLQIPGGRTVAAACDLQLLHKDQORQLGSKADFLDIKNHVFSPINWDDL 300  
 QY 301 YHKRLTPFPNPNVEGPADLKHFDPEFTQBAVSKSIGCTPDTVASSSGASSAFLGFSYAQD 360  
 Db 301 YHKRLTPFPNPNVTGPADLKHFDPEFTQBAVSKSIGCTPDTVASSSGASSAFLGFSYAPE 360  
 QY 361 DDDILD 366  
 Db 361 DDDILD 366  
 RESULT 9  
 AAM25594  
 ID AAM25594 standard; protein; 382 AA.  
 XX  
 AC AAM25594;  
 XX

DT	16-OCT-2001	(first entry)	
DE	Human protein sequence SEQ ID NO:1109.		
XX	Human; cancer; ulcer; HIV infection; human immunodeficiency virus;		
KW	antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;		
KW	antibacterial; endocrine; cardiant; central nervous system; virucide;		
KW	anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;		
KW	antiaggregant; haemostatic; vulnerary; antitumor; osteopathic; eczema;		
KW	dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;		
KW	neuroprotective; antidepressant; neurotropic; antiparkinsonian; infection;		
KW	immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;		
KW	antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;		
KW	cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;		
KW	genetic disease; haematopoietic disorder; platelet disorder; asthma;		
KW	thrombocytopaenia; osteoporosis; severe combined immunodeficiency;		
KW	allergic rhinitis; diabetes; multiple sclerosis; depression;		
KW	Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;		
XX	neurological disorder.		
OS	Homo sapiens.		
XX	WO200153455-A2.		
PN	26-JUL-2001.		
XX	22-DEC-2000; 2000WO-US035017.		
PF	23-DEC-1999; 99US-00471275.		
PR	21-JAN-2000; 2000US-00488725.		
PR	25-APR-2000; 2000US-00552317.		
XX	(HYSE-) HYSEQ INC.		
PA	Tang YT, Liu C, Drmanac RT;		
PI	WPI; 2001-457603/49.		
XX	N-PSDB; AAH99535.		
DR	Isolated human polynucleotides encoding polypeptides, useful for the		
PT	treatment and diagnosis of e.g. cancer, ulcers and HIV infection.		
XX	Claim 20; Page 227; 1217pp; English.		
PS	AAH99166 to AAH99904 encode the human proteins given in AAM25225 to		
XX	AAM25963. The proteins can have activities based on the tissues and cells		
CC	they are expressed in, such as: antiinflammatory; antirheumatic;		
CC	antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;		
CC	central nervous system; virucide; anti-HIV; fungicide; antimutagen;		
CC	cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;		
CC	antitumor; osteopathic; dermatological; antiallergic; antiasthmatic;		
CC	antidiabetic; cytostatic; neuroprotective; antidepressant; neurotropic;		
CC	antiparkinsonian; and immunostimulant. The proteins and polynucleotides		
CC	encoding them can be used in gene therapy, antisense therapy and vaccine		
CC	production. The proteins and polynucleotides are useful for screening for		
CC	agonists or antagonists of a protein and for the treatment and diagnosis		
CC	of disorders associated with the activity of a protein e.g. inflammation,		
CC	rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,		
CC	neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal		
CC	infections, autoimmunity, genetic diseases, haematopoietic disorders,		
CC	anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,		
CC	osteoporosis, severe combined immunodeficiency, eczema, allergic		
CC	rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression.		
CC	Alzheimer's disease, Parkinson's disease, neurodegenerative and		
CC	neurological disorders		
XX	Sequence 382 AA;		
SQ	Query Match 94.3%; Score 1848; DB 4; Length 382;		
	Best Local Similarity 94.3%; Pred. No. 2.6e-177;		
	Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;		
QY	1 MASSPVGVPSOPSRANGNINLPSANPNARPTDFDLKVIKGNKGVLLAKRKS DGAF 60		



CC detecting lung cancer-specific gene products and their expression levels  
CC in animal models of cancer. (I) is also useful for diagnosing, treating  
CC or preventing lung cancer, and also disorders related to abnormal  
CC cellular differentiation, proliferation or degeneration.

XX SQ Sequence 396 AA;

Query Match 94.3%; Score 1848; DB 9; Length 396;  
Best Local Similarity 94.3%; Pred. No. 2.8e-177;  
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MASSPVGVPSPPSRANGNINLGPANPNARPTDFELKVIKGNVGVLLAKRKSDDGAF 60  
DB 30 MNSSPAGTSPQPSRANGNINLGPANPNARPTDFELKVIKGNVGVLLAKRKSDDGAF 89  
QY 61 YAVKVLQKKSILKNKEQNHMAERNVLLKNVRHPPFLVGLRYSFQTPEKLYFVLDYVNGGE 120  
DB 90 YAVKVLQKKSILKNKEQNHMAERSVLLKNVRHPPFLVGLRYSFQTPEKLYFVLDYVNGGE 149  
QY 121 LFFHLQRRERFLEPRARFYTAEVASAIQYLHSLNIIYRDLKPEINILLDCQGHVLTDFGL 180  
DB 150 LFFHLQRRERFLEPRARFYAAEVAESAIGYLHSLNIIYRDLKPEINILLDCQGHVLTDFGL 209  
QY 181 CKECVEPEETTTFCGTPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFNTDVA 240  
DB 210 CKEGVEPEDTTTFCGTPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYSQDVS 269  
QY 241 QMYENILHQPLOIPGGRTVAACDLQLGLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 300  
DB 270 QMYENILHQPLOIPGGRTVAACDLQLGLLHKDQRLGSKADFLDIKNHVFSPINWDDL 329  
QY 301 YHKRLTPPNPNVVEGPADLKHFDPPTQBAVSKSIGCTPDTVASSSGASSAFGLFSYAQD 360  
DB 330 YHKRLTPPNPNVGTGPADLKHFDPPTQBAVSKSIGCTPDTVASSSGASSAFGLFSYAPE 389  
QY 361 DDDILD 366  
DB 390 DDDILD 395

RESULT 11  
AAY95276  
ID AAY95276 standard; protein; 427 AA.

XX AC AAY95276;  
XX DT 12-SEP-2000 (first entry)  
XX DE Human serum and glucocorticoid-induced protein kinase 2-beta.  
XX KW Serum and glucocorticoid-induced protein kinase 2; SGK2-beta; human;  
XX KW phosphorylation; cancer; diabetes; ischaemia; therapy.

XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT Modified-site 339 /note= "O-phosphorylated"  
FT Modified-site 394 /note= "O-phosphorylated"  
XX WO200035946-A1.  
XX PD 22-JUN-2000.  
XX PF 14-DEC-1999; 99WO-GB004232.  
XX PR 14-DEC-1998; 98US-0112121P.  
XX PR 19-AUG-1999; 99GB-00019676.  
XX PA (UYDU-) UNIV DUNDEE.  
XX PI Cohen P, Kobayashi T, Deak M;

XX WPI; 2000-442364/38.  
DR N-PSDB; AAA27857.  
XX Modulation of serum and glucocorticoid-induced protein kinase (SGK) by  
PT phosphorylation with 3-phosphoinositide-dependent protein kinase-1 (PDK1)  
PT or dephosphorylation, useful for treatment of cancer, diabetes and  
PT ischemic diseases.  
XX Disclosure; Page 6-7; 127pp; English.

XX The present sequence is that of human serum and glucocorticoid-induced  
CC protein kinase (SGK) isoform 2-beta. SGK (see AAY95276) was initially  
CC identified as a glucocorticoid and osmotic stress-responsive gene. Novel  
CC isoforms, SGK2 and SGK3, were isolated from EST database searches, and 2  
CC splice variants of SGK2, i.e. SGK2-beta and -alpha (see AAY95275), which  
CC contains 60 fewer N-terminal residues, were identified. SGK2-beta is  
CC expressed in liver and kidney. It is activated by phosphorylation in a  
CC similar manner to SGK. The invention provides methods of activating SGK  
CC activity by phosphorylation using 3-phosphoinositide-dependent protein  
CC kinase-1 (PDK1), and of reducing the activity of SGK by  
CC dephosphorylation. The invention also provides a method of identifying a  
CC compound that modulates the activity of SGK. Such compounds are useful  
CC for treating patients requiring modulation of SGK, such as patients with  
CC cancer, diabetes or ischaemic disease

SQ Sequence 427 AA;

Query Match 94.3%; Score 1848; DB 3; Length 427;  
Best Local Similarity 94.3%; Pred. No. 3.1e-177;  
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MASSPVGVPSPPSRANGNINLGPANPNARPTDFELKVIKGNVGVLLAKRKSDDGAF 60  
DB 61 MNSSPAGTSPQPSRANGNINLGPANPNARPTDFELKVIKGNVGVLLAKRKSDDGAF 120  
QY 61 YAVKVLQKKSILKNKEQNHMAERNVLLKNVRHPPFLVGLRYSFQTPEKLYFVLDYVNGGE 120  
DB 121 YAVKVLQKKSILKNKEQNHMAERSVLLKNVRHPPFLVGLRYSFQTPEKLYFVLDYVNGGE 180  
QY 121 LFFHLQRRERFLEPRARFYTAEVASAIQYLHSLNIIYRDLKPEINILLDCQGHVLTDFGL 180  
DB 181 LFFHLQRRERFLEPRARFYAAEVAESAIGYLHSLNIIYRDLKPEINILLDCQGHVLTDFGL 240  
QY 181 CKECVEPEETTTFCGTPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFNTDVA 240  
DB 241 CKEGVEPEDTTTFCGTPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYSQDVS 300  
QY 241 QMYENILHQPLOIPGGRTVAACDLQLGLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 300  
DB 301 QMYENILHQPLOIPGGRTVAACDLQLGLLHKDQRLGSKADFLDIKNHVFSPINWDDL 360  
QY 301 YHKRLTPPNPNVVEGPADLKHFDPPTQBAVSKSIGCTPDTVASSSGASSAFGLFSYAQD 360  
DB 361 YHKRLTPPNPNVGTGPADLKHFDPPTQBAVSKSIGCTPDTVASSSGASSAFGLFSYAPE 420  
QY 361 DDDILD 366  
DB 421 DDDILD 426

RESULT 12  
ADQ88284

ID ADQ88284 standard; protein; 427 AA.

XX AC ADQ88284;  
XX DT 21-OCT-2004 (first entry)  
XX DE Human 54946 protein, a Ser/Thr protein kinase SGK2.  
XX KW human; cardiovascular disorder; thrombotic disorder;  
KW differential expression; gene therapy; aberrant vascularisation;



KW atherosclerosis; thrombosis; coronary artery disease; hyperlipidaemia;  
 KW dyslipidaemia; high blood pressure; heart failure; cardiomyopathy;  
 KW thrombolytic; anticoagulant; antilipemic; hypotensive; cardiant;  
 KW Ser/Thr protein kinase; SGK2; EC 2.7.1.37; enzyme.

OS Homo sapiens.

XX WO2004063340-A2.

XX 29-JUL-2004.

XX 13-JAN-2004; 2004WO-US000393.

XX 13-JAN-2003; 2003US-0439693P.

XX 05-FEB-2003; 2003US-0445216P.

XX 18-FEB-2003; 2003US-0448036P.

XX 12-MAR-2003; 2003US-0454189P.

XX 25-MAR-2003; 2003US-0457541P.

XX 23-APR-2003; 2003US-0466411P.

XX 08-MAY-2003; 2003US-0469041P.

XX 10-JUN-2003; 2003US-0477414P.

XX 13-JUN-2003; 2003US-0478560P.

XX 24-JUL-2003; 2003US-0489772P.

XX 03-SEP-2003; 2003US-0490860P.

XX 22-SEP-2003; 2003US-0504786P.

XX 24-SEP-2003; 2003US-0505570P.

XX 17-OCT-2003; 2003US-0512418P.

XX 27-OCT-2003; 2003US-0514660P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Stagliano NE, Healy A, Acton SL, Galvin KM, Donoghue MA;

XX Rogrigue-Way A, Tomlinson JB;

XX WPI; 2004-553729/53.

XX N-PSDB; ADQ88283.

XX Identifying a compound for treating a cardiovascular or thrombotic

XX disorder by combining a compound to be tested with e.g., a 9380, 9462,

XX 8701 or 2419 polypeptide or with a host cell expressing the polypeptide

XX and detecting the binding.

XX Claim 1; SEQ ID NO 126; 512pp; English.

XX This invention relates to a novel compound that is capable of treating a

XX cardiovascular or thrombotic disorder. Specifically, it refers to the

XX identification of nucleic acid molecules, and the encoded proteins

XX thereof, which are differentially expressed in cardiovascular disease

XX states relative to their normal expression in non-diseased tissues. The

XX present invention describes test compounds (i.e. small molecules,

XX peptides or antibodies) that can bind to and modulate the activity of

XX these differentially expressed membrane-bound polypeptides, where binding

CC Query Match 94.3%; Score 1848; DB 8; Length 427;

CC Best Local Similarity 94.3%; Pred. No. 3.1e-177;

CC Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

CC 1 MASSPVGVPSPQSRANGINLPSANPNARPTDFDLKVGKNGYGVLLAKRKSDDGAF 60

CC 61 MNSSPAGTSPQSRANGINLPSANPNARPTDFDLKVGKNGYGVLLAKRKSDDGAF 120

QY 61 YAVKVLQKKSILKNKQNHMAERNVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGE 120

DB 121 YAVKVLQKKSILKKKQSHIMAERSVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGE 180

QY 121 LFFHLQRRRFLPRARFYTAEVASAIYGLHLSNIIYRDLKPNILLDCQGHVVLDTFGL 180

DB 181 LFFHLQRRRFLPRARFYAAEVASAIYGLHLSNIIYRDLKPNILLDCQGHVVLDTFGL 240

QY 181 CKECVPEETTSFCTGPEVLAPEVLRKPYDRAVDMWCLGAVLYEMLHGLPPFNTDVA 240

DB 241 CKEGVPEETTSFCTGPEVLAPEVLRKPYDRAVDMWCLGAVLYEMLHGLPPFYSQDVS 300

QY 241 QMYENILHQPLOIPGGRITVAACDQLQLLHKDQRLGSKEDFLDKNHNFFSPINWDDL 300

DB 301 QMYENILHQPLOIPGGRITVAACDQLQLLHKDQRLGSKADFLKHNHFFSPINWDDL 360

QY 301 YHKRLTPPNPNVGGPADLKHDPPEFTQEAIVSKSICGCTPDVTASSSGASSAFILGFSYAQD 360

DB 361 YHKRLTPPNPNVGTGADLKHDPPEFTQEAIVSKSICGCTPDVTASSSGASSAFILGFSYAPE 420

QY 361 DDDILD 366

DB 421 DDDILD 426

RESULT 13

AAB65708

ID AAB65708 standard; protein; 367 AA.

AC AAB65708;

XX 27-MAR-2001 (first entry)

XX Novel protein kinase, SEQ ID NO: 237.

XX Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;

XX immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;

XX dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;

XX immune disorder; cardiovascular disease; neurodegenerative disease;

XX cancer; autoimmune disorder; stroke; inflammatory bowel disease;

XX inflammatory pelvic disease; multiple sclerosis; psoriasis.

OS Homo sapiens.

XX WO2000073469-A2.

XX 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US014842.

XX 28-MAY-1999; 99US-0136503P.

XX (SUGB-) SUGEN INC.

XX Plowman GD, Martinez R, Whyte D, Sudersanam S;

XX WPI; 2001-032161/04.

XX N-PSDB; AAP44737.

XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and

XX treating immune-related diseases and disorders, cardiovascular disease,

XX neurodegenerative diseases and/or cancers.

XX Claim 10; Fig 1; 310pp; English.

XX The present sequence is a novel protein kinase. The novel protein kinases

XX and the nucleic acids that encode them may be used in the treatment and

XX diagnosis of diseases associated with inappropriate kinase expression

XX such as immune-related diseases and disorders, cardiovascular disease,

XX neurodegenerative diseases and/or cancers. The nucleic acids and

XX complementary sequences may also be used as DNA probes in diagnostic

XX assays. The kinase polypeptides may be used as antigens in the production

XX of antibodies of kinase expression and activity. Anti-kinase antibodies

CC and kinase antagonists may also be used to down regulate kinase  
CC expression and activity. Diseases related to kinase expression and  
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune  
CC disorders, complications of organ transplantation, myocardial infarction,  
CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-  
CC stress related disorders, chronic inflammatory bowel disease, chronic  
CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,  
CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive  
CC disorders  
XX

Sequence 367 AA;

Query Match 94.2%; Score 1846; DB 4; Length 367;  
Best Local Similarity 94.0%; Pred. No. 3.9e-177;  
Matches 344; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MASSPVGVSPQPSRANGNINLGPSANPNARPTDFDLKVIKGNYGKVLAKRKSDDGAF 60

Db 1 MNSSPAGTSPQPSRANGNINLGPSANPNARPTDFDLKVIKGNYGKVLAKRKSDDGAF 60

Qy 61 YAVKVLQKKSILKNKEQHIMAEARNVLLKNVRHPLVGLRYSFQTPKEKLYFVLDYVNGGE 120

Db 61 YAVKVLQKKSILKKKEQHIMAEARNVLLKNVRHPLVGLRYSFQTPKEKLYFVLDYVNGGE 120

Qy 121 LFFHLQRRERFLEPRAREVTAEVAISAIGYLHSINIYRDLKPNILLDCQGHVLTDFGL 180

Db 121 LFFHLQRRERFLEPRAREVTAEVAISAIGYLHSINIYRDLKPNILLDCQGHVLTDFGL 180

Qy 181 CRECEPEPTTFTFCGTPPEYLAPEVLRLKEPYPYDRAVDWVCLGAVLYEMLHGLPFFNTDVA 240

Db 181 CREGEPEPTTFTFCGTPPEYLAPEVLRLKEPYPYDRAVDWVCLGAVLYEMLHGLPFFNSQDVS 240

Qy 241 QMYENILHQPLOIPGQRTVAACDLQLGLLHKDQRLGSKEDFLDITKNHFFSPINWDDL 300

Db 241 QMYENILHQPLOIPGQRTVAACDLQLGLLHKDQRLGSKEDFLDITKNHFFSPINWDDL 300

Qy 301 YHKRLTPPNPNVGGPADLKHDPDPTQEAIVSKSGCTPDTVASSSGASSAFLGESYAOD 360

Db 301 YHKRLTPPNPNVGGPADLKHDPDPTQEAIVSKSGCTPDTVASSSGASSAFLGESYAPE 360

Qy 361 DDDILD 366

Db 361 DDDILD 366

RESULT 14

ADA05780

ID ADA05780 standard; protein; 398 AA.

AC ADA05780;

XX 06-NOV-2003 (first entry)

XX Human NOV33a protein SEQ ID NO:140.

XX human; NOV3; antidiabetic; anorectic; antibacterial; virucide;  
KW immunomodulator; cytostatic; neurotropic; neuroprotective;  
KW antiparkinsonian; antilipaeamic; gene therapy; human disease;  
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;  
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;  
KW immune disorder; haematopoietic disorder; dyslipidaemia.

XX Homo sapiens.

XX WO2003029424-A2.

XX 10-APR-2003.

XX 02-OCT-2002; 2002WO-US031373.

XX 02-OCT-2001; 2001US-0326483P.

XX 05-OCT-2001; 2001US-0327435P.

XX 05-OCT-2001; 2001US-0327449P.

PR 09-OCT-2001; 2001US-0327917P.  
PR 09-OCT-2001; 2001US-0328029P.  
PR 09-OCT-2001; 2001US-0328044P.  
PR 09-OCT-2001; 2001US-0328056P.  
PR 12-OCT-2001; 2001US-0328849P.  
PR 15-OCT-2001; 2001US-0329414P.  
PR 17-OCT-2001; 2001US-0330142P.  
PR 18-OCT-2001; 2001US-0330309P.  
PR 22-OCT-2001; 2001US-0341058P.  
PR 24-OCT-2001; 2001US-0339266P.  
PR 24-OCT-2001; 2001US-0343629P.  
PR 29-OCT-2001; 2001US-0349575P.  
PR 01-NOV-2001; 2001US-0346357P.  
PR 17-APR-2002; 2002US-0373260P.  
PR 19-APR-2002; 2002US-0373815P.  
PR 19-APR-2002; 2002US-0373826P.  
PR 19-APR-2002; 2002US-0373884P.  
PR 22-APR-2002; 2002US-0374977P.  
PR 16-MAY-2002; 2002US-0381037P.  
PR 16-MAY-2002; 2002US-0381038P.  
PR 16-MAY-2002; 2002US-0381042P.  
PR 17-MAY-2002; 2002US-0381642P.  
PR 28-MAY-2002; 2002US-0383656P.  
PR 29-MAY-2002; 2002US-0383831P.  
PR 25-JUN-2002; 2002US-0391335P.  
PR 01-OCT-2002; 2002US-00262511.

(CURA-) CURAGEN CORP.

Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;  
Patturajan M, Sytek KA, Edinger SR, Ellerman K, Malyankar UM; B;  
Ott T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;  
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;  
Shinkens RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;  
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

WPI; 2003-381626/36.

N-PSDB; ADA05779.

New NOVX polypeptides and nucleic acids, useful for diagnosing,  
preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,  
cancer or dyslipidemia, and in chromosome mapping, tissue typing or  
pharmacogenomics.

Claim 1; Page 219; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55  
(e.g. NOV1). Also described: (1) a composition comprising a polypeptide  
described above and a carrier; (2) a kit comprising, in one or more  
containers, the composition described above; (3) an isolated nucleic acid  
molecule which encodes a NOVX protein of the invention; (4) a vector  
comprising the nucleic acid molecule described above; (5) a cell  
comprising the above vector; (6) an antibody that immunospecifically  
binds to the polypeptide described above; (7) methods for determining the  
presence or amount of the above polypeptide or nucleic acid molecule in a  
sample; (8) methods for determining the presence of or predisposition to a  
disease associated with altered levels of expression of the above  
polypeptide or nucleic acid molecule in a first mammalian subject; (9) a  
method of identifying an agent that binds to the polypeptide described  
above; (10) a method for identifying a potential therapeutic agent for  
use in treating a pathology that is related to an aberrant expression or  
aberrant physiological interactions of the polypeptide; (11) a method of  
screening for a modulator of activity of or latency or predisposition to  
a pathology associated with the polypeptide; (12) a method for modulating  
the activity of the polypeptide described above; (13) methods of treating  
or preventing a pathology associated with the above polypeptide in a  
mammal; and (14) a method for producing the above polypeptide. NOVX  
sequences have antidiabetic, anorectic, antibacterial, virucide,  
immunomodulator, cytostatic, neurotropic, neuroprotective, antiparkinsonian  
and antilipaeamic activities, and can be used in gene therapy. The  
polypeptide is useful in manufacturing a medicament for treating a  
syndrome associated with a human disease. The polypeptide or the nucleic

CC acid molecule may be used to diagnose, treat or prevent metabolic  
CC disorders such as diabetes or obesity, infections, cachexia, cancer,  
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's  
CC disease, immune disorders, hematopoietic disorders and various  
CC dyslipidaemias. The nucleic acids can also be used as hybridisation  
CC probes, in chromosome mapping, tissue typing, preventive medicine and  
CC pharmacogenomics. The present sequence represents a human NOVX from the  
CC present invention.

XX SQ Sequence 398 AA;

Query Match 85.5%; Score 1674.5; DB 6; Length 398;  
Best Local Similarity 86.9%; Pred. No. 9.1e-160;  
Matches 318; Conservative 9; Mismatches 10; Indels 29; Gaps 1;  
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QY 61 YAVKVLQKKSILKNKEQHIMARNVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGE 120  
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QY 181 CKECVPEETTSFCGTPPEVLAEVLRKEPYDRAVDWMCGLGAVLYEMLHGLRPPFNTDVA 240  
DB 231 -----YLAPEVLRKEPYDRAVDWMCGLGAVLYEMLHGLRPPFYSDVS 271  
QY 241 QMYENILHQLQIPGGRRTVAACDLQGLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 300  
DB 272 QMYENILHQLQIPGGRRTVAACDLQGLLHKDQRLGSKADFLIKNVHFFSPINWDDL 331  
QY 301 YHKRLTPPNPNVEGADLKHFDPEFTQEAIVSKSIGCTPTDVASSGASSAFILGFSYAQD 360  
DB 332 YHKRLTPPNPNVTGPADLKHFDPEFTQEAIVSKSIGCTPTDVASSGASSAFILGFSYAPE 391  
QY 361 DDDILD 366  
DB 392 DDDILD 397

RESULT 15

ADN62944

ID ADN62944 standard; protein; 398 AA.

XX AC ADN62944;

XX DT 01-JUL-2004 (first entry)

XX DE Human NOV33a.

XX human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;  
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;  
KW Alzheimer's disease; Parkinson's disease; immune disorder;  
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;  
KW wasting disorder.

XX OS Homo sapiens.

XX PN US2004038223-A1.

XX PD 26-FEB-2004.

XX PF 01-OCT-2002; 2002US-00262511.

XX PR 02-OCT-2001; 2001US-0326483P.

XX PR 05-OCT-2001; 2001US-0327435P.

XX PR 09-OCT-2001; 2001US-0327449P.

XX PR 09-OCT-2001; 2001US-0328029P.

PR 09-OCT-2001; 2001US-0328044P.  
PR 09-OCT-2001; 2001US-0328056P.  
PR 12-OCT-2001; 2001US-0328849P.  
PR 15-OCT-2001; 2001US-0329414P.  
PR 17-OCT-2001; 2001US-0330142P.  
PR 18-OCT-2001; 2001US-0330309P.  
PR 22-OCT-2001; 2001US-0341058P.  
PR 24-OCT-2001; 2001US-0339266P.  
PR 29-OCT-2001; 2001US-0343629P.  
PR 29-OCT-2001; 2001US-0349575P.  
PR 01-NOV-2001; 2001US-0346357P.  
PR 17-APR-2002; 2002US-0373260P.  
PR 19-APR-2002; 2002US-0373815P.  
PR 19-APR-2002; 2002US-0373817P.  
PR 19-APR-2002; 2002US-0373826P.  
PR 22-APR-2002; 2002US-0373884P.  
PR 16-MAY-2002; 2002US-0381037P.  
PR 16-MAY-2002; 2002US-0381038P.  
PR 17-MAY-2002; 2002US-0381042P.  
PR 28-MAY-2002; 2002US-0381642P.  
PR 29-MAY-2002; 2002US-0383656P.  
PR 25-JUN-2002; 2002US-0383831P.  
XX XX

(SMIT/) SMITHSON G.

(MILL/) MILLET I.

(PEYM/) PEYMAN J. A.

(KEKU/) KEKUDA R.

(JUJU/) JU J.

(LILL/) LI L.

(GUOX/) GUO X.

(PATT/) PATTURAJAN M.

(SPYT/) SPYTEK K. A.

(EDIN/) EDINGER S. R.

(ELLE/) ELLERMAN K.

(MALY/) MALYANKAR U. M.

(ORTT/) ORT T.

(GORM/) GORMAN L.

(ZERR/) ZERHUSEN B. D.

(ANDE/) ANDERSON D. W.

(ZHON/) ZHONG M.

(CATT/) CATTERTON E.

(JIWV/) JI W.

(MILL/) MILLER C. E.

(RAST/) RASTELLI L.

(STON/) STONE D. J.

(PENA/) PENNA C. E. A.

(SHEN/) SHENOY S. G.

(SHIM/) SHIMKETS R. A.

(ROTH/) ROTHENBERG M. E.

(LEAC/) LEACH M. D.

(AGER/) AGER M. L.

(BERG/) BERGHS C.

(DIPI/) DIPPO V. A.

(EISE/) EISEN A.

(GANG/) GANGOLLI B. A.

(RIEG/) RIEGER D. K.

(SPAD/) SPADERNA S. K.

XX XX

PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;

PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;

PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;

PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoj SG;

PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;

PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;

XX WPI: 2004-213931/20.

DR N-PSDB; ADN62943.

XX XX

PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,

XX diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:21:11 ; Search time 17.3113 Seconds  
(without alignments)  
1752.724 Million cell updates/sec

Title: US-09-868-131A-3  
Perfect score: 1959  
Sequence: 1 MASSPVGVSPQPSRANGNI.....ASSAFLGFSYAODDDILDLS 367

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/H COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfilese1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1387	70.8	407	2	US-10-067-977-4
2	1387	70.8	445	2	US-10-067-977-2
3	1383	70.6	431	2	US-09-031-295-2
4	1383	70.6	431	2	US-10-000-039-2
5	1380.5	70.5	430	1	US-08-712-709-9
6	1380.5	70.5	430	2	US-09-111-444-9
7	1380.5	70.5	430	2	US-09-541-228-9
8	1379	70.4	431	1	US-08-712-709-5
9	1379	70.4	431	2	US-09-111-444-5
10	1379	70.4	431	2	US-09-541-228-5
11	863	44.1	479	2	US-09-771-161A-246
12	863	44.1	479	2	US-09-771-161A-247
13	863	44.1	479	2	US-09-771-161A-248
14	860	43.9	465	2	US-09-526-043-2
15	858	43.8	454	2	US-09-526-043-17
16	851.5	43.5	480	2	US-09-590-740-6
17	851	43.5	480	2	US-09-526-043-13
18	851	43.4	481	2	US-09-538-092-1054
19	847.5	43.3	480	2	US-09-091-058-2
20	847.5	43.3	480	2	US-09-590-740-2
21	847.5	43.3	480	2	US-09-538-092-1053
22	847.5	43.3	480	2	US-09-526-043-14
23	847.5	43.3	480	2	US-09-771-161A-223
24	847.5	43.3	726	2	US-09-417-197-71
25	847.5	43.3	727	2	US-09-417-197-139
26	831.5	42.4	470	2	US-09-248-796A-18482
27	829	42.3	417	2	US-09-590-740-4

28	822.5	42.0	480	2	US-09-205-658-157	Sequence 157, App
29	794.5	40.6	482	2	US-09-430-564-2	Sequence 2, Appli
30	794.5	40.6	495	2	US-09-430-564-3	Sequence 3, Appli
31	794.5	40.6	495	2	US-09-762-258-2	Sequence 2, Appli
32	792	40.4	637	2	US-09-817-310-2	Sequence 2, Appli
33	792	40.4	637	2	US-10-355-724A-2	Sequence 2, Appli
34	780.5	39.8	502	2	US-09-538-092-996	Sequence 996, App
35	780.5	39.8	525	1	US-08-749-902-7	Sequence 7, Appli
36	780.5	39.8	525	1	US-08-749-902-8	Sequence 8, Appli
37	780.5	39.8	525	2	US-09-430-564-16	Sequence 16, Appli
38	780.5	39.8	525	2	US-09-762-258-4	Sequence 4, Appli
39	778.5	39.7	587	1	US-08-313-274-2	Sequence 2, Appli
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41	777.5	39.7	546	2	US-09-205-658-155	Sequence 155, App
42	773	39.5	541	2	US-09-205-658-154	Sequence 154, App
43	764	39.0	568	2	US-09-949-016-7970	Sequence 7970, Ap
44	764	39.0	584	2	US-09-842-307-2	Sequence 2, Appli
45	750	38.3	737	2	US-09-772-647-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-10-067-977-4  
; Sequence 4, Application US/10067977  
; Patent No. 6830911  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Chunhua and KE, Zhaoxi  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001313  
; CURRENT APPLICATION NUMBER: US/10/067,977  
; CURRENT FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 407  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-067-977-4

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Best Local Similarity	71.1%;	Pred. No. 8.8e-127;		
Matches	256;	Conservative 51;	Mismatches 49;	Indels 4; Gaps 2;
QY	9	PSQPSPRANGNINLGPSANPNARPTDFLKVIGKNGYGVLLAKRSGDGFYAVKVLQK	68	
Db	49	PSPPSPSPSQ-QINLGSPSNPHAKPSDFHLKVIGKSGFGKVLARHKAEEVFYAVKVLQK	107	
QY	69	KAILKKEQNHMAERNVLLKNVRHFFLVGLRYSFQTPPEKLYPVLGYVNGGELFFHLORE	128	
Db	108	KAILKKEKHIMSERNVLLKNVRHFFLVGLRYSFQTPPEKLYPVLGYVNGGELFFHLORE	167	
QY	129	RFLEPRARFYAEVASAIGYLSHNLIIYRDLKPENILLDCQGHVLTDPGLCKECVEPE	188	
Db	168	RFLEPRARFYAEVASAIGYLSHNLIIYRDLKPENILLDCQGHVLTDPGLCKECVEPE	227	
QY	189	ETTSTFCGTPPEYLAPEVLREKPYDRAVDWMCGLGAVLYEMLHGLPPFPFNTDVAQMYENILH	248	
Db	228	ETTSTFCGTPPEYLAPEVLREKPYDRAVDWMCGLGAVLYEMLHGLPPFPFNTDVAQMYENILH	287	
QY	249	QLOIPIGGRTVACDILLOGLLHKDQQRORIGSKEDFLDIKNHMPFSPINMDDLXHKRLTTPP	308	
Db	288	KPLQLKPNITNSARHLLGLELQKDRTKRLGAKDDFMEIKSHVFFSLINMDDLINKKITTPP	347	
QY	309	FNPVVEGPDALXHFDPFTQEAHSVKSIGCTPDTV---ASSSGASSAFLGFSYAODDDIL	365	
Db	348	FNPVSGPNDLRHDFDPFTQEAHSVKSIGCTPDTV---ASSSGASSAFLGFSYAODDDIL	407	

RESULT 2

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US-10-067-977-2
; Sequence 2, Application US/10067977
; Patent No. 6830911
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua and KE, Zhaoxi
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THREEOF
; FILE REFERENCE: CLO01313
; CURRENT APPLICATION NUMBER: US/10/067,977
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-977-2
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Query Match 70.8%; Score 1387; DB 2; Length 445;
Best Local Similarity 71.1%; Pred. No. 1e-126;
Matches 256; Conservative 51; Mismatches 49; Indels 4; Gaps 2;

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DB 87 PSPPPSPSQ-QINLGFSSNPHAKPSDFHFLKVIKGSFGKVLARHKAEEVFVAVKVLQK 145
QY 69 KSILKNKQNHIMAERNVLLKNVRHPLVGLRYSFQTPEKLYFVLVDYVNGGELFFHLORE 128
DB 146 KAILKKKEKHIMSERVLLKNVKHPLVGLHFSFQTADKLYFVLVDYINGGELFFHLORE 205
QY 129 RRLPRARFYTAVASAGYLHSLNIYRDLPENILLDCQGHVVLTDFGLCKECVEPE 188
DB 206 RCLEPRARFYAAEIASALGYLHSLNIYRDLPENILLDSQGHIVLTDFGLCKENIEHN 265
QY 189 ETTSTFCGTPEYLAPVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFFNTDVAQMYENILH 248
DB 266 STTSTFCGTPEYLAPVLRHQPYDRTVDWVCLGAVLYEMLYGLPPYSRTAEMYNILN 325
QY 249 QPLQIPGRTVAACDLQGLLHKQRLGSKEDFLDIKNHMFPSPINWDDLHYHKLTPP 308
DB 326 KPLQLKPNITNSARHLEGLLQKRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPP 385
QY 309 FNPVVEGPADLKHFDPEFTQEAHSVKSIGCTPTDV---ASSSGASSAFLGFSYAQDDDDL 365
DB 386 FNPVSGPNDLRHFDPEFTPEVPNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSFL 445
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RESULT 3
US-09-031-295-2
; Sequence 2, Application US/09031295
; Patent No. 6326181
; GENERAL INFORMATION:
; APPLICANT: LANG, Florian
; APPLICANT: WALDEGGER, Tübingen
; TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,295
; FILING DATE: 26-FEB-1998
; CLASSIFICATION: 435
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 197-08-173.8
; FILING DATE: 28-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 058315/0123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 431 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-031-295-2

Query Match 70.6%; Score 1393; DB 2; Length 431;
Best Local Similarity 70.8%; Pred. No. 2.3e-126;
Matches 255; Conservative 52; Mismatches 49; Indels 4; Gaps 2;

QY 9 PSPQSRANGINILGPSANPNARPTDFDLKVIKGNVGVLLAKRKSQDGAFAVAVKVLQK 68
DB 73 PSPPPSPSQ-QINLGFSSNPHAKPSDFHFLKVIKGSFGKVLARHKAEEVFVAVKVLQK 131
QY 69 KSILKNKQNHIMAERNVLLKNVRHPLVGLRYSFQTPEKLYFVLVDYVNGGELFFHLORE 128
DB 132 KAILKKKEKHIMSERVLLKNVKHPLVGLHFSFQTADKLYFVLVDYINGGELFFHLORE 191
QY 129 RRLPRARFYTAVASAGYLHSLNIYRDLPENILLDCQGHVVLTDFGLCKECVEPE 188
DB 192 RCLEPRARFYAAEIASALGYLHSLNIYRDLPENILLDSQGHIVLTDFGLCKENIEHN 251
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DB 252 STTSTFCGTPEYLAPVLRHQPYDRTVDWVCLGAVLYEMLYGLPPYSRTAEMYNILN 311
QY 249 QPLQIPGRTVAACDLQGLLHKQRLGSKEDFLDIKNHMFPSPINWDDLHYHKLTPP 308
DB 312 KPLQLKPNITNSARHLEGLLQKRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPP 371
QY 309 FNPVVEGPADLKHFDPEFTQEAHSVKSIGCTPTDV---ASSSGASSAFLGFSYAQDDDDL 365
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RESULT 4
US-10-000-039-2
; Sequence 2, Application US/10000039
; Patent No. 6855520
; GENERAL INFORMATION:
; APPLICANT: LANG, Florian
; APPLICANT: WALDEGGER, Tübingen
; TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/000,039
; FILING DATE: 04-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US/09/031.295  
FILING DATE: 26-FEB-1998  
APPLICATION NUMBER: DE 197-08-173.8  
FILING DATE: 28-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Sandercock, Colin G.  
REGISTRATION NUMBER: 31.298  
REFERENCE/DOCKET NUMBER: 058315/0123  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 431 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-000-039-2

Query Match 70.6%; Score 1383; DB 2; Length 431;  
Best Local Similarity 70.8%; Pred. No. 2.3e-126;  
Matches 255; Conservative 52; Mismatches 49; Indels 4; Gaps 2;  
QY 9 PPSQPSRANGINILGPSANPNARPTDFDLKVIKGNVGVKVLAKRSGDGAFAVAVKVLQK 68  
Db 73 PPSPPSPSQ-QINLGSSNPHAKPSDFHFLKVIKGSFGKVLARHAKAEVFAVAVKVLQK 131  
QY 69 KSLKKNQNHMAERNVLLKNVRHPLVGLRYSFQTPKLYFLVDYVNGGELFFHLORE 128  
Db 132 KALKKKEKHMSERNVLLKNVHPFLVGLHFSFQADKLYFLVDYINGGELFFHLORE 191  
QY 129 RRELEPRARYTAEVASAIYHLSNLIYRDLPENILLDCQGHVLTDFGLCKECVEPE 188  
Db 192 RCLEPRARYAEIASALGYLHSLNIVYRDLPENILLDSQGHIVLTDFGLCKENIEHN 251  
QY 189 ETTSTFCGTPPEYLAPEVLKRPYDRAVDWMCGLGAVLYEMLHGLPPFFNTDVAQMYENILH 248  
Db 252 STTSTFCGTPPEYLAPEVLKRPYDRTVDWMCGLGAVLYEMLYGLPPFSYRNTAEYDNLN 311  
QY 249 QPLQIPGGRTVACDLLOGLLHKQORLGSKEDFLDIKNHMFSPINWDDLYHKRLTTP 308  
Db 312 KPLQLKNTNSARHLEGLLQKDRKRLGAKDDFMEIKSHVFFSLINWDDLINKKITTP 371  
QY 309 FNPVNEGPAADLKHFDEFTQEAYSKISGCTPTDV---ASSSGASSAFLGFSYAQDDDDIL 365  
Db 372 FNPVSGPNELRHDFDEFTPEEPVNSIGKSPDSVLVTASVKAAEAFLGFSYAPPTDSDL 431

RESULT 5  
US-08-712-709-9  
Sequence 9, Application US/08712709  
Patent No. 5863780  
GENERAL INFORMATION:  
APPLICANT: Au-Young, Janice  
APPLICANT: Guegler, Karl J.  
APPLICANT: Hawkins, Phillip R.  
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/712,709

FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0118 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 430 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 294637  
US-08-712-709-9  
Query Match 70.5%; Score 1380.5; DB 1; Length 430;  
Best Local Similarity 71.1%; Pred. No. 4.1e-126;  
Matches 256; Conservative 53; Mismatches 46; Indels 5; Gaps 3;  
QY 9 PPSQPSRANGINILGPSANPNARPTDFDLKVIKGNVGVKVLAKRSGDGAFAVAVKVLQK 68  
Db 73 PPSPPSPSQ-QINLGSSNPHAKPSDFHFLKVIKGSFGKVLARHAKAEVFAVAVKVLQK 131  
QY 69 KSLKKNQNHMAERNVLLKNVRHPLVGLRYSFQTPKLYFLVDYVNGGELFFHLORE 128  
Db 132 KALKKKEKHMSERNVLLKNVHPFLVGLHFSFQADKLYFLVDYINGGELFFHLORE 191  
QY 129 RRELEPRARYTAEVASAIYHLSNLIYRDLPENILLDCQGHVLTDFGLCKECVEPE 188  
Db 192 RCLEPRARYAEIASALGYLHSLNIVYRDLPENILLDSQGHIVLTDFGLCKENIEHN 251  
QY 189 ETTSTFCGTPPEYLAPEVLKRPYDRAVDWMCGLGAVLYEMLHGLPPFFNTDVAQMYENILH 248  
Db 252 GTTSTFCGTPPEYLAPEVLKRPYDRTVDWMCGLGAVLYEMLYGLPPFSYRNTAEYDNLN 311  
QY 249 QPLQIPGGRTVACDLLOGLLHKQORLGSKEDFLDIKNHMFSPINWDDLYHKRLTTP 308  
Db 312 KPLQLK-NITNSARHLEGLLQKDRKRLGAKDDFMEIKSHIFFSLINWDDLINKKITTP 370  
QY 309 FNPVNEGPAADLKHFDEFTQEAYSKISGCTPTDV---ASSSGASSAFLGFSYAQDDDDIL 365  
Db 371 FNPVSGPSDLRHDFDEFTPEEPVSSIGRSPDSILVTASVKAAEAFLGFSYAPPMDSFL 430

RESULT 6  
US-09-111-444-9  
Sequence 9, Application US/09111444  
Patent No. 6045792  
GENERAL INFORMATION:  
APPLICANT: Au-Young, Janice  
APPLICANT: Guegler, Karl J.  
APPLICANT: Hawkins, Phillip R.  
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/111,444

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/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/712,709
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0118 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 430 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 294637
/
US-09-111-444-9
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Query Match 70.5%; Score 1380.5; DB 2; Length 430;
Best Local Similarity 71.1%; Pred. No. 4.1e-126;
Matches 256; Conservative 53; Mismatches 46; Indels 5; Gaps 3;

QY 9 PSPQSRANGNINLGSANPNARPTDFDLKVGKGNKYLAKRKSDFYAVKVLQK 68
DB 73 PSPSPSPSQ-QINLGSSNPHAKPSDFHLKVGKSGFKVLLARHKAEEAFYAVKVLQK 131
QY 69 KSILKNKEQHIMAEARNVLLKNVRHPLVGLRYSPQTPEKLYFVLDYVNGGELFFHLORE 128
DB 132 KAILKKKEKHIMSERNVLLKNVHPFLVGLHFSQTDADKLYFVLDYINGGELFFHLORE 191
QY 129 RFLPRARFYTAESAIGYLHSLNIIVRDLPENILLDCQGHVLTDFGLCKECVEPE 188
DB 192 RCFLEPRARFYAAETASALGYLHSLNIIVRDLPENILLDSQGHIVLTDFGLCKENIEHN 251
QY 189 ETTSTFCGTPEYLAPEVLKPEYDRAVDWCLGAVLYEMLHGLPPFFNTDVAQMYENILH 248
DB 252 GTTSTFCGTPEYLAPEVLKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMVDNINL 311
QY 249 QPLQIPGGRTVAACDLQGLLHKQORLGSKEDEFLDIKNHMFPSINWDDLHYKRLTTP 308
DB 312 KPLQLK-NITNSARHLLEGLLQKRTKRLGAKDDFMEIKSHIFFSLINWDDLINKKITPP 370
QY 309 FNPVNEGADLKHFDPEFTQEAIVSKSIGCTPPTV---ASSSGASSAFLGFSVAQDDDDIL 365
DB 371 FNPVSGPSDLRHFDEFTPEEPVPSSIGRSPSILVTASVKEAAEAFLGFSYAPPMDSFL 430
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RESULT 7
US-09-541-228-9
/ Sequence 9, Application US/09541228
/ Patent No. 6232077
/ GENERAL INFORMATION:
/ APPLICANT: Au-Young, Janice
/ APPLICANT: Guegler, Karl J.
/ APPLICANT: Hawkins, Phillip R.
/ TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
/ NUMBER OF SEQUENCES: 9
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: U.S.
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
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/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/541,228
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/712,709
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0118 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 430 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 294637
/
US-09-541-228-9

Query Match 70.5%; Score 1380.5; DB 2; Length 430;
Best Local Similarity 71.1%; Pred. No. 4.1e-126;
Matches 256; Conservative 53; Mismatches 46; Indels 5; Gaps 3;

QY 9 PSPQSRANGNINLGSANPNARPTDFDLKVGKGNKYLAKRKSDFYAVKVLQK 68
DB 73 PSPSPSPSQ-QINLGSSNPHAKPSDFHLKVGKSGFKVLLARHKAEEAFYAVKVLQK 131
QY 69 KSILKNKEQHIMAEARNVLLKNVRHPLVGLRYSPQTPEKLYFVLDYVNGGELFFHLORE 128
DB 132 KAILKKKEKHIMSERNVLLKNVHPFLVGLHFSQTDADKLYFVLDYINGGELFFHLORE 191
QY 129 RFLPRARFYTAESAIGYLHSLNIIVRDLPENILLDCQGHVLTDFGLCKECVEPE 188
DB 192 RCFLEPRARFYAAETASALGYLHSLNIIVRDLPENILLDSQGHIVLTDFGLCKENIEHN 251
QY 189 ETTSTFCGTPEYLAPEVLKPEYDRAVDWCLGAVLYEMLHGLPPFFNTDVAQMYENILH 248
DB 252 GTTSTFCGTPEYLAPEVLKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMVDNINL 311
QY 249 QPLQIPGGRTVAACDLQGLLHKQORLGSKEDEFLDIKNHMFPSINWDDLHYKRLTTP 308
DB 312 KPLQLK-NITNSARHLLEGLLQKRTKRLGAKDDFMEIKSHIFFSLINWDDLINKKITPP 370
QY 309 FNPVNEGADLKHFDPEFTQEAIVSKSIGCTPPTV---ASSSGASSAFLGFSVAQDDDDIL 365
DB 371 FNPVSGPSDLRHFDEFTPEEPVPSSIGRSPSILVTASVKEAAEAFLGFSYAPPMDSFL 430
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RESULT 8
US-08-712-709-5
/ Sequence 5, Application US/08712709
/ Patent No. 5863780
/ GENERAL INFORMATION:
/ APPLICANT: Au-Young, Janice
/ APPLICANT: Guegler, Karl J.
/ APPLICANT: Hawkins, Phillip R.
/ TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
/ NUMBER OF SEQUENCES: 9
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: U.S.
/ ZIP: 94304
/ COMPUTER READABLE FORM:
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MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/712,709  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PP-0118 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 431 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE: Consensus  
US-08-712-709-5

Query Match 70.4%; Score 1379; DB 1; Length 431;  
Best Local Similarity 70.8%; Pred. No. 5.7e-126;  
Matches 255; Conservative 51; Mismatches 50; Indels 4; Gaps 2;  
QY 9 PPSQPSRANGNINLGSANPNARPTDFLKVIGKNGYKVLAKRSDGAFYAVKVLQK 68  
DB 73 PPSPPSPSQ-QINLGPSSNPHAKPSDFHLKVIGKSGFGKVLARHKAEEVFYAVKVLQK 131  
QY 69 KSLTKNKEQNHMAERNVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGELFFHLORE 128  
DB 132 KALKKKEKHIMSERVLLKNVHPFLVGLHFSFQTDKLYFVLDYINGGELFYHLORE 191  
QY 129 RRFLEPRARFYTAEVASAIYGLHSLNIIYRDLPENILLDCQGHVLTDFGLCKECVEPE 198  
DB 192 RCFLEPRARSYAEIASALYGLHSLNIVYRDLPENILLDSQGHIVLTDGFCCKENIEHN 251  
QY 189 ETTSTFCGTPYLAPEVLKPEYDRAVDMWCLGAVLYEMLHGLPPFFNTDVAQMYENILH 248  
DB 252 STTSTFCGTPYLAPEVLKPEYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNILN 311  
QY 249 OPLQIPGGRTVAACDLLOGLLHKQORLGSKEDFLDIKNHMFSPINWDDLYHKRLTTP 308  
DB 312 KPLQLKPNITNSARHLLGLLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLINKKITPP 371  
QY 309 FNPVNEGPDADLKHFDPEFTQEAIVSKSIGCTPDTV---ASSSGASSAFLGFSYAQDDDDIL 365  
DB 372 FNPVNSGPNDRHFDPEFTPEEPVNSIGKSPSVLVTASVKEAAEAFLGFSYAPPTDSDL 431

RESULT 9  
US-09-111-444-5  
Sequence 5, Application US/09111444  
Patent No. 6045792  
GENERAL INFORMATION:  
APPLICANT: Au-Young, Janice  
APPLICANT: Guegler, Karl J.  
APPLICANT: Hawkins, Phillip R.  
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/111,444  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/712,709  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PP-0118 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 431 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: Consensus  
US-09-111-444-5

Query Match 70.4%; Score 1379; DB 2; Length 431;  
Best Local Similarity 70.8%; Pred. No. 5.7e-126;  
Matches 255; Conservative 51; Mismatches 50; Indels 4; Gaps 2;  
QY 9 PPSQPSRANGNINLGSANPNARPTDFLKVIGKNGYKVLAKRSDGAFYAVKVLQK 68  
DB 73 PPSPPSPSQ-QINLGPSSNPHAKPSDFHLKVIGKSGFGKVLARHKAEEVFYAVKVLQK 131  
QY 69 KSLTKNKEQNHMAERNVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGELFFHLORE 128  
DB 132 KALKKKEKHIMSERVLLKNVHPFLVGLHFSFQTDKLYFVLDYINGGELFYHLORE 191  
QY 129 RRFLEPRARFYTAEVASAIYGLHSLNIIYRDLPENILLDCQGHVLTDFGLCKECVEPE 198  
DB 192 RCFLEPRARSYAEIASALYGLHSLNIVYRDLPENILLDSQGHIVLTDGFCCKENIEHN 251  
QY 189 ETTSTFCGTPYLAPEVLKPEYDRAVDMWCLGAVLYEMLHGLPPFFNTDVAQMYENILH 248  
DB 252 STTSTFCGTPYLAPEVLKPEYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNILN 311  
QY 249 OPLQIPGGRTVAACDLLOGLLHKQORLGSKEDFLDIKNHMFSPINWDDLYHKRLTTP 308  
DB 312 KPLQLKPNITNSARHLLGLLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLINKKITPP 371  
QY 309 FNPVNEGPDADLKHFDPEFTQEAIVSKSIGCTPDTV---ASSSGASSAFLGFSYAQDDDDIL 365  
DB 372 FNPVNSGPNDRHFDPEFTPEEPVNSIGKSPSVLVTASVKEAAEAFLGFSYAPPTDSDL 431

RESULT 10  
US-09-541-228-5  
Sequence 5, Application US/09541228  
Patent No. 6232077  
GENERAL INFORMATION:  
APPLICANT: Au-Young, Janice  
APPLICANT: Guegler, Karl J.  
APPLICANT: Hawkins, Phillip R.  
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA

; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/541,228
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/712,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 431 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
;
US-09-541-228-5

Query Match 70.4%; Score 1379; DB 2; Length 431;
Best Local Similarity 70.8%; Pred. No. 5.7e-126;
Matches 255; Conservative 51; Mismatches 50; Indels 4; Gaps 2;

QY 9 PSPQSRANGNTNLGSPANPNARPTDFELKVTIGKNGYKVLAKKSDGAFYAVKVLQK 68
DB 73 PSPSPSQ-QNLGSPSPHAKPSDFELKVTIGKSGFGKVLARHAKBEVFYAVKVLQK 131
QY 69 KSLKNKEQHMAERNVLLKNVRHPPFLVGLRYSFQTPPEKLYFVLDYVNGGELFFHLQRE 128
DB 132 KAILKKKEKHMSERNVLLKNVKHPPFLVGLHESFQTADKLYFVLDYINGGELFYHLQRE 191
QY 129 RPLPRAPRYAEVASAIGYLHSLNIIVRDLPKPNILDCQGHVVLTDGFLCKECVPE 188
DB 192 RCFLEPRARSYAETAASALGYLHSLNIIVRDLPKPNILDSOCHI VLTDFGLCKENIEHN 251
QY 189 ETTSTFCGTPPEYLAPEVLKPEYDRAVDWMLGAVLYEMLHGLPPFNTDVAQMYENILH 248
DB 252 STTSTFCGTPPEYLAPEVLKHPQYDRTVDWMLGAVLYEMLYGLPPPYSRNTAEYDNIILN 311
QY 249 QPLQIPGGRVTAACDLLOGLLHKDQRLGSKEDFLDIKNHMPFSPINWDDLHYKRLTTP 308
DB 312 KPQLKPNITNSARHLEGLLQKRTKRLGAKDDFWEIKSHVFFSLINWDDLINKKITPP 371
QY 309 FNPVNGPADLKHDFEPTQEAHSVIGCTPTDV-----ASSSGASSAFLGFSYAQDDDDIL 365
DB 372 FNPVNSGPNDLRHFDFEPTQEAHSVIGKSPSVLVTASVKEAAEAFLGFSYAPPTDSEL 431

RESULT 11
US-09-771-161A-246
; Sequence 246, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 246
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-771-161A-246

Query Match 44.1%; Score 863; DB 2; Length 479;
Best Local Similarity 48.4%; Pred. No. 1.5e-75;
Matches 171; Conservative 53; Mismatches 107; Indels 22; Gaps 5;

QY 18 GNINLGPSANPNARPT--DFDFLKVIGKNGYKVLAKKSDGAFYAVKVLQKKSILKNK 75
DB 129 GEEEMDASTTHHKRKTMDNDFYLLKLGKTFCKVILVREKASGYVAMKILKEVIIAKD 188
QY 76 EQNHMAERNVLLKNVRHPPFLVGLRYSFQTPPEKLYFVLDYVNGGELFFHLQERRFLRPR 135
DB 189 EVAHTLTESRV-LKNTRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSERVFSEDR 247
QY 136 ARFYTAEVASAIGYLHSLNIIVRDLPKPNILDCQGHVVLTDGFLCKECVPEETTSTFC 195
DB 248 TRFYGAEIVSAUDYLHSGKIVYRDLPKPNILDCQGHVVLTDGFLCKEGITDAATWKTF 307
QY 196 GTPEYLAPEVLKPEYDRAVDWMLGAVLYEMLHGLPPFNTDVAQMYENILHQLQIPG 255
DB 308 GTPEYLAPEVLDEDNDYGRAVDWMLGAVLYEMLHGLPPFNTDVAQMYENILHQLQIPG 367
QY 256 GRTVAACDLLOGLLHKDQRL--GSKEDFLDIKNHMPFSPINWDDLHYKRLTTPPNPNV 314
DB 368 TLSSDAKSLLSGLLIKDPNKRILGGGPDDAKEIMRHSFFSGVNMQVDYDKLVPPPKPQVT 427
QY 315 GPADLKHDFEPTQEAHSVIGCTPTDVASSSGASSAFLGFSYAQDDDDILDS 367
DB 428 SETDTRYFDEEPT---AQTTITITPE-----KYDEGDMCDMN 462

RESULT 12
US-09-771-161A-247
; Sequence 247, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-771-161A-247

Query Match 44.1%; Score 863; DB 2; Length 479;
Best Local Similarity 48.4%; Pred. No. 1.5e-75;
Matches 171; Conservative 53; Mismatches 107; Indels 22; Gaps 5;

QY 18 GNINLGPSANPNARPT--DFDFLKVIGKNGYKVLAKKSDGAFYAVKVLQKKSILKNK 75
DB 129 GEEEMDASTTHHKRKTMDNDFYLLKLGKTFCKVILVREKASGYVAMKILKEVIIAKD 188

QY 76 EQNHMAERNVLLKNVRHPLVGLRYVSFQTPKLYFVLDYVNGGELFFHLQRRERFLEPR 135  
Db 189 EVAHTLTESRV-LKNTRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLRSRVSSEDR 247  
QY 136 ARFYTAESAIGVLSHNLIIYRDLKPNILLDCQGHVLTDFGLCKECVEPETTSTFC 195  
Db 248 TRFYGAIEVSALDYLSHGKIVYRDLKLENMLDKDGHKIKITDFGLCKEGITDAATWKTF 307  
QY 196 GTPYLAPEVLKPEYDRAVDMWCLGAVLYEMLHGLPPFFNTDVAQMYENILHQPLOIPG 255  
Db 308 GTPYLAPEVLEDNDYGRAVDMWGLGVVMYEMCGRLPFYNQDHEKLFELILMEDIKFPR 367  
QY 256 GRTVAACDLLOGLLHKDQORL-GSKEDFLDIKNHMFSPINWDDLYHKRLTPFPNPV 314  
Db 368 TLSSDAKSLLSGLLIKDPNKRLLGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPPKPQVT 427  
QY 315 GPADLKHDFEPTQEAHSVKSIGCTPTDVASSGSAFLGFSYAQDDDDILDS 367  
Db 428 SETDTRYFDEEFT---AQITITTPPE-----KYDEBGMDCMDN 462

RESULT 13  
US-09-771-161A-248  
; Sequence 248, Application US/09771161A  
; Patent No. 6936450  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 248  
; LENGTH: 479  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-771-161A-248

Query Match 44.1%; Score 863; DB 2; Length 479;  
Best Local Similarity 48.4%; Pred. No. 1.5e-75;  
Matches 171; Conservative 53; Mismatches 107; Indels 22; Gaps 5;

QY 18 GNINLGPSANPNARPT--DFDFLKIVGKGNKYGVLLAKRKSDFGAFYAVKVLQKKSILKNK 75  
Db 129 GEEEMDASTTHHKRTMNDFDYLLKLGKTFGKVLVREKASGKYVAMKILKEVIK 188  
QY 76 EQNHMAERNVLLKNVRHPLVGLRYVSFQTPKLYFVLDYVNGGELFFHLQRRERFLEPR 135  
Db 189 EVAHTLTESRV-LKNTRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLRSRVSSEDR 247  
QY 136 ARFYTAESAIGVLSHNLIIYRDLKPNILLDCQGHVLTDFGLCKECVEPETTSTFC 195  
Db 248 TRFYGAIEVSALDYLSHGKIVYRDLKLENMLDKDGHKIKITDFGLCKEGITDAATWKTF 307  
QY 196 GTPYLAPEVLKPEYDRAVDMWCLGAVLYEMLHGLPPFFNTDVAQMYENILHQPLOIPG 255  
Db 308 GTPYLAPEVLEDNDYGRAVDMWGLGVVMYEMCGRLPFYNQDHEKLFELILMEDIKFPR 367  
QY 256 GRTVAACDLLOGLLHKDQORL-GSKEDFLDIKNHMFSPINWDDLYHKRLTPFPNPV 314  
Db 368 TLSSDAKSLLSGLLIKDPNKRLLGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPPKPQVT 427  
QY 315 GPADLKHDFEPTQEAHSVKSIGCTPTDVASSGSAFLGFSYAQDDDDILDS 367  
Db 428 SETDTRYFDEEFT---AQITITTPPE-----KYDEBGMDCMDN 462

RESULT 14  
US-09-526-043-2  
; Sequence 2, Application US/09526043  
; Patent No. 6881555  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Kun  
; APPLICANT: Pagnoni, Marco  
; APPLICANT: Clark, Kenneth  
; APPLICANT: Ivashchenko, Yuri  
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF  
; FILE REFERENCE: A3278A-US  
; CURRENT APPLICATION NUMBER: US/09/526,043  
; CURRENT FILING DATE: 2000-03-14  
; EARLIER APPLICATION NUMBER: 60/125,108  
; EARLIER FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 465  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-526-043-2

Query Match 43.9%; Score 860; DB 2; Length 465;  
Best Local Similarity 51.6%; Pred. No. 2.8e-75;  
Matches 164; Conservative 50; Mismatches 100; Indels 4; Gaps 3;

QY 18 GNINLGPSANPNARPT--DFDFLKIVGKGNKYGVLLAKRKSDFGAFYAVKVLQKKSILKNK 75  
Db 129 GEEEMDASTTHHKRTMNDFDYLLKLGKTFGKVLVREKASGKYVAMKILKEVIK 188  
QY 76 EQNHMAERNVLLKNVRHPLVGLRYVSFQTPKLYFVLDYVNGGELFFHLQRRERFLEPR 135  
Db 189 EVAHTLTESRV-LKNTRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLRSRVSSEDR 247  
QY 136 ARFYTAESAIGVLSHNLIIYRDLKPNILLDCQGHVLTDFGLCKECVEPETTSTFC 195  
Db 248 TRFYGAIEVSALDYLSHGKIVYRDLKLENMLDKDGHKIKITDFGLCKEGITDAATWKTF 307  
QY 196 GTPYLAPEVLKPEYDRAVDMWCLGAVLYEMLHGLPPFFNTDVAQMYENILHQPLOIPG 255  
Db 308 GTPYLAPEVLEDNDYGRAVDMWGLGVVMYEMCGRLPFYNQDHEKLFELILMEDIKFPR 367  
QY 256 GRTVAACDLLOGLLHKDQORL-GSKEDFLDIKNHMFSPINWDDLYHKRLTPFPNPV 314  
Db 368 TLSSDAKSLLSGLLIKDPNKRLLGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPPKPQVT 427  
QY 315 GPADLKHDFEPTQEAHSVKSIGCTPTDVASSGSAFLGFSYAQDDDDILDS 367  
Db 428 SETDTRYFDEEFT---AQITITTPPE-----KYDEBGMDCMDN 462

RESULT 15  
US-09-526-043-17  
; Sequence 17, Application US/09526043  
; Patent No. 6881555  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Kun  
; APPLICANT: Pagnoni, Marco  
; APPLICANT: Clark, Kenneth  
; APPLICANT: Ivashchenko, Yuri  
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF  
; FILE REFERENCE: A3278A-US  
; CURRENT APPLICATION NUMBER: US/09/526,043  
; CURRENT FILING DATE: 2000-03-14  
; EARLIER APPLICATION NUMBER: 60/125,108  
; EARLIER FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 454  
; TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-09-526-043-17

Query Match      43.8%; Score 858; DB 2; Length 454;
Best Local Similarity 51.6%; Pred. No. 4.2e-75;
Matches 164; Conservative 50; Mismatches 100; Indels 4; Gaps 3;

Qy 18 GNINLGPSANPNARPT--DFDFLKVIKGNYGKVKLLAKRKSDGAFYAVKVLQKKSLKNK 75
Db | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
129 GEEEMDASTTHHKRKTMDFDYLLKLGKGTFGKVLVREKASGKYAMKILKEVIIAKD 188
Qy 76 EQNHMAERNVLLKNVRHPLVGLRYSFQTPEKLYFVLDYNGGELFFHLQRRRLEPR 135
Db | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
189 EVAHTLTESRV-LKNTRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLRERVSEDR 247
Qy 136 ARFYTAEVASAGYLHSLNIIVRDLPENILLDCQGHVLTDFGLCKECVEPEETTSTFC 195
Db | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
248 TRFYGAEIVSALDYLHSGKIVYRDLEKLEMLDKOGHIKITDFGLCKEGITDAATWKTC 307
Qy 196 GTPPYLAPEYLKPEYDRAVDMMCLGAVLYEMLHGLPPFFNTDVAQMYENILHQLQIPG 255
Db | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
308 GTPPYLAPEVLENDYGRAVDMMGLGVVMYEMWCGRLPFYNQDHEKLFELILMEDIKFPR 367
Qy 256 GRTVAACDLLQGLLHKQORQL-GSKEDFLDIKNHMFSPINWDDLYHKRLTPPPNPVE 314
Db | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
368 TLSSDAKSLLSGLLIKDPNKRLLGGPDPKEMRHSFFSGVNMQDVYDKKLVPPPKPQVT 427
Qy 315 GPADLKHFDPEFTOEAVS 332
Db | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
428 SETDTRYFDEEFTAQIT 445
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Search completed: January 27, 2006, 23:33:30  
Job time : 18.3113 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:31:20 ; Search time 64.3981 Seconds  
(without alignments)  
2381.178 Million cell updates/sec

Title: US-09-868-131A-3  
Perfect score: 1959  
Sequence: 1 MASSPVGVSPQPSRANGNI.....ASSAFLGFSYAQDDDLDS 367

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_Main:\*

- 1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1848	94.3	367	3	US-09-971-118-2
2	1848	94.3	367	4	US-10-291-172-256
3	1848	94.3	367	4	US-10-429-160-52
4	1848	94.3	367	4	US-10-221-278-256
5	1848	94.3	367	4	US-10-380-235-6
6	1848	94.3	382	4	US-10-296-115-1109
7	1848	94.3	396	5	US-10-526-543-83
8	1848	94.3	427	5	US-10-753-267-126
9	1674.5	85.5	398	4	US-10-262-511-140
10	1387	70.8	388	4	US-10-131-410-104
11	1387	70.8	407	4	US-10-067-977-4
12	1387	70.8	407	4	US-10-827-272-4
13	1387	70.8	431	3	US-09-981-353-7
14	1387	70.8	431	4	US-10-403-161-2
15	1387	70.8	431	4	US-10-403-161-2
16	1387	70.8	445	4	US-10-067-977-2
17	1387	70.8	445	4	US-10-827-272-2
18	1387	70.8	526	4	US-10-094-749-1861
19	1383	70.6	431	4	US-10-000-039-2
20	1383	70.6	431	4	US-10-353-690-12
21	1383	70.6	431	5	US-10-756-149-5279
22	1383	70.6	431	6	US-11-044-570-2
23	1381.5	70.5	594	5	US-10-732-923-10768
24	1380.5	70.5	430	3	US-09-810-808-9
25	1379	70.4	431	3	US-09-810-808-9
26	1377.5	70.3	433	5	US-10-732-923-10767
27	1325.5	67.7	340	4	US-10-217-555-17

28	1325.5	67.7	340	4	US-10-217-555-17	Sequence 17, Appl
29	1297.5	66.2	429	4	US-10-295-027-116	Sequence 116, Appl
30	1297.5	66.2	496	3	US-09-784-249-2	Sequence 2, Appli
31	1297.5	66.2	496	3	US-09-764-875-746	Sequence 746, App
32	1297.5	66.2	496	3	US-09-764-875-900	Sequence 900, Appl
33	1297.5	66.2	496	5	US-10-737-450-4	Sequence 4, Appli
34	1286.5	65.7	496	4	US-10-755-889-42	Sequence 42, Appl
35	1141.5	58.3	308	4	US-10-664-421-85	Sequence 85, Appl
36	1141.5	58.3	308	5	US-10-941-635-85	Sequence 85, Appl
37	981	50.1	422	4	US-10-369-493-7027	Sequence 7027, Ap
38	863	44.1	479	3	US-09-771-161A-246	Sequence 246, App
39	863	44.1	479	3	US-09-771-161A-247	Sequence 247, App
40	863	44.1	479	3	US-09-771-161A-248	Sequence 248, App
41	863	44.1	479	4	US-10-394-322A-3	Sequence 3, Appli
42	863	44.1	479	4	US-10-217-574-33	Sequence 33, Appl
43	863	44.1	479	4	US-10-217-555-33	Sequence 33, Appl
44	863	44.1	479	5	US-10-753-267-108	Sequence 108, App
45	860	43.9	465	3	US-09-526-043-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-971-118-2  
; Sequence 2, Application US/09971118  
; Patent No. US20020123056A1  
; GENERAL INFORMATION:  
; APPLICANT: DELANEY, ALLEN  
; APPLICANT: YOGANATHAN, THILLAINATHAN  
; TITLE OF INVENTION: SGK2 AND ITS USES  
; FILE REFERENCE: KINE025CIP  
; CURRENT APPLICATION NUMBER: US/09/971,118  
; CURRENT FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: PCT/US01/21479  
; PRIOR FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/237,419  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 367  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-971-118-2

Query Match	94.3%;	Score	1848;	DB	3;	Length	367;
Best Local Similarity	94.3%;	Pred. No.	4.8e-140;				
Matches	345;	Conservative	10;	Mismatches	11;	Indels	0;
		Gaps	0;				
QY	1	MASSPVGVSPQPSRANGNINILGPSANPNARPTDPLKVIKGNKGVLLAKRSDGAF	60				
Db	1	MSSSAGTSPQPSRANGNINILGPSANPNARPTDPLKVIKGNKGVLLAKRSDGAF	60				
QY	61	YAVKVLQKKSILKNEQNHMAERNVLLKNVRHPLVGLRYSFQTEPKLYFVLDDYNGGE	120				
Db	61	YAVKVLQKKSILKKEQSHMAERSVLLKNVRHPLVGLRYSFQTEPKLYFVLDDYNGGE	120				
QY	121	LFPHLQRRRFLPRARFYTAASVAGYLSLNIYYRLKPNILLDCQGHVLTDFGL	180				
Db	121	LFPHLQRRRFLPRARFYTAASVAGYLSLNIYYRLKPNILLDCQGHVLTDFGL	180				
QY	181	CKECVEPETTTCGTPPEYLAPEVLKPEYDRAVDWMCIGAVLYEMLHGLPPFFNTDVA	240				
Db	181	CKECVEPETTTCGTPPEYLAPEVLKPEYDRAVDWMCIGAVLYEMLHGLPPFFNTDVA	240				
QY	241	QMYENILHOPLOIPGGRTVAACDLQLGLHKDQORLGSKEPDFLDIKNHMFSPINWDDL	300				
Db	241	QMYENILHOPLOIPGGRTVAACDLQLGLHKDQORLGSKEPDFLDIKNHMFSPINWDDL	300				
QY	301	YHKRLTTPPNPNVEGPAULKHPDPTQBAVSKSIGCTPDTVAASSGASSAFILGFSYAQD	360				
Db	301	YHKRLTTPPNPNVEGPAULKHPDPTQBAVSKSIGCTPDTVAASSGASSAFILGFSYAQD	360				

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QY 361 DDILD 366
DB 361 DDILD 366

RESULT 2
US-10-291-172-256
; Sequence 256, Application US/10291172
; Publication No. US20030228584A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/291,172
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 256
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-172-256

Query Match 94.3%; Score 1848; DB 4; Length 367;
Best Local Similarity 94.3%; Pred. No. 4.8e-140;
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MASSPVGVSPQPSRANGINILGPSANPNARPTDFDLKVIKGNVGVKLLAKRKS DGAF 60
DB 1 MNSSPAGTFSPQPSRANGINILGPSANPNARPTDFDLKVIKGNVGVKLLAKRKS DGAF 60
QY 61 YAVKVLQKKSILKNKEQHMAERNVLLKNVRHPPFLVGLRYSFQTPEKLYFVLDYVNGGE 120
DB 61 YAVKVLQKKSILKKKEQSHMAERSVLLKNVRHPPFLVGLRYSFQTPEKLYFVLDYVNGGE 120
QY 121 LFFHLQRRERFLEPRARFYTAEVASAIGYLHSLNIYRDLKPENILLDCQGHVLTDFGL 180
DB 121 LFFHLQRRERFLEPRARFYTAEVASAIGYLHSLNIYRDLKPENILLDCQGHVLTDFGL 180
QY 181 CKECVEPEETSTFCGTPPEYLAPEVLKPEPYDRAVDWCLGAVLYEMLHGLPPFNTDVA 240
DB 181 CKEGVEPEDTSTFCGTPPEYLAPEVLKPEPYDRAVDWCLGAVLYEMLHGLPPFYSQDVS 240
QY 241 QMYENILHQLQIPGGRTVAAACDLLQGLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 300
DB 241 QMYENILHQLQIPGGRTVAAACDLLQGLLHKDQRLGSKADFLBKHNHVFSPINWDDL 300
QY 301 YHKRLTPPNPNVEGPADLKHDPFTQEAHSVSKSIGCTPDTVASSSGASSAFLGFSYAQD 360
DB 301 YHKRLTPPNPNVTGPADLKHDPFTQEAHSVSKSIGCTPDTVASSSGASSAFLGFSYAPE 360
QY 361 DDILD 366
DB 361 DDILD 366

RESULT 3
US-10-429-160-52
; Sequence 52, Application US/10429160
; Publication No. US20040023276A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Teresa R
; APPLICANT: Mao, Mao
; APPLICANT: Linsley, Peter S
; APPLICANT: Lund, Lund
; TITLE OF INVENTION: LXR Ligand Induced Genes and Proteins
; FILE REFERENCE: RS0200
; CURRENT APPLICATION NUMBER: US/10/429,160
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/377,714
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-160-52

Query Match 94.3%; Score 1848; DB 4; Length 367;
Best Local Similarity 94.3%; Pred. No. 4.8e-140;
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MASSPVGVSPQPSRANGINILGPSANPNARPTDFDLKVIKGNVGVKLLAKRKS DGAF 60
DB 1 MNSSPAGTFSPQPSRANGINILGPSANPNARPTDFDLKVIKGNVGVKLLAKRKS DGAF 60
QY 61 YAVKVLQKKSILKNKEQHMAERNVLLKNVRHPPFLVGLRYSFQTPEKLYFVLDYVNGGE 120
DB 61 YAVKVLQKKSILKKKEQSHMAERSVLLKNVRHPPFLVGLRYSFQTPEKLYFVLDYVNGGE 120
QY 121 LFFHLQRRERFLEPRARFYTAEVASAIGYLHSLNIYRDLKPENILLDCQGHVLTDFGL 180
DB 121 LFFHLQRRERFLEPRARFYTAEVASAIGYLHSLNIYRDLKPENILLDCQGHVLTDFGL 180
QY 181 CKECVEPEETSTFCGTPPEYLAPEVLKPEPYDRAVDWCLGAVLYEMLHGLPPFNTDVA 240
DB 181 CKEGVEPEDTSTFCGTPPEYLAPEVLKPEPYDRAVDWCLGAVLYEMLHGLPPFYSQDVS 240
QY 241 QMYENILHQLQIPGGRTVAAACDLLQGLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 300
DB 241 QMYENILHQLQIPGGRTVAAACDLLQGLLHKDQRLGSKADFLBKHNHVFSPINWDDL 300
QY 301 YHKRLTPPNPNVEGPADLKHDPFTQEAHSVSKSIGCTPDTVASSSGASSAFLGFSYAQD 360
DB 301 YHKRLTPPNPNVTGPADLKHDPFTQEAHSVSKSIGCTPDTVASSSGASSAFLGFSYAPE 360
QY 361 DDILD 366
DB 361 DDILD 366
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QY 241 OMZENILHQPLOIPGGRVVAACDLLOGLLHKDQORLQSGKEDFLDIKXHMFFSPINWDDL 300
Db 256 OMZENILHQPLOIPGGRVVAACDLQSLHKDQORLQSGKADFLKIKHVFVFPINWDDL 315
QY 301 YHKRLTPFPNPNVEGPADLKHFDPBFTQEAUVSKSIGCTPDTVAASSGGASSAFLGFSYAQD 360
Db 316 YHKRLTPFPNPNVVTGPADLKHFDPBFTQEAUVSKSIGCTPDTVAASSGGASSAFLGFSYAPE 375
QY 361 DDDILD 366
Db 376 DDDILD 381

RESULT 7
US-10-926-543-83
; Sequence 83, Application US/10926543
; Publication No. US20050048589A1
; GENERAL INFORMATION:
; APPLICANT: Jendoubt, Moncef
; TITLE OF INVENTION: LUNG CANCER SPECIFIC GENE PRODUCTS: THEIR CODING SEQUENCES
; TITLE OF INVENTION: ANTIBODIES AND THEIR USE IN DIAGNOSTIC, THERAPEUTIC AND
; TITLE OF INVENTION: MANAGEMENT OF LUNG CANCER
; FILE REFERENCE: 705403.4004
; CURRENT APPLICATION NUMBER: US/10/926,543
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: US 60/497,790
; PRIOR FILING DATE: 2003-08-25
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 83
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-926-543-83

```

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1  / APPLICANT: Millennium Pharmaceuticals, Inc.
2  / APPLICANT: Stagliano, Nancy E.
3  / APPLICANT: Healy, Aileen
4  / APPLICANT: Acton, Susan L.
5  / APPLICANT: Galvin, Katherine M.
6  / APPLICANT: Donoghue, Mary A.
7  / APPLICANT: Rodrigue-Way, Amelie
8  / APPLICANT: Tomlinson, James E.
9  / TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
10 / TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553.
11 / TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,
12 / TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701,
13 / TITLE OF INVENTION: 3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 33770,
14 / TITLE OF INVENTION: 9380, 2569654, 33556, 53656, 44143, 32612, 10671, 261,
15 / TITLE OF INVENTION: 4370, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955,
16 / TITLE OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408,
17 / TITLE OF INVENTION: 42028, 112091, 13886, 13942, 1673, 54946 OR 2419
18 / FILE REFERENCE: MPI03-003PIRNM0TM
19 / CURRENT APPLICATION NUMBER: US/10/753,267
20 / CURRENT FILING DATE: 2004-01-08
21 / PRIOR APPLICATION NUMBER: US 60/439,683
22 / PRIOR FILING DATE: 2003-01-13
23 / PRIOR APPLICATION NUMBER: US 60/445,216
24 / PRIOR FILING DATE: 2003-02-05
25 / PRIOR APPLICATION NUMBER: US 60/448,036
26 / PRIOR FILING DATE: 2003-02-18
27 / PRIOR APPLICATION NUMBER: US 60/454,189
28 / PRIOR FILING DATE: 2003-03-12
29 / PRIOR APPLICATION NUMBER: US 60/457,541
30 / PRIOR FILING DATE: 2003-03-25
31 / PRIOR APPLICATION NUMBER: US 60/466,411
32 / PRIOR FILING DATE: 2003-04-29
33 / PRIOR APPLICATION NUMBER: US 60/469,041
34 / PRIOR FILING DATE: 2003-05-08
35 / PRIOR APPLICATION NUMBER: US 60/477,414
36 / PRIOR FILING DATE: 2003-06-10
37 / PRIOR APPLICATION NUMBER: US 60/478,560
38 / PRIOR FILING DATE: 2003-06-13
39 / PRIOR APPLICATION NUMBER: US 60/489,772
40 / PRIOR FILING DATE: 2003-07-24
41 / Remaining Prior Application data removed - See File Wrapper or PALM.
42 / NUMBER OF SEQ ID NOS: 130
43 / SOFTWARE: FastSeq for Windows Version 4.0
44 / SEQ ID NO 126
45 / LENGTH: 427
46 / TYPE: PRT
47 / ORGANISM: Homo Sapiens
48 / IS-10-753-267-126

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QY 301 YHKLTPPPNPNVEGPADLKHDFEFTQEAUVSKSIGCTPDTVASSSGASSAFILGFSYAQD 360  
Db 361 YHKLTPPPNPNVTGPADLKHDFEFTQEAUVSKSIGCTPDTVASSSGASSAFILGFSYAPE 420  
QY 361 DDDILD 366  
Db 421 DDDILD 426

RESULT 9

US-10-262-511-140  
; Sequence 140, Application US/10262511  
; Publication No. US20040038223A1  
; GENERAL INFORMATION:  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Peyman, John A.  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Ju, Jingfang  
; APPLICANT: Li, Li  
; APPLICANT: Guo, Xiaojia (Sasha)  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Edinger, Shlomik R.  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Ort, Tatiana  
; APPLICANT: Gorman, Linda  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Catterton, Elina  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Stone, David J.  
; APPLICANT: Pena, Carol E. A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Rothenberg, Mark E.  
; APPLICANT: Leach, Martin D.  
; APPLICANT: Agee, Michele L.  
; APPLICANT: Berghs, Constance  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-462C  
; CURRENT APPLICATION NUMBER: US/10/262,511  
; CURRENT FILING DATE: 2003-05-28  
; PRIOR APPLICATION NUMBER: 60/326,483  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: 60/373,815  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: 60/327,917  
; PRIOR FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: 60/381,642  
; PRIOR FILING DATE: 2002-05-17  
; PRIOR APPLICATION NUMBER: 60/328,029  
; PRIOR FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: 60/381,038  
; PRIOR FILING DATE: 2002-05-16  
; PRIOR APPLICATION NUMBER: 60/328,056  
; PRIOR FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: 60/373,260  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: 60/373,826  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: 60/327,435  
; PRIOR FILING DATE: 2001-10-05  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 439  
; SOFTWARE: CuraSequist version 0.1  
; SEQ ID NO 140  
; LENGTH: 398  
; TYPE: PRT

; ORGANISM: Homo sapiens  
US-10-262-511-140  
Query Match 85.5%; Score 1674.5; DB 4; Length 398;  
Best Local Similarity 86.9%; Pred. No. 4.6e-126;  
Matches 318; Conservative 9; Mismatches 10; Indels 29; Gaps 1;  
QY 1 MASSPVGVSPQPSRANGINILGSPANPNARPTDFDLKVIKGNKGVLLAKRKSDGAF 60  
Db 61 MNSSPAGTSPQPSRANGINILGSPANPNARPTDFDLKVIKGNKGVLLAKRKSDGAF 120  
QY 61 YAVKVLQKKSILKNKEQNHMAERNVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGE 120  
Db 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGE 180  
QY 121 LPFHLOERRERLEPRARFYTAEVASAIYGLHSNIIYRDLKPENILLDCQGHVVLTPDGL 180  
Db 181 LPFHLOERRERLEPRARFYAAEVASAIYGLHSNIIYRDLKPENILLDCQ----- 230  
QY 181 CKECVEPEETTTSTFCGTPPEYLAPVLRKEPYDRAVDWVCLGAVLYEMLHGLPFPFNTDVA 240  
Db 231 -----YLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPFPYSQDVS 271  
QY 241 QMYENILHQPLOIPGORTVAACDLLOGLLHKQORQLGSKEDFLDKNHFPPSPINWDDL 300  
Db 272 QMYENILHQPLOIPGORTVAACDLLOGLLHKQORQLGSKADFLKIKNHVFFSPINWDDL 331  
QY 301 YHKRLTPPNPNVVEGPADLKHDFEFTQEAUVSKSIGCTPDTVASSSGASSAFILGFSYAQD 360  
Db 332 YHKRLTPPNPNVTGPADLKHDFEFTQEAUVSKSIGCTPDTVASSSGASSAFILGFSYAPE 391  
QY 361 DDDILD 366  
Db 392 DDDILD 397

RESULT 10

US-10-131-410-104  
; Sequence 104, Application US/10131410  
; Publication No. US20030235915A1  
; GENERAL INFORMATION:  
; APPLICANT: SPECHT, THOMAS  
; APPLICANT: HINZMANN, BERND  
; APPLICANT: SCHMITT, ARMIN  
; APPLICANT: PILARSKY, CHRISTIAN  
; APPLICANT: DAHL, EDGAR  
; APPLICANT: ROSENTHAL, ANDRE  
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST  
; FILE REFERENCE: SCH-1763  
; CURRENT APPLICATION NUMBER: US/10/131,410  
; PRIOR APPLICATION NUMBER: 09/646,673  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: PCT/DE99/00908  
; PRIOR FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 202  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 104  
; LENGTH: 388  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-131-410-104  
Query Match 70.8%; Score 1387; DB 4; Length 388;  
Best Local Similarity 71.1%; Pred. No. 5.4e-103;  
Matches 256; Conservative 51; Mismatches 49; Indels 4; Gaps 2;  
QY 9 BSPQPSRANGINILGSPANPNARPTDFDLKVIKGNKGVLLAKRKSDGAFYAVKVLQK 68  
Db 30 PSPPPSPSQ-QINLGPSPNHPAKPSDFHLKVIKGNKGVLLAKRKAEVFAVKVLQK 88  
QY 69 KSLKNKEQNHMAERNVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGELFFHLORE 128

Db 89 KAILKKKEKHIMSERVLLKNVGFPLVGLHFSFQTADKLYFVLDYINGGELFYHLQRE 148  
QY 129 RRFLEPRARFYTAEVASAIQYLHSLNIIYRDLKPNILLDCQGHVVLTDFGLCKECVEPE 188  
Db 149 RCFLEPRARFYAAETASALGYLHSLNIVYRDLKPNILLDSQGHIVLTDFGLCKENIEHN 208  
QY 189 ETTSTFCGTPYLAPEVLKPEYDRADVWCLGAVLYEMLHGLPPFNTDVAQMYENILH 248  
Db 209 STTSTFCGTPYLAPEVLHQPVDRTVDWCLGAVLYEMLYGLPPFYSRNTAEYDNILN 268  
QY 249 QPLQIPGGRTVAACDLLOGLLHKDQRLGSKEDFLDIKNHMFSPINWDDLYHKRLTTP 308  
Db 269 KPQLQKPNITNSARHLLEGLLQKDRTKRLGAKDDFMEIKSHVFFSLINWDDLLINKKITPP 328  
QY 309 FNPVNEGPGADLKHDFEFTQEAIVSKSIGCTPDTV---ASSSGASSAFLGFSYAQDDDDTL 365  
Db 329 FNPVNSGPNDLRHDFEFTTEEPVPNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSDL 388

RESULT 11  
US-10-067-977-4  
; Sequence 4, Application US/10067977  
; Publication No. US20030157679A1  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Chunhua and KE, Zhaoxi  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001313  
; CURRENT APPLICATION NUMBER: US/10/067,977  
; CURRENT FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 407  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-067-977-4

Query Match 70.8%; Score 1387; DB 4; Length 407;  
Best Local Similarity 71.1%; Pred. No. 5.8e-103;  
Matches 256; Conservative 51; Mismatches 49; Indels 4; Gaps 2;  
QY 9 PSPQPSRANGINLGPSANPNARPTDFDLKVIKGNYGKVLAKRKSDFGAFYAVKVLQK 68  
Db 49 PSPPPSPSQ-QINLGPSSNPHAKPSDFHLKVIKGSFGKVLARHKAEEVFYAVKVLQK 107  
QY 69 KSILKNKEQNHIMAEARNVLLKNVRHPPFLVGLRYSFQTPKLYFVLDYVNGGELFYHLQRE 128  
Db 108 KAILKKKEKHIMSERVLLKNVGFPLVGLHFSFQTADKLYFVLDYINGGELFYHLQRE 167  
QY 129 RRFLEPRARFYTAEVASAIQYLHSLNIIYRDLKPNILLDCQGHVVLTDFGLCKECVEPE 188  
Db 168 RCFLEPRARFYAAETASALGYLHSLNIVYRDLKPNILLDSQGHIVLTDFGLCKENIEHN 227  
QY 189 ETTSTFCGTPYLAPEVLKPEYDRADVWCLGAVLYEMLHGLPPFNTDVAQMYENILH 248  
Db 228 STTSTFCGTPYLAPEVLHQPVDRTVDWCLGAVLYEMLYGLPPFYSRNTAEYDNILN 287  
QY 249 QPLQIPGGRTVAACDLLOGLLHKDQRLGSKEDFLDIKNHMFSPINWDDLYHKRLTTP 308  
Db 288 KPQLQKPNITNSARHLLEGLLQKDRTKRLGAKDDFMEIKSHVFFSLINWDDLLINKKITPP 347  
QY 309 FNPVNEGPGADLKHDFEFTQEAIVSKSIGCTPDTV---ASSSGASSAFLGFSYAQDDDDTL 365  
Db 348 FNPVNSGPNDLRHDFEFTTEEPVPNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSDL 407

RESULT 12  
US-10-827-272-4  
; Sequence 4, Application US/10827272  
; Publication No. US20040203127A1

; GENERAL INFORMATION:  
; APPLICANT: KE, Zhaoxi  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001313-DIV  
; CURRENT APPLICATION NUMBER: US/10/827,272  
; CURRENT FILING DATE: 2004-04-20  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 407  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-827-272-4

Query Match 70.8%; Score 1387; DB 4; Length 407;  
Best Local Similarity 71.1%; Pred. No. 5.8e-103;  
Matches 256; Conservative 51; Mismatches 49; Indels 4; Gaps 2;  
QY 9 PSPQPSRANGINLGPSANPNARPTDFDLKVIKGNYGKVLAKRKSDFGAFYAVKVLQK 68  
Db 49 PSPPPSPSQ-QINLGPSSNPHAKPSDFHLKVIKGSFGKVLARHKAEEVFYAVKVLQK 107  
QY 69 KSILKNKEQNHIMAEARNVLLKNVRHPPFLVGLRYSFQTPKLYFVLDYVNGGELFYHLQRE 128  
Db 108 KAILKKKEKHIMSERVLLKNVGFPLVGLHFSFQTADKLYFVLDYINGGELFYHLQRE 167  
QY 129 RRFLEPRARFYTAEVASAIQYLHSLNIIYRDLKPNILLDCQGHVVLTDFGLCKECVEPE 188  
Db 168 RCFLEPRARFYAAETASALGYLHSLNIVYRDLKPNILLDSQGHIVLTDFGLCKENIEHN 227  
QY 189 ETTSTFCGTPYLAPEVLKPEYDRADVWCLGAVLYEMLHGLPPFNTDVAQMYENILH 248  
Db 228 STTSTFCGTPYLAPEVLHQPVDRTVDWCLGAVLYEMLYGLPPFYSRNTAEYDNILN 287  
QY 249 QPLQIPGGRTVAACDLLOGLLHKDQRLGSKEDFLDIKNHMFSPINWDDLYHKRLTTP 308  
Db 288 KPQLQKPNITNSARHLLEGLLQKDRTKRLGAKDDFMEIKSHVFFSLINWDDLLINKKITPP 347  
QY 309 FNPVNEGPGADLKHDFEFTQEAIVSKSIGCTPDTV---ASSSGASSAFLGFSYAQDDDDTL 365  
Db 348 FNPVNSGPNDLRHDFEFTTEEPVPNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSDL 407

RESULT 13  
US-09-981-353-7  
; Sequence 7, Application US/09981353  
; Patent No. US20020160382A1  
; GENERAL INFORMATION:  
; APPLICANT: Lasek, Amy W.  
; APPLICANT: Jones, David A.  
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER  
; FILE REFERENCE: PA-0039 US  
; CURRENT APPLICATION NUMBER: US/09/981,353  
; CURRENT FILING DATE: 2001-10-11  
; NUMBER OF SEQ ID NOS: 194  
; SOFTWARE: PERL Program  
; SEQ ID NO 7  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20020160382A1 3819039CD1  
US-09-981-353-7

Query Match 70.8%; Score 1387; DB 3; Length 431;  
Best Local Similarity 71.1%; Pred. No. 6.1e-103;  
Matches 256; Conservative 51; Mismatches 49; Indels 4; Gaps 2;  
QY 9 PSPQPSRANGINLGPSANPNARPTDFDLKVIKGNYGKVLAKRKSDFGAFYAVKVLQK 68

Db 73 PPSPPSPSQ-QINLGPSNPNHAKPSDFHFLKVIKGSFGKVLARHAKAEVFAVAVKLOK 131  
Qy 69 KSILKKEQNHMAERNVLLKNVRHPPFLVGLRYSFQTPKLYFVLDVYNGGELFFHLORE 128  
Db 132 KAILKKEKHIMSERVLLKNVHPFLVGLHFSFQADKLYFVLDVYNGGELFFHLORE 191  
Qy 129 RRFLEPRARFYTAESAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGLCKECVEPE 188  
Db 192 RCFLEPRARFYAAEIASALGTLHSLNIIYRDLKPENILLDCQGHVLTDFGLCKENIEHN 251  
Qy 189 ETTSTFCGTPEYLAPEVLRKEPYDRAVDWNCGLGAVLYEMHLGLPPFFNTDVAQMYENILH 248  
Db 252 STTSTFCGTPEYLAPEVLRKEPYDRTVDWNCGLGAVLYEMLYGLPPFYSRNTAEYDNLN 311  
Qy 249 QPLQIPGRTVAACDLLOGLLHKDQOROLGSKEDFLDIKNHMFSPINWDDLYHKRLTTP 308  
Db 312 KPLQLKKNITNSARHLLEGLLQKORTKRLGAKODFMEIKSHVFFSLNWDLLINKKTIPT 371  
Qy 309 FNPVVEGPADLKHPDPFTQEAHSVKSIGCTPDTV---ASSSGASSAFLGFSYAQDDDDIL 365  
Db 372 FNPVSGNDLRHDPDEFTPEPVPNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSFL 431

## RESULT 14

US-10-403-161-2  
; Sequence 2, Application US/10403161  
; Publication No. US20040043930A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, David et al.  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-573C  
; CURRENT APPLICATION NUMBER: US/10/403,161  
; CURRENT FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: 60/370349  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 60/384543  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: 60/370969  
; PRIOR FILING DATE: 2002-04-08  
; PRIOR APPLICATION NUMBER: 60/403748  
; PRIOR FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: 60/372019  
; PRIOR FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: 60/374379  
; PRIOR FILING DATE: 2002-04-22  
; PRIOR APPLICATION NUMBER: 09/779679  
; PRIOR FILING DATE: 2001-02-08  
; PRIOR APPLICATION NUMBER: 60/181045  
; PRIOR FILING DATE: 2000-02-08  
; PRIOR APPLICATION NUMBER: 10/055877  
; PRIOR FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: 60/262892  
; PRIOR FILING DATE: 2001-01-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 173  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 2  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-403-161-2

Query Match 70.8%; Score 1387; DB 4; Length 431;  
Best Local Similarity 71.1%; Pred. No. 6.1e-103;  
Matches 256; Conservative 51; Mismatches 49; Indels 4; Gaps 2;  
Qy 9 PPSPPSRANGINLGPSANPNARPTDFDLKVIKGSFGKVLARHAKAEVFAVAVKLOK 68  
Db 73 PPSPPSPSQ-QINLGPSNPNHAKPSDFHFLKVIKGSFGKVLARHAKAEVFAVAVKLOK 131  
Qy 69 KSILKKEQNHMAERNVLLKNVRHPPFLVGLRYSFQTPKLYFVLDVYNGGELFFHLORE 128  
Db 132 KAILKKEKHIMSERVLLKNVHPFLVGLHFSFQADKLYFVLDVYNGGELFFHLORE 191  
Qy 129 RRFLEPRARFYTAESAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGLCKECVEPE 188  
Db 192 RCFLEPRARFYAAEIASALGTLHSLNIIYRDLKPENILLDCQGHVLTDFGLCKENIEHN 251

Qy 129 RRFLEPRARFYTAESAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGLCKECVEPE 188  
Db 192 RCFLEPRARFYAAEIASALGTLHSLNIIYRDLKPENILLDCQGHVLTDFGLCKENIEHN 251  
Qy 189 ETTSTFCGTPEYLAPEVLRKEPYDRAVDWNCGLGAVLYEMHLGLPPFFNTDVAQMYENILH 248  
Db 252 STTSTFCGTPEYLAPEVLRKEPYDRTVDWNCGLGAVLYEMLYGLPPFYSRNTAEYDNLN 311  
Qy 249 QPLQIPGRTVAACDLLOGLLHKDQOROLGSKEDFLDIKNHMFSPINWDDLYHKRLTTP 308  
Db 312 KPLQLKKNITNSARHLLEGLLQKORTKRLGAKODFMEIKSHVFFSLNWDLLINKKTIPT 371  
Qy 309 FNPVVEGPADLKHPDPFTQEAHSVKSIGCTPDTV---ASSSGASSAFLGFSYAQDDDDIL 365  
Db 372 FNPVSGNDLRHDPDEFTPEPVPNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSFL 431

## RESULT 15

US-10-403-161-4  
; Sequence 4, Application US/10403161  
; Publication No. US20040043930A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, David et al.  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-573C  
; CURRENT APPLICATION NUMBER: US/10/403,161  
; CURRENT FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: 60/370349  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 60/384543  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: 60/370969  
; PRIOR FILING DATE: 2002-04-08  
; PRIOR APPLICATION NUMBER: 60/403748  
; PRIOR FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: 60/372019  
; PRIOR FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: 60/374379  
; PRIOR FILING DATE: 2002-04-22  
; PRIOR APPLICATION NUMBER: 09/779679  
; PRIOR FILING DATE: 2001-02-08  
; PRIOR APPLICATION NUMBER: 60/181045  
; PRIOR FILING DATE: 2000-02-08  
; PRIOR APPLICATION NUMBER: 10/055877  
; PRIOR FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: 60/262892  
; PRIOR FILING DATE: 2001-01-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 173  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 4  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-403-161-4

Query Match 70.8%; Score 1387; DB 4; Length 431;  
Best Local Similarity 71.1%; Pred. No. 6.1e-103;  
Matches 256; Conservative 51; Mismatches 49; Indels 4; Gaps 2;  
Qy 9 PPSPPSRANGINLGPSANPNARPTDFDLKVIKGSFGKVLARHAKAEVFAVAVKLOK 68  
Db 73 PPSPPSPSQ-QINLGPSNPNHAKPSDFHFLKVIKGSFGKVLARHAKAEVFAVAVKLOK 131  
Qy 69 KSILKKEQNHMAERNVLLKNVRHPPFLVGLRYSFQTPKLYFVLDVYNGGELFFHLORE 128  
Db 132 KAILKKEKHIMSERVLLKNVHPFLVGLHFSFQADKLYFVLDVYNGGELFFHLORE 191  
Qy 129 RRFLEPRARFYTAESAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGLCKECVEPE 188  
Db 192 RCFLEPRARFYAAEIASALGTLHSLNIIYRDLKPENILLDCQGHVLTDFGLCKENIEHN 251

Qy	189	ETTSTFCGTPPEYLAPVLRKEPYDRAVDWCLGAVLYEMLHGLPPRENTDVAOMYENILH	248
Db	252	STTSTFCGTPPEYLAPVLRKEPYDRAVDWCLGAVLYEMLHGLPPRENTDVAOMYENILH	311
Qy	249	QPLQIPGGRITVAACDLQGLLHKDQRQLGSKEDFLDIKNHMFSPINWDDLYHKRLTPP	308
Db	312	KPLQKPNITNSARHLLLEGULLQDRTKRLGAKDDFWEIKSHVFFSLINWDDLINKKITPP	371
Qy	309	FNPVSGPADLKHFDPEFTQEA VSKIGCTPDV---ASSSGASSAFLGFSYAQDDDDIL	365
Db	372	FNPVSGPNDLRHFDPEFTQEA VSKIGCTPDV---ASSSGASSAFLGFSYAQDDDDIL	431

Search completed: January 27, 2006, 23:57:31  
Job time : 64.3981 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:32:16 ; Search time 9.46352 Seconds  
(without alignments)  
419.957 Million cell updates/sec

Title: US-09-868-131A-3

Perfect score: 1959

Sequence: 1 MASSPVGVPSPQSPRANGNI.....ASSAFLGFSYAQDDDDILDS 367

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_New:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pap:\*  
2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pap:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pap:\*  
4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pap:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pap:\*  
6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pap:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pap:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1387	70.8	543	6	US-10-821-234-1158
2	847.5	43.3	480	7	US-11-109-156-18
3	794.5	40.6	495	6	US-10-770-726-81
4	750	38.3	737	7	US-11-152-366-28
5	713	36.4	740	6	US-10-878-556A-129
6	705.5	36.0	341	7	US-11-092-168-4
7	698.5	35.7	343	7	US-11-092-168-3
8	697	35.6	351	7	US-11-132-142-13
9	696.5	35.6	462	7	US-11-132-142-10
10	695.5	35.5	351	7	US-11-132-142-14
11	688.5	35.1	942	6	US-10-770-726-76
12	685.5	35.0	350	6	US-10-497-767-4
13	683.5	34.9	381	7	US-11-132-142-9
14	675.5	34.5	395	7	US-11-132-142-12
15	673	34.4	353	7	US-11-132-142-11
16	668	34.1	705	6	US-10-995-561-856
17	668	34.1	706	6	US-10-995-561-855
18	668	34.1	706	7	US-11-099-958-1
19	665	33.9	351	7	US-11-099-958-2
20	662	33.8	398	7	US-11-132-142-7
21	658	33.6	515	7	US-11-132-142-8
22	651.5	33.3	548	7	US-11-132-142-5
23	645	32.9	480	7	US-11-132-142-6
24	535.5	27.3	1732	6	US-10-055-877-147
25	521.5	26.6	1663	6	US-10-055-877-148

Sequence 146, Appl  
Sequence 72, Appl  
Sequence 183, Appl  
Sequence 20, Appl  
Sequence 8, Appl  
Sequence 10, Appl  
Sequence 4, Appl  
Sequence 16, Appl  
Sequence 45, Appl  
Sequence 145, Appl  
Sequence 144, Appl  
Sequence 21, Appl  
Sequence 11, Appl  
Sequence 9, Appl  
Sequence 48, Appl  
Sequence 49, Appl  
Sequence 11, Appl  
Sequence 9, Appl  
Sequence 47, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-821-234-1158

; Sequence 1158, Application US/10821234

; Publication No. US20050255114A1

; GENERAL INFORMATION:

; APPLICANT: Labat, Ivan

; APPLICANT: Stache-Crain, Birgit

; APPLICANT: Andarmani, Susan

; APPLICANT: Tang, Y. Tom

; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

; FILE REFERENCE: 821A

; CURRENT APPLICATION NUMBER: US/10/821,234

; CURRENT FILING DATE: 2004-04-07

; PRIOR APPLICATION NUMBER: US 60/462,047

; PRIOR FILING DATE: 2003-04-07

; NUMBER OF SEQ ID NOS: 1704

; SOFTWARE: pt\_seq\_genes Version 1.0

; SEQ ID NO 1158

; LENGTH: 543

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-821-234-1158

Query Match 70.8%; Score 1387; DB 6; Length 543;

Best Local Similarity 71.1%; Pred. No. 1.6e-120;

Matches 256; Conservative 51; Mismatches 49; Indels 4; Gaps 2;

QY 9 PSPQSPRANGNINLGSPSNAPNAPPTDFLKVIGKNGYKVLAKRSGDAFYAVKVLQK 68

Db 185 PPSPPSPSQ-QINLGSPSNPHAKPSDFHLKVIKSGFGKVLARHAKAEVFAVKVLQK 243

QY 69 KSLTKNKEQNHMAERNVLLKNVRHPLVCLRSFQTPKLYFVLDYVNGELFFHLORE 128

Db 244 KALKKKBEKHMSERNVLLKNVHPFLVGLHFSFQTADKLYFVLDYVNGELFFHLORE 303

QY 129 RRFLEPRARFYAEVASAIGYLHSLNIIYRDLPENILLDCQGHVLTDFGLCKECVEPE 188

Db 304 RCFLEPRARFYAEIASALGYLHSLNIVYRDLPENILLDSQGHVLTDFGLCKENIEHN 363

QY 189 ETTSTFCGTPPEYLAPEVLARKEPYDRAVDMWCLGAVLYEMLHGLPPFPNTDVAQMYENILH 248

Db 364 STTSTFCGTPPEYLAPEVLHKKQPYDRTVDWVCLGAVLYEMLYGLPPFYSRNTAEMYDNLN 423

QY 249 QPLOIFGGTVAACDILLOGLHKKDQORLGSKDEFLDKNHFESPTNWDLLVHKRLTTP 308

Db 424 KPLQLKPNITNSARHLLLEGLLQKORTKRGAKDDFMEIKSHVFFSLINWDLLINKKITPP 483

QY 309 FNPVNEGPDALKHFDPEFTQEAHSVKSIGCTPTDV---ASSSGASSAFLGFSYAQDDDDIL 365



; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-152-366-28

Query Match
Best Local Similarity 38.3%; Score 750; DB 7; Length 737;
Matches 157; Conservative 69; Mismatches 115; Indels 34; Gaps 7;

QY 2 ASSPVG-VPSQPSRANGNINLGPSANPNARPTDFLKVIGKNGYKVLAKRKSQDAF 60
DB 379 ASSPDGQLMSP---GENGEVRQQAQRLGL--DEFNFIKVLGKSGFGKWLAEILKGDE 433
QY 61 YAVKVLQKSLTKNKEONHMAERNVLLKNVRHPELVGLRYSFOTPEKLVFLDYVNGGE 120
DB 434 YAVKVLKDVILQDDVDCTWTEKRIILALARKHPELTQLCCFQTKORLFFVMEYVNGGD 493
QY 121 LFFHLQRRERFLEPRARFYTAEVASAIYGLHSLNIIYRDLKPNILLDCOCHVVLTDFGL 180
DB 494 LMFQIQSRKFDPRSRFYAEVTSALMFLHQHGVIRDLKLNILLDAEGHCKLADFGM 553
QY 181 CKECVEPEETSTPCGTPPEYLAPVLKPEYDRAVDWMCIGAVLYEMLHGLPPFFNTDVA 240
DB 554 CKEGILNGVTTTFCGTPDVIAPBILQLELYGPSVDWVALGVLMYEMWAGQPPPEADNED 613
QY 241 QMVENILHQPLOTIPGGRITVAACDLLOGLLHKDQORLG-----SKDFLDIKNMFPSPI 295
DB 614 DLFESILHDDVLYPVWLVSKEAVSILKAFMTKNPKHRLGCVASONGED--AIKQHPFPKEI 671
QY 296 NWDDLHYHKLTPPPNPNVEGPADLKHFPDPBFTQ-----EAVSKSIGCTPDTVASS 346
DB 672 DWLLEQKKIKPPKPKRIKTRDVNNFDDFTREBPVLTLDVAIVKQIN----- 721
QY 347 GASSAFGFSYAQDD 361
DB 722 --QBEFKGFSYFGED 734

RESULT 5
US-10-878-556A-129
; Sequence 129, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 740
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw\_hum/k6a3\_human
; DATABASE ENTRY DATE: 1996-10-01
US-10-878-556A-129

Query Match
Best Local Similarity 36.4%; Score 713; DB 6; Length 740;
Matches 157; Conservative 63; Mismatches 130; Indels 40; Gaps 8;

QY 6 VGVSPQPSRAN-----GNINLGP-----SANPNARPTDFDLK 39
DB 13 MAVESDSSENQQIMDEPMBGEEINPQTEVSIKEIATHVKEGKADSPQELLK 72
QY 40 VIGKNGYKVLAKRKSQD---AFYAVKVLQKSLTKNKEONHMAERNVLLKNVRHPEL 96
DB 73 VLGGSGFGKVLVKKISGSDARQLYAMKVL--KKATLKVDRVTRTKMERDILVE-VNHFFI 130

QY 97 VGLRYSFQTPKLYFVLVDYVNGGELFFHLQRRERFLEPRARFYTAEVASAIYGLHSLNII 156
DB 131 VKLHYAFQTEGKLYLIULDFLRGGDLFTRLSKSEVMFTEDVKFYLAELALDHLHSLGII 190
QY 157 YRDLKPNILLDCOCHVVLTDFGLCKECVEPEETSTTFCGTPPEYLAPVLKPEYDRAVD 216
DB 191 YRDLKPNILLDBEGHIKLTDFGLSKESIDHEKKAVSFCGTVETMAPEVNVRRGHTQSAD 250
QY 217 WMCIGAVLYEMLHGLPPFFNTDVAQMYENILHQPLOTIPGGRITVAACDLLOGLLHKDQOR 276
DB 251 WNSFGVLMPEMLTGTLPFQOKDKRETWTMLTKAKLGMPOFLSPBEAQSLRLMLFKRNPNR 310
QY 277 LGSKEPDFL-DIKNMFPSPINWDDLHYHKLTPPPNPNVEGPADLKHFPDPBFTQBAVSKSI 335
DB 311 LGAGPDGVEIKRHSFSTIDWNKLYRREIHPFKPATGPEDTFYFDPBFTAKTPKDSP 370
QY 336 GCTPDTVASSSGASSAPLGFPSY---AQDD 362
DB 371 GIPP-----SANAHQLFRGFSFVAITSDE 395

RESULT 6
US-11-092-168-4
; Sequence 4, Application US/11092168
; Publication No. US20050277658A1
; GENERAL INFORMATION:
; APPLICANT: Arizona Board of Regents on behalf of The University of Arizona
; APPLICANT: Montigen Pharmaceuticals, Inc.
; APPLICANT: Hurlay, Laurence H.
; APPLICANT: Mahadevan, Daruka
; APPLICANT: Han, Haiyong
; APPLICANT: Bears, David J.
; APPLICANT: Vankayalapati, Hariprasad
; APPLICANT: Bashyam, Sridevi
; APPLICANT: Munoz, Ruben M.
; APPLICANT: Warner, Steven L.
; APPLICANT: Della Croce, Kimiko
; APPLICANT: Von Hoff, Daniel D.
; APPLICANT: Grand, Cory L.
; TITLE OF INVENTION: PROTEIN KINASE INHIBITORS
; FILE REFERENCE: 920214.00003CONT3
; CURRENT APPLICATION NUMBER: US/11/092,168
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: US 10/965,313
; US 60/608,529
; US 60/511,486
; US 60/511,489
; PRIOR FILING DATE: 2004-10-14
; 2004-09-09
; 2003-10-14
; 2003-10-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-092-168-4

Query Match
Best Local Similarity 36.0%; Score 705.5; DB 7; Length 341;
Matches 138; Conservative 61; Mismatches 107; Indels 7; Gaps 5;

QY 24 PSANPNARPTDFDLKVIKGNKYGKVLAKRKSQDAFYAVKVLQKSLTKNKEONHMAE 83
DB 24 PSQN-TAQLDQDFRIKTLTGTSFGRVLMVKHESGNHYAMKILDKQVVKLQKIEHTLNE 82
QY 84 RNVLKNVRHPELVGLRYSFQTPKLYFVLVDYVNGGELFFHLQRRERFLEPRARFYTAEV 143
DB 83 KRI-LQAVNFPFLVKLEFSFKNSNLYVMVEYVAGGEMFSLRRIGRFAEPHARFYAAQI 141
QY 144 ASAIYGLHSLNIIYRDLKPNILLDCOCHVVLTDFGLCKECVEPEETSTTFCGTPPEVLAP 203

Db 142 VLTFEYLHSDLIYRLDKPENLLIDQGGYIQVTDGFAKRV---KGRWTWLTGTPPYLAP 198  
QY 204 EVLRKEPYDRAVDWNCGLGAVLYEMLHGLPPFFNTDVAQMYENILHQPLOIPGGRTVAACD 263  
Db 199 EILSKGYNKAVDWWALGVLIYEMAAGYPPFFADQPIQYIEKIVSGKVRFPFHFSSDLKD 258  
QY 264 LLOGLLHKDQORLGS-KEDFLDIKNHMFSPINWDDLHYKELTPPENNVGSPADLKHF 322  
Db 259 LLRNLLQVLDLTKRFGNLKGVNDIKNHKWFATTDWIAIYQKVEAPFIPKFKGPGDTSNF 318  
QY 323 DPEFTQEAUSKSI 335  
Db 319 D-DYEEERIVSI 330

## RESULT 7

US-11-092-168-3  
; Sequence 3, Application US/11092168  
; Publication No. US2005027658A1  
; GENERAL INFORMATION:  
; APPLICANT: Arizona Board of Regents on behalf of The University of Arizona  
; APPLICANT: Montigen Pharmaceuticals, Inc.  
; APPLICANT: Hurley, Laurence H.  
; APPLICANT: Mahadevan, Daruka  
; APPLICANT: Han, Huiyong  
; APPLICANT: Bears, David J.  
; APPLICANT: Vankayalapati, Hariprasad  
; APPLICANT: Bashyam, Sridevi  
; APPLICANT: Munoz, Ruben M.  
; APPLICANT: Warner, Steven L.  
; APPLICANT: Della Croce, Kimiko  
; APPLICANT: Von Hoff, Daniel D.  
; APPLICANT: Grand, Cory L.  
; TITLE OF INVENTION: PROTEIN KINASE INHIBITORS  
; FILE REFERENCE: 920214.00003CONT3  
; CURRENT APPLICATION NUMBER: US/11/092,168  
; CURRENT FILING DATE: 2005-03-29  
; PRIOR APPLICATION NUMBER: US 10/965,313  
; US 60/608,529  
; US 60/511,486  
; US 60/511,489  
; PRIOR FILING DATE: 2004-10-14  
; 2004-09-09  
; 2003-10-14  
; 2003-10-14  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 343  
; TYPE: PRT  
; ORGANISM: Bos taurus  
US-11-092-168-3

Query Match 35.7%; Score 698.5; DB 7; Length 343;  
Best Local Similarity 43.5%; Pred. No. 3.6e-57;  
Matches 136; Conservative 64; Mismatches 106; Indels 7; Gaps 5;

QY 24 PSANPNARPTDFDLKLVIGKNGYGVLLAKRSDGAFYAVKVLQKKSILKNKEONHIMAE 83  
Db 26 PAQN-TAHLDPFRITLGTGSGFRVNLVKHKTGNHFKAMKLLDKQKVKLKQIEHTINE 84  
QY 84 RNVLLKNVRHPFLVGLRYSFQTPKELYFVLDDYVNGGELFFHLQRRERFLEPRARFYTAEV 143  
Db 85 KRI-LQAVNPFVLKLEYSFKDNLNLYMVEYVPGGEMFSLRRIGRFSEPHARFYAAQI 143  
QY 144 ASAIGYLHSLNIYRDLKPNILLDCQGHVLTDFGLCKECVEPEBTSTTCGTPPYLAP 203  
Db 144 VLTFEYLHSDLIYRLDKPENLLIDQGGYIQVTDGFAKRV---KGRWTWLTGTPPYLAP 200  
QY 204 EVLRKEPYDRAVDWNCGLGAVLYEMLHGLPPFFNTDVAQMYENILHQPLOIPGGRTVAACD 263  
Db 201 EILSKGYNKAVDWWALGVLIYEMAAGYPPFFADQPIQYIEKIVSGKVRFPFHFSSDLKD 260

QY 264 LLOGLLHKDQORLGSKEDFL-DIKNHMFSPINWDDLHYKELTPPENNVGSPADLKHF 322  
Db 261 LLRNLLQVLDLTKRFGNLKGVNDIKNHKWFATTDWIAIYQKVEAPFIPKFKGPGDTSNF 320  
QY 323 DPEFTQEAUSKSI 335  
Db 321 D-DYEEERIVSI 332  
RESULT 8  
US-11-132-142-13  
; Sequence 13, Application US/11132142  
; Publication No. US20050276818A1  
; GENERAL INFORMATION:  
; APPLICANT: The Burnham Institute  
; APPLICANT: Sikora, Sergey  
; APPLICANT: Godzik, Adam  
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A  
; FILE REFERENCE: 8014-011-US  
; CURRENT APPLICATION NUMBER: US/11/132,142  
; CURRENT FILING DATE: 2005-05-17  
; PRIOR APPLICATION NUMBER: 60/571,698  
; PRIOR FILING DATE: 2004-05-17  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 13  
; LENGTH: 351  
; TYPE: PRT  
; ORGANISM: Xenopus sp.  
US-11-132-142-13

Query Match 35.6%; Score 697; DB 7; Length 351;  
Best Local Similarity 43.9%; Pred. No. 5e-57;  
Matches 133; Conservative 61; Mismatches 103; Indels 6; Gaps 4;

QY 34 DFDFLKVIGKNGYGVLLAKRSDGAFYAVKVLQKKSILKNKEONHIMAEVNLLKNVRH 93  
Db 43 DFDRMKTLTGSGFRVNLVKHKGASQYAMKLLDKQKVKLKQIEHTLNEKRI-LQAVNF 101  
QY 94 PELVGLRYSFQTPKELYFVLDDYVNGGELFFHLQRRERFLEPRARFYTAEVASIGYLHSL 153  
Db 102 PELVRLSEYFKDNLNLYMVEYVPGGEMFSLRRIGRFSEPHARFYAAQIVLTFEYLHSL 161  
QY 154 NIYRDLKPNILLDCQGHVLTDFGLCKECVEPEBTSTTCGTPPYLAPVLRKEPYDR 213  
Db 162 DLIIYRDLKPNILLIDQGGYIQVTDGFAKRV---KGRWTWLTGTPPYLAPVLRKEPYDR 218  
QY 214 AVDWNLGAVLYEMLHGLPPFFNTDVAQMYENILHQPLOIPGGRTVAACDLQGLLHKDQ 273  
Db 219 AVDWNLGAVLYEMLHGLPPFFNTDVAQMYENILHQPLOIPGGRTVAACDLQGLLHKDQ 278  
QY 274 RORLGS-KEDFLDIKNHMFSPINWDDLHYKELTPPENNVGSPADLKHFDPFTQEAUS 332  
Db 279 TKRYGNLKNVNDIKNHKWFATTDWIAIYQKVEAPFIPKFKGPGDTSNF-DYEEEDIR 337  
QY 333 KSI 335  
Db 338 VSL 340

## RESULT 9

US-11-132-142-10  
; Sequence 10, Application US/11132142  
; Publication No. US20050276818A1  
; GENERAL INFORMATION:  
; APPLICANT: The Burnham Institute  
; APPLICANT: Sikora, Sergey  
; APPLICANT: Godzik, Adam  
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A  
; FILE REFERENCE: 8014-011-US



```
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Amblyomma
US-11-132-142-10

Query Match      35.6%; Score 696.5; DB 7; Length 462;
Best Local Similarity 44.7%; Pred. No. 8.1e-57;
Matches 138; Conservative 58; Mismatches 106; Indels 7; Gaps 5;

QY 24 PSANPNRPTDFDLKLVIGKNGYGVKLLAKRKSDGAFYAVKVLQKKSILKNKEQHIMAE 83
DB 145 PSSN-TASLDDFDRIKLTGTSGFGRVNLVQHKQKDYFAMKILDKQVVKLKQVEHTLNE 203

QY 84 RNVLKNVRHPFLVGLRYSFQTPKLYFVLDDYVNGGELFFHLQRRERFLEPRARFYTAEV 143
DB 204 KRI-LOAVEFPFLVKLAHYFKDNSLYMWLEVLGGEMFSLRKSGRFSEPHARFYCAQI 262

QY 144 ASAGYLHSLNIYRDLKPNILDDCOGHVVLTDGFLCKECVEPEETTSTFCGTPPEYLAP 203
DB 263 VLAQYILHSLDLYRDLKPNLLIDHTGYIKVTDGFAKRV---RGRTWTLCGTPEYLAP 319

QY 204 EVLRKEPYDRAVDWMCILGAVLYEMLHGLPPFNTDVAQMYENILHQLQIPGGRTVAACD 263
DB 320 EILSKYGNKAVDWMALGVLIYEMAAGYPPFFADQPIQIYEKIVSGKVRFPFSHFTSLDK 379

QY 264 LLOGLLHKDQORLGS-KEDFLDIKNHMFSPINWDDLHYHKLTPPPNPNVVEGPADLKH 322
DB 380 LLRNLLQVLDLTKRFGNLKNGVNDIKNHWKFAATTDWIAIYQKVEAPFPKPGCDTSNF 439

QY 323 DPEFTQEA 331
DB 440 D-EYEESAL 447

RESULT 10
US-11-132-142-14
; Sequence 14, Application US/11/132,142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-132-142-14

Query Match      35.5%; Score 695.5; DB 7; Length 351;
Best Local Similarity 43.5%; Pred. No. 6.9e-57;
Matches 136; Conservative 62; Mismatches 108; Indels 7; Gaps 5;

QY 24 PSANPNRPTDFDLKLVIGKNGYGVKLLAKRKSDGAFYAVKVLQKKSILKNKEQHIMAE 83
DB 34 PAQN-TAHLDDQFERIKLTGTSGFGRVNLVQHKGTGNHAWKILDKQVVKLKQIEHTLNE 92

QY 84 RNVLKNVRHPFLVGLRYSFQTPKLYFVLDDYVNGGELFFHLQRRERFLEPRARFYTAEV 143
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DB 93 KRI-LOAVNFPFLVKLEFSFKDNSLYMWMEYVPGGMFSLHRRIGRFSSEPHARFYAAQI 151
QY 144 ASAGYLHSLNIYRDLKPNILDDCOGHVVLTDGFLCKECVEPEETTSTFCGTPPEYLAP 203
DB 152 VLTFEYLHSLDLYRDLKPNLLIDQOQYIQVTDGFAKRV---KGRWTLCGTPEYLAP 208
QY 204 EVLRKEPYDRAVDWMCILGAVLYEMLHGLPPFNTDVAQMYENILHQLQIPGGRTVAACD 263
DB 209 EILSKYGNKAVDWMALGVLIYEMAAGYPPFFADQPIQIYEKIVSGKVRFPFSHFTSLDK 268
QY 264 LLOGLLHKDQORLGS-KEDFLDIKNHMFSPINWDDLHYHKLTPPPNPNVVEGPADLKH 322
DB 269 LLRNLLQVLDLTKRFGNLKNGVNDIKNHWKFAATTDWIAIYQKVEAPFPKPGCDTSNF 328
QY 323 DPEFTQEA 335
DB 329 D-EYEESAL 340

RESULT 11
US-10-770-726-76
; Sequence 76, Application US/10/770,726
; Publication No. US20050286409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76
; LENGTH: 942
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-76

Query Match      35.1%; Score 688.5; DB 6; Length 942;
Best Local Similarity 41.5%; Pred. No. 1.2e-55;
Matches 154; Conservative 64; Mismatches 132; Indels 21; Gaps 8;

QY 3 SSPVGVFSP-QPSRA-----NGNINLGPSANPNARPT-----DPDFLKVIGKNGYGVKLL 51
DB 572 SSPSSLSSTQESTAPELPSETQETGFCALCSPLRKSPLTLEDFKFLAVILGRGHFGKVL 631

QY 52 AKRKSDGAFYAVKVLQKKSILKNKEQHIMAEARNVL--LKNVRHPFLVGLRYSFQTPPEKL 109
DB 632 SEFRPSGELFAIKALKKGGIVARDEVESLMCEKRIILAAVNTSAGHPFLVNLFGCFQTPPEHV 691

QY 110 YFVLDYVNGGELFFHLQRRERFLEPRARFYTAEVAISAIGYLHSLNIYRDLKPNILDDC 169
DB 692 CFVMEYSAGGDLMLHISD-VFSEPRAFVYACVVLGLQLFLHEHKIVYRDLKLDNLDDT 750

QY 170 QGHVLTDFGLCKECVEPEETTSTFCGTPPEYLAPVLRKEPYDRAVDWMCILGAVLYEMLH 229
DB 751 EGYVKIADFGLCKEKGMYGDRSTSTFCGTPPEYLAPVLTDTSTYTRAVDWMWGLVLLYEMLV 810

QY 230 GLPPFNTDVAQMYENILHQLQIPGGRTVAACDQLLQKLDKORORLGSKE-DFLDIKN 288
DB 811 GSPFFGDDDEEVFDSIVNDEVYRFLSAEIGIMRLLRRNPERLGRSSERDAEDVKK 870

QY 289 HMFSPINWDDLHYHKLTPPPNPNVVEGPADLKHFDPEFTQEA--VSKSIGCTPDTVASSS 346
DB 871 QPFRTLGWEALLARLPPFPVPTLSGRDVSNFDEEFTGEAPTLPSPRDARPLTAAE-- 928

QY 347 GASSAPLGF 357
DB 929 --QAAPLDFDF 937
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RESULT 12
US-10-497-767-4
; Sequence 4, Application US/10497767
; Publication No. US20050261836A1
; GENERAL INFORMATION:
; APPLICANT: VERTEX PHARMACEUTICALS INCORPORATED
; APPLICANT: MENG, WUYI
; APPLICANT: SWENSON, LOWORKA
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF MITOGEN-ACTIVATED PROTEIN
; TITLE OF INVENTION: KINASE-ACTIVATED PROTEIN KINASE 2 AND BINDING POCKETS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: VP1/01-13 PCT
; CURRENT APPLICATION NUMBER: US/10/497,767
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/337,513
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD.RES
; LOCATION: (10)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD.RES
; LOCATION: (338)
; OTHER INFORMATION: Variable amino acid
US-10-497-767-4
```

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Query Match 35.0%; Score 685.5; DB 6; Length 350;
Best Local Similarity 42.8%; Pred. No. 5.8e-56;
Matches 134; Conservative 62; Mismatches 110; Indels 7; Gaps 5;

QY 24 PSANPNARPTDFPDLKVGKNGYKVLAKRKSOGAFYAVKVLQKKSILKNKEQNHIAMAE 83
DB 33 PAQN-TAHLDFQRIKRTLTGSGFRVLMVKHMETGNHYAMKILDKQVVKLKQIEHTLNE 91

QY 84 RNVLKNVRHPLVLGLRYSFQTPPEKLYFVLDYVNGGELFFHLQRRERFLEPRARFYTAEV 143
DB 92 KRI-LQAVNPFVLKLEFSGKNSNLYMVNVEYVPGGEMSHLRIGRFSEPHARFYAAQI 150

QY 144 ASAIGLHLSNIIYRDLKPENILDCQGHVLLTDFGLCKECVEPEETTTSTFCGTPEYLAP 203
DB 151 VLTFEYLHSLDLYRDLKPENILDCQGYIQVTDGFAKRV---KGRWTLCGTPEYLAP 207

QY 204 EVLRKEPYDAVDWVCLGAVLYEMHLGLPPFFNTDVAQMYENILHQLPQIPGQRTVAACD 263
DB 208 EITLSKGYNKAVDWMALGVLYEMAAAGYPPFFADQPIQIYEKIVSGKVRFPFSFSDLDK 267

QY 264 LLQGLLHKQORQLGS-KEDFLDIKNHMFSPINWDDLYHKRLTTPPNPNVVEGPADLKH 322
DB 268 LLRNLLQVLTGKFGNLKGVNDIKNHKWFATTDIAIYQKVEAPFIPKFGPGDTSNF 327

QY 323 DPEFTQEAIVSKSI 335
DB 328 D-DYEEIEIRVXI 339
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RESULT 13
US-11-132-142-9
; Sequence 9, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: 8014-011-US
```

```
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Leishmania sp.
US-11-132-142-9

Query Match 34.9%; Score 683.5; DB 7; Length 381;
Best Local Similarity 42.0%; Pred. No. 1e-55;
Matches 136; Conservative 65; Mismatches 110; Indels 13; Gaps 5;

QY 33 TDFDLKVGKNGYKVLAKRKSOGAFYAVKVLQKKSILKNKEQNHIAMERNVLLKNVR 92
DB 70 SDFELKNTLTGSGFRVIAHRKGTETEEYVAIKLRKEIILKMKQOQHVQAEKILME-LC 128

QY 93 HPFLVGLRYSFQTPPEKLYFVLDYVNGGELFFHLQRRERFLEPRARFYTAEVASAIYLHS 152
DB 129 HPFIVNMCSFQDEKKVYFLLEFVNGGEMFTHLRTAGRPNDVAKFYHAELVLAPEYLHS 188

QY 153 LNIYRDLKPENILDCQGHVLLTDFGLCKECVEPEETTTSTFCGTPEYLAPVLRKEPYD 212
DB 189 LDVIYRDLKPENILDKNGHVMTDFGFAKVV---PDRFTLCGTPEYLAPVIOSKGHG 245

QY 213 RAVDWVCLGAVLYEMHLGLPPFFNTDVAQMYENILHQLPQIPGQRTVAACDILLQGLLHK 272
DB 246 KAVDWVWVGLLYEYFIAGYPYDDTPFRIYEKILAGRLKFPNWFDRARDLVKGLQTD 305

QY 273 QRQRLGS-KEDFLDIKNHMFSPINWDDLYHKRLTTPPNPNVVEGPADLKHDPPEFTQEA 331
DB 306 HTKRLGTLKGGPADVKNHPYFHGANWDLKLYARYYPAPIVRVKSPGDTSNFE-KYPDSPV 364

QY 332 SKSIGCTPDTVASSSGASSAFLGF 355
DB 365 DR-----TPALTSAAQQAELKGF 381
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RESULT 14
US-11-132-142-12
; Sequence 12, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Danio
US-11-132-142-12

Query Match 34.5%; Score 675.5; DB 7; Length 395;
Best Local Similarity 41.8%; Pred. No. 5.7e-55;
Matches 135; Conservative 58; Mismatches 115; Indels 15; Gaps 5;
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```
QY 34 DFDLKVIGKNGYKVLAKRKSOGAFYAVKVLQKKSILKNKEQNHIAMERNVLLKNVRH 93
DB 87 DFDLKLTLTGSGFRVLMVKHKSQSQYFAMKILDKLVKVLKQIEHTLNEKKI-LQAVSF 145
QY 94 PFLVGLRYSFQTPPEKLYFVLDYVNGGELFFHLQRRERFLEPRARFYTAEVASAIYLHSL 153
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Job time : 10.4635 secs

Db 146 PFLVLECAFKDNLNLYMRYIQGEMFSLHRRIGRSEQNARFYAAQIVLTPEYLHML 205  
QY 154 NIIVRLKPNILLDCGHVVLTDGLCKECVEPEETSTFCGTPEYLAPVLRKEPYDR 213  
Db 206 DLIYRLKPNILLIDHOGYIQVTDGFAKRV---KGRWTLCGTPEYLAPVLRKEPYDR 262  
QY 214 AVDMWCLGAVLYEMLHGLPPFNTDVAQMYENILHQLIPGGRTVAACDLLOGLLHKDQ 273  
Db 263 AVDMWALGLIYEMAAGYPPFADQPIQIVEKIVSGKVRYPFSSDLKLLRNLQVDL 322  
QY 274 RORLGS-KEFDLTKNMFSPINWDDLYHKRLTPPNVVEGADLKHFDPFTQEAUS 332  
Db 323 TKRFGNLKNGVSDIKNHRWFASTDWIAIYEKKVDAPIPKRCGEGDTSNFD-EYDEEVR 381  
QY 333 KSIGCTPTVASSSGASSAFLGF 355  
Db 382 VSV-----SEQCKEFLDF 395

RESULT 15  
US-11-132-142-11  
; Sequence 11, Application US/11132142  
; Publication No. US20050276818A1  
; GENERAL INFORMATION:  
; APPLICANT: The Burnham Institute  
; APPLICANT: Sikora, Sergey  
; APPLICANT: Godzik, Adam  
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A  
; FILE OF INVENTION: CYCLIC-AMP-DEPENDENT KINASE AND A TARGET FOR SARS THERAPY  
; CURRENT APPLICATION NUMBER: US/11/132,142  
; PRIOR FILING DATE: 2005-05-17  
; PRIOR FILING DATE: 2004-05-17  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 11  
; LENGTH: 353  
; TYPE: PRT  
; ORGANISM: Anopheles sp.  
US-11-132-142-11

Query Match 34.4%; Score 673; DB 7; Length 353;  
Best Local Similarity 41.4%; Pred. No. 8 4e-55;  
Matches 132; Conservative 67; Mismatches 110; Indels 10; Gaps 6;  
QY 27 NP--NARPTDPLKVGKNGYKVLAKKSDGAFYAVKVLQKSKILKNKEQHMAER 84  
Db 36 NPTNTAALDDFERIKTLTGSGFGRVMIVQHKSTKYVAMKILDKQVKVLLKQVEHTLNEK 95  
QY 85 NVLLKNVRHPFLVGLRYSPQTEPKLYFLVDYVNGGELFHLQREPRLEPRAPYTAEVA 144  
Db 96 RI--LQAISFPFLVSLKFXHNSNLYMVEYVPGEMFSLHRRIGRSEQNARFYAAQIV 154  
QY 145 SAIGYLHSLNIIYRLKPNILLDCGHVVLTDGLCKECVEPEETSTFCGTPEYLAPV 204  
Db 155 LAEYLHYLDLIYRLKPNILLIDHOGYIQVTDGFAKRV---KGRWTLCGTPEYLAPV 211  
QY 205 VLKSPYDRAVDWMLGAVLYEMLHGLPPFNTDVAQMYENILHQLIPGGRTVAACDL 264  
Db 212 IILSKGYNKAVDMWALGLVYEMAAGYPPFADQPIQIVEKIVSGKVRYPFSSDLKLLRNLQVDL 271  
QY 265 LQGLLHKDQORLGS-KEFDLTKNMFSPINWDDLYHKRLTPPNVVEGADLKHFDPFTQEAUS 332  
Db 272 LRNLLQVDLTFRYGNLKGAVNDIKHRWFASTDWIAIYEKKVDAPIPKRCGEGDTSNFD 381  
QY 324 PEFTQEA--VSKSIGCTPD 340  
Db 332 -DYEETLRISSTEKCAKE 349

Search completed: January 27, 2006, 23:58:24

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:12:00 ; Search time 10.8484 Seconds  
(without alignments)  
3254.993 Million cell updates/sec

Title: US-09-868-131A-3  
Perfect score: 1959  
Sequence: 1 MASSPVGVSPQPSRANGNI.....ASSAFLGFSYAQDDDDILDS 367

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1389	70.9	431	2 A48094	serum and glucocorticoid-regulated kinase - rat
2	981	50.1	422	2 T26334	hypothetical prote
3	863	44.1	479	1 A59380	protein kinase (EC
4	860	43.9	462	1 T17287	protein kinase (EC
5	858	43.8	454	1 JC4345	protein kinase (EC
6	851.5	43.5	480	1 S33364	protein kinase (EC
7	851.5	43.5	763	1 A40831	gag-akt polyprotei
8	851	43.4	481	1 A46288	protein kinase (EC
9	848.5	43.3	480	1 JC2437	protein kinase (EC
10	848	43.3	680	2 S37955	protein kinase YPK
11	847.5	43.3	480	1 A39360	protein kinase (EC
12	845.5	43.2	480	1 S62117	protein kinase (EC
13	837	42.7	481	1 JC2438	protein kinase (EC
14	834	42.6	479	2 A38578	protein kinase 2 (
15	833	42.5	677	2 JS0178	protein kinase YKR
16	827.5	42.2	611	1 A55888	protein kinase (EC
17	795	40.6	481	2 JE0377	p70 S6 kinase (EC
18	794	40.5	569	2 T50414	probable prolifera
19	783.5	40.0	1016	1 A46079	protein kinase C (
20	780.5	39.8	525	1 A41887	ribosomal protein
21	780.5	39.8	525	1 S12906	probable ribosomal
22	778.5	39.7	586	2 A53758	protein kinase C (
23	778.5	39.7	587	2 A49509	protein kinase C (
24	777.5	39.7	546	1 T43233	protein kinase (EC
25	773	39.5	541	1 T43232	protein kinase (EC
26	772.5	39.4	646	2 T38171	probable serine/th
27	771.5	39.4	525	1 TVRTK6	ribosomal protein
28	768	39.2	634	1 B32392	protein kinase C (
29	763	38.9	592	2 JN0877	protein kinase C (

ALIGNMENTS

RESULT 1

A48094  
serum and glucocorticoid-regulated kinase - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 31-Dec-2004  
C;Accession: A48094  
R;Webster, M.K.; Goya, L.; Ge, Y.; Maiyar, A.C.; Firestone, G.L.  
Mol. Cell. Biol. 13, 2031-2040, 1993  
A;Title: Characterization of sgk, a novel member of the serine/threonine protein kinase  
A;Reference number: A48094; MUID:93204949; PMID:8455596  
A;Accession: A48094  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-431 <WEB>  
A;Cross-references: UNIPARC:UPI000017A3E8  
A;Experimental source: Con5.hdc mammary epithelial tumor cells  
A;Note: sequence extracted from NCBI backbone (NCBIN:127618, NCBIPI:127619)  
C;Keywords: ATP  
F;96-355/Domain: protein kinase homology <KIN>  
F;104-112/Region: protein kinase ATP-binding motif

Query Match	70.9%	Score 1389;	DB 2;	Length 431;
Best Local Similarity	71.1%;	Pred. No. 2.3e-58;		
Matches	256;	Conservative 53;	Mismatches 47;	Indels 4; Gaps 2;
QY	9	PSQPSPRANGNINLGPSANPNARPTDFDLKVIKGNVKGVLAKRSGDAFYAVKVLQK	68	
Db	73	PSPPSPSQ-QINLGPSSNPFAKPSDFHLKVIKGSFGKVLARHKAEEAFYAVKVLQK	131	
QY	69	KSILKKEQNHIWAERNVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGELFFHLORE	128	
Db	132	KALKKKKBEKHINSERNVLLKNVHPLVGLHFSQTDKLYFVLDYINGGELFYHLORE	191	
QY	129	RRFLPRARFYTAEVASATGYLHSLNIIYRDLKPNILLDCQGHVLTDFGLCKECVPE	188	
Db	192	RCEFLPRARFYAAETASALGYLHSLNIVYRDLKPNILLDSQQGHI VLTDFGLCKENTEHN	251	
QY	189	ETTSTFCGTPPYLAPEVLKPEPYDRAVDWMCAGVLYEMLHGLPPFPNTDVAQMYENILH	248	
Db	252	GTTSTFCGTPPYLAPEVLKPYDRTVDWMCAGVLYEMLYGLPPFVSRTAEYDNLN	311	
QY	249	QPLQIPGGTVAACDILGLLHKDQORLGSKEDEFLDKNMHFFSPINWDDLHYKRLTTPP	308	
Db	312	KPLQLKPNITNSARHLEGLLQKORTKRLGAKDDFMEIKSHIFFSINWDDLINKKITPP	371	
QY	309	FNPVNEGPDALKHFDPEFTQEAHSVKSIGCTPDTV---ASSSGASSAPLGFSAQDDDDIL	365	
Db	372	FNPVNSGSDLRHFDPEFTTEEPVSSIGRSPSILVTASVKEAREAPLGFSAAPPMDSFL	431	
RESULT 2				
T26334				

RESULT 2

T26334

hypothetical protein W10G6.2 - Caenorhabditis elegans  
A;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 05-Oct-2004  
C;Accession: T26334  
submitted to the EMBL Data Library, October 1996  
A;Reference number: Z20201  
A;Accession: T26334  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-422 <WIL>  
A;Cross-references: UNIPROT:Q94365; UNIPARC:UPI000007852E; EMBL:Z81140; PIDN:CAB03485.1;  
A;Experimental source: clone W10G6  
C;Genetics:  
A;Gene: CRSP:W10G6.2  
A;Map position: X  
A;Introns: 14/3; 60/2; 88/2; 135/3; 179/3; 217/2; 290/3; 393/1  
Query Match 50.1%; Score 981; DB 2; Length 422;  
Best Local Similarity 54.3%; Pred.No.2.4e-19;  
Matches 175; Conservative 57; Mismatches 90; Indels 0; Gaps 0;  
QY 13 PSRANGNINLSPSANPNARPTDFDLKVIKGNKGVKLLAKRKSDGAFYAVKVLQKKSIL 72  
DB 72 PDDENNVDLGPSEKRTATANDFDYLTTCGSGFGRVYQVRHKEKTKKIYAMKILSKHEIR 131  
QY 73 KKEQNHMAERNVLLKNVRHPFLVGLRYSFQTPKLYFVLDVYNGGELFFHLQRRERFL 132  
DB 132 KKEVHVMAERNVLLNFKHPFLVSLHFSFQNKELKLYFVLDHLNGGELFFSHLQREKHS 191  
QY 133 EPRARFVTARVASAIGVLSLNIYYRDLKPENILLDCQGHVLTDFGLCKECVEPEETTS 192  
DB 192 ESRSFVAEACALGVLEKNIYYRDLKPENILLDCQGHVLTDFGLCKEDQGGKTS 251  
QY 193 TFCGTPEYLAPEVLKREPYDRAVDWMLGAVLYEMHLGLPPFPFNTDVAQMYENILHQPLQ 252  
DB 252 TFCGTPEYLAPEILKKPYDKTVDWMLGSLVYEMIFGLPPFYSKDHNEYDKIINQPLR 311  
QY 253 IPGGRTVAACDLLOGLLHKDQORLGSKEGDFLDIKNHMFFSPINWDDLYHKRLTPFPNPN 312  
DB 312 LKGNISVPCSELITGLLQKRSRLGHRNDFRIDRHPFLPVDWDLNRELKAPFIRK 371  
QY 313 VEGPADLKHDFDPEFTQSAVSKS 334  
DB 372 VKNAMDTSNISKFEVFIQIDPS 393  
RESULT 3  
A59380  
protein kinase (EC 2.7.1.37) akt3 long splice form [similarity] - human  
N;Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific protei  
C;Species: Homo sapiens (man)  
C;Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C;Accession: A59380; A59379  
R;Brobeck, D.; Cron, P.; Hemmings, B.A.  
J. Biol. Chem. 274, 9133-9136, 1999  
A;Title: A human protein kinase Bgamma with regulatory phosphorylation sites in the acti  
A;Reference number: A59380; MUID:99194749; PMID:10092583  
A;Accession: A59380  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-479 <BRO>  
A;Cross-references: UNIPROT:Q9Y243; UNIPARC:UPI00000335E8; GB:AAD29089; NID:g4757579; PI  
R;Masure, S.; Haefner, B.; Weeselink, J.J.; Hofnagel, E.; Mortier, E.; Verhasselt, P.;  
Eur. J. Biochem. 265, 353-360, 1999  
A;Title: Molecular cloning, expression and characterization of the human serine/threonin  
A;Reference number: A59379; MUID:99421751; PMID:10491192  
A;Accession: A59379  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-479 <MAS>  
A;Cross-references: UNIPARC:UPI00000335E8; GB:CAB53537; NID:g5804886; PIDN:CAB53537.1  
C;Genetics:

A;Gene: GDB:AKT3; PKBG: PRKBG; RAC-gamma  
A;Cross-references: GDB:9954867  
A;Map position: 1q44-1q44  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonil  
A;Pathway: signal transduction pathways regulating various processes  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen  
F;108/Domain: pleckstrin repeat homology <PLK>  
F;149-408/Domain: protein kinase ATP-binding motif  
F;157-165/Region: protein kinase ATP-binding motif  
F;177/Active site: Lys #statute Predicted  
F;305/Binding site: phosphate (Thr) (covalent) #statute predicted  
F;474/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #statute predict  
Query Match 44.1%; Score 863; DB 1; Length 479;  
Best Local Similarity 48.4%; Pred.No.8.5e-34;  
Matches 171; Conservative 53; Mismatches 107; Indels 22; Gaps 5;  
QY 18 GNINLGPSANPNARPT--DFDLKVIKGNKGVKLLAKRKSDGAFYAVKVLQKKSILKNK 75  
DB 129 GBEEMDASTTHKRKTMDNDFYLLKLGKGTGFKVILVREKASGKYAMKILKEVIAKD 188  
QY 76 EQNHMAERNVLLKNVRHPFLVGLRYSFQTPKLYFVLDVYNGGELFFHLQRRERFLR 135  
DB 189 EVAVILTESRV-LKNTRHPFLTSLKYSFQTKORLCFVMEYVNGGELFFHLSRERVFSEDR 247  
QY 136 AFPTAETAVASATGYLHSLNIYYRDLKPENILLDCQGHVLTDFGLCKECVEPEETTSFTFC 195  
DB 248 TRFYGAEIVSALDYLSHGKIVYRDLKLENLMDKDGHIKITDFGLCKEGITDAATMKTFC 307  
QY 196 GTPPEYLAPEVLKREPYDRAVDWMLGAVLYEMHLGLPPFPFNTDVAQMYENILHQPLQIPC 255  
DB 308 GTPPEYLAPEVLSDNDYGRAVDWMLGAVLYEMHMCGRLLPFYNQDHKLFELIMEDIKFPR 367  
QY 256 GRTVAACDLLOGLLHKDQORQL-GSKEDPLDIKNHMFPSPINWDDLYHKRLTPFPNPNVE 314  
DB 368 TLSSDAKSLLSGLLIKDPNKRLLGGGPDDAKEIMRHSFFSGVNWQVYDKLVPPFKPQVT 427  
QY 315 GPADLKHDFDPEFTQSAVSKSIQCTPDTVASSSGASSAFGLFSYAQDDDDILDS 367  
DB 428 SETDTRYFDEFT---AQITITITPPE-----KYDEGDMCDMN 462  
RESULT 4  
T17287  
protein kinase (EC 2.7.1.37) akt3 short splice form - human  
N;Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific protei  
C;Species: Homo sapiens (man)  
C;Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C;Accession: T17287  
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, September 1999  
A;Reference number: Z18723  
A;Accession: T17287  
A;Molecule type: mRNA  
A;Residues: 1-462 <POU>  
A;Cross-references: UNIPARC:UPI000016AC77; EMBL:AL117525; GB:CAB55977; NID:g5912043; PI  
A;Experimental source: adult testis; clone DKEZp434N0250  
R;Nakatani, K.; Thompson, D.A.; Barthel, A.; Sakaue, H.; Liu, W.; Weigel, R.J.; Roth, R.  
J. Biol. Chem. 274, 21528-21532, 1999  
A;Title: Up-regulation of Akt3 in estrogen receptor-deficient breast cancers and amdrp  
A;Reference number: A64199; PMID:10419456  
A;Contents: annotation  
C;Comment: This protein is increased in estrogen receptor-negative breast cancers and a  
C;Genetics:  
A;Gene: GDB:AKT3  
A;Cross-references: GDB:9954867  
A;Map position: 1q44-1q44  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonil  
A;Pathway: signal transduction pathways regulating various processes  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein

C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase  
F;4-105/Domain: pleckstrin repeat homology <PLK>  
F;146-405/Domain: protein kinase homology <KIN>  
F;154-162/Region: protein kinase ATP-binding motif  
F;177/Active site: Lys #status predicted

Query Match 43.9%; Score 860; DB 1; Length 462;  
Best Local Similarity 51.6%; Pred. No. 1.1e-33;  
Matches 164; Conservative 50; Mismatches 100; Indels 4; Gaps 3;

QY 18 GNINLGPSANPNARPT--DFDFLVIGKNGYKVLAKRSDGAFYAVKVLQKKSILKNK 75  
DB 129 GEEEMDASTTHKKRTKNDYDFYKLGKGTFGKVLVREKASGYAMKILKEVIAKD 188  
QY 76 EQNHMAERNVLLKNVRHPLVGLRYSFQPEKLYFVLDYVNGGELFFHLQRERRFLEPR 135  
DB 189 EVAHTLTESRV-LKNTRHPPLTSLKYSFQTKDRLCFVMEYVNGGELFFHLRSRVFSEDR 247  
QY 136 ARFYTAEVASAIYGLHSINIYRDLPENILLDCQGHVLTDFGLCKECVEPEETTSTFC 195  
DB 248 TRFYGAEIVSALDYLSHGKIYVRDLKLENMLDKDGHIKITDFGLCKEGITDAATMTKTC 307  
QY 196 GTPPYLAPEVLKRPYDRAVDWMLGAVLYEMHLGLPFPNTDVAQMYENILHQPLQIPG 255  
DB 308 GTPPYLAPEVLEDNDYGRAVDWMLGAVLYEMHCGRLPFPYVQDHEKLFELIMEDIKPPR 367  
QY 256 GRTVAACDLQGLLHKDQORL-GSKEDFLDIKNHMFSPINWDDLHYKRLTPPFPNVVE 314  
DB 368 TLSSDAKSLGLLKDNPKNRLGGPDPAKEIMRHSFFSGVNWQDVYDKLVPPFKQVIT 427  
QY 315 GPADLKHDFDEFTQEAWS 332  
DB 428 SETDTRYFDEEFTAQIT 445

## RESULT 5

JC4345  
protein kinase (EC 2.7.1.37) akt3 [validated] - rat  
N;Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific protein kinase  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C;Accession: JC4345  
R;Koniishi, H.; Kuroda, S.; Tanaka, M.; Matsuzaki, H.; Ono, Y.; Kameyama, K.; Haga, T.; K  
Biochem. Biophys. Res. Commun. 216, 526-534, 1995  
A;Title: Molecular cloning and characterization of a new member of the RAC protein kinase  
e C subtypes and beta gamma subunits of G proteins.  
A;Reference number: JC4345; MUID: 96063640; PMID: 7488143  
A;Accession: JC4345  
A;Molecule type: mRNA  
A;Residues: 1-454 <KON>  
A;Cross-references: UNIPROT:Q63484; UNIPARC:UPI000012577F; DDBJ:D49836; NID:g1136777; PI  
A;Experimental source: brain  
C;Function:

A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating various processes  
A;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k  
F;4-105/Domain: pleckstrin repeat homology <PLK>  
F;146-405/Domain: protein kinase homology <KIN>  
F;154-162/Region: protein kinase ATP-binding motif  
F;177/Active site: Lys #status predicted

Query Match 43.8%; Score 858; DB 1; Length 454;  
Best Local Similarity 51.6%; Pred. No. 1.4e-33;  
Matches 164; Conservative 50; Mismatches 100; Indels 4; Gaps 3;

QY 18 GNINLGPSANPNARPT--DFDFLVIGKNGYKVLAKRSDGAFYAVKVLQKKSILKNK 75  
DB 129 GEEEMDASTTHKKRTKNDYDFYKLGKGTFGKVLVREKASGYAMKILKEVIAKD 188  
QY 76 EQNHMAERNVLLKNVRHPLVGLRYSFQPEKLYFVLDYVNGGELFFHLQRERRFLEPR 135  
DB 189 EVAHTLTESRV-LKNTRHPPLTSLKYSFQTKDRLCFVMEYVNGGELFFHLRSRVFSEDR 247

QY 136 ARFYTAEVASAIYGLHSINIYRDLPENILLDCQGHVLTDFGLCKECVEPEETTSTFC 195  
DB 248 TRFYGAEIVSALDYLSHGKIYVRDLKLENMLDKDGHIKITDFGLCKEGITDAATMTKTC 307  
QY 196 GTPPYLAPEVLKRPYDRAVDWMLGAVLYEMHLGLPFPNTDVAQMYENILHQPLQIPG 255  
DB 308 GTPPYLAPEVLEDNDYGRAVDWMLGAVLYEMHCGRLPFPYVQDHEKLFELIMEDIKPPR 367  
QY 256 GRTVAACDLQGLLHKDQORL-GSKEDFLDIKNHMFSPINWDDLHYKRLTPPFPNVVE 314  
DB 368 TLSSDAKSLGLLKDNPKNRLGGPDPAKEIMRHSFFSGVNWQDVYDKLVPPFKQVIT 427  
QY 315 GPADLKHDFDEFTQEAWS 332  
DB 428 SETDTRYFDEEFTAQIT 445

## RESULT 6

S33364  
protein kinase (EC 2.7.1.37) akt1 [similarity] - mouse  
N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prote  
C;Species: Mus musculus (house mouse)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Aug-2004  
C;Accession: S33364  
R;Bellacosa, A.; Franke, T.F.; Gonzalez-Portal, M.E.; Datta, K.; Taguchi, T.; Gardner,  
Oncogene 8, 745-754, 1993  
A;Title: Structure, expression and chromosomal mapping of c-akt: relationship to v-akt  
A;Reference number: S33364; MUID: 93173519; PMID: 8437858  
A;Accession: S33364  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-480 <BEL>  
A;Cross-references: UNIPROT:P31750; UNIPARC:UPI0000001726; EMBL:X65687; NID:g287806; PI

C;Genetics:  
A;Gene: MGI:Akt  
A;Cross-references: MGI:87986  
A;Map position: 12  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating various processes  
A;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen  
F;4-106/Domain: pleckstrin repeat homology <PLK>  
F;148-408/Domain: protein kinase homology <KIN>  
F;156-164/Region: protein kinase ATP-binding motif  
F;179/Active site: Lys #status predicted  
F;308/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predict  
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predict

Query Match 43.5%; Score 851.5; DB 1; Length 480;  
Best Local Similarity 48.8%; Pred. No. 2.9e-33;  
Matches 175; Conservative 55; Mismatches 115; Indels 15; Gaps 7;

QY 7 GVPSQPSRANGNINLGPSANPNARPT--DFDFLVIGKNGYKVLAKRSDGAFYAVK 64  
DB 123 GSPSDNSGAEMEVSLS--AKPHRYTMNEFEVLKLGKGTFGKVLVREKATGRYYAMK 179  
QY 65 VLOKKSILKNKQNHMAERNVLLKNVRHPLVGLRYSFQPEKLYFVLDYVNGGELFFH 124  
DB 180 ILKKEVIVAKDEVAHTLSE-NRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFH 238  
QY 125 LQERRFLEPRARFYTAEVASAIYGLHS-LNIYYRDLKPENILLDCQGHVLTDFGLCKE 183  
DB 239 LGRERVFSRDRARFYGAETVSALDYLSHGKIYVRDLKLENMLDKDGHIKITDFGLCKE 298  
QY 184 CVEPEETTSTFCQTPPYLAPEVLKRPYDRAVDWMLGAVLYEMHLGLPFPNTDVAQMY 243  
DB 299 GIKDGYATMTKTCQTPPYLAPEVLEDNDYGRAVDWMLGAVLYEMHCGRLPFPYVQDHEKLF 358  
QY 244 ENILHQPLQIPGRTVAACDLQGLLHKDQORL-GSKEDFLDIKNHMFSPINWDDLHY 302  
DB 359 ELILMEIEIRPRTLGPPEAKSLGLLKDQPTQRLGGSGSEDAKEIMQHRFPANIVWQDVYE 418







submitted to the EMBL Data Library, July 1991  
A:Reference number: S20836  
A:Accession: S20836  
A:Molecule type: mRNA  
A:Residues: 63-70,'TPSSAACGSLSNAPSMWRLRSRGVDNRHPCGRRPQ','BAGGGDGLPVGLTQRLGRRRDGV  
A:Cross-references: UNIPARC:UPI00001725AC; EMBL:X61037  
A>Note: this sequence has been revised in reference S24423  
R:Alessi, D.R.; Andjelkovic, M.; Caudwell, B.; Cron, P.; Morrice, N.; Cohen, P.; Hemming  
EMBO J. 15, 6541-6551, 1996  
A:Title: Mechanism of activation of protein kinase B by insulin and IGF-1.  
A:Reference number: A64192; MUID:97133284; PMID:8978681  
A:Contents: annotation; phosphorylation sites  
R:Toker, A.; Newton, A.C.  
J. Biol. Chem. 275, 8271-8274, 2000  
A:Title: Akt/protein kinase B is regulated by autophosphorylation at the hypothetical PD  
A:Reference number: A64193; MUID:20187529; PMID:10722653  
A:Contents: annotation; autophosphorylation site  
C:Comment: Akt1 is ubiquitous as an inactive multimeric complex. It binds phosphatidy1-3  
nt protein kinase 1 complex. Akt1 can then autophosphorylate and become fully active.  
C:Genetics:  
A:Gene: GDB:AKT1; RAC; PKB  
A:Cross-references: GDB:118989; OMIM:164730  
A:Map position: 14q32.32-14q32.32  
C:Function:  
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
e production  
A:Pathway: signal transduction pathways regulating various processes including insulin a  
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C:Keywords: ATP; autophosphorylation; phosphotransferase; proto-oncogene  
F;4-106/Domain: pleckstrin repeat homology <PK>  
F;148-408/Domain: protein kinase homology <KIN>  
F;156-164/Region: protein kinase ATP-binding motif  
F;179/Active site: Lys #status predicted  
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki  
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status experime

Query Match 43.3%; Score 847.5; DB 1; Length 480;  
Best Local Similarity 48.3%; Pred. No. 4.5e-33;  
Matches 174; Conservative 56; Mismatches 115; Indels 15; Gaps 7;  
QY 7 GVSPQPSRANGNINLGPSANPNARPT--DFDFLVKVGKNGYKVLAKRKSDGAFYAVK 64  
Db 123 GSPSDNSGAEMEVSLS--AKPKHRYTMNEFEYVLLKLGKTFGKVLVKEKATRYAMK 179  
QY 65 VLQKKSILKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGSELPFH 124  
Db 180 ILKKEVIVAKDEVAHTLTE-NRVLQNSRHPLTALKYSFQTHDRLCFVMEYANGGELFFH 238  
QY 125 LQEREFLEPPRPFYTAEVASAIYGLHS-LNIIYRDLKPNILLDCQGHVLTDFGLCKE 183  
Db 239 LSRERFSEDRARFYGAIEVSALDYLHSEKNVYRDLKLENMLDKDGHIKITDFGLCKE 298  
QY 184 CVPEETTSFTCGTPEYLAPEVLKPEYDRAVDWCLGAVLYEMLHGLPFPFNTDVAQMY 243  
Db 299 GIKDGAATMTFCGTPEYLAPEVLNDYGRAVDWGLGVVYEMWCGRLPFPYQDHEKLF 358  
QY 244 ENILHQLQIPGGRTVAACDLLOGLLHKDQRL--GSKEDFLDIKNHMFSPINWDDLYH 302  
Db 359 ELIMBEIRFPRTLGPPEAKSLLSGLLKDPKQRLGGSGSEDAKEIMQHRFFAGIVMQRVYE 418  
QY 303 KRLLTPFPNVEGPADLKHDPDPEFTQBAVSKSIGCTPDTVASSSGASSA----FLGFSYA 358  
Db 419 KKLSPFPKPVQVTSYDTRYFDEEFTAQMITIT--PPQDDDSMECVDSERRRPHFPQFSYS 475

RESULT 12  
S62117  
protein kinase (EC 2.7.1.37) akt1 [similarity] - bovine  
N:Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific protei  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 16-Aug-2004  
C:Accession: S62117; S24423; S17999; S15714; S36388  
R:Coffer, P.J.; Woodgett, J.R.

submitted to the EMBL Data Library, December 1991  
A:Reference number: S62117  
A:Accession: S62117  
A:Molecule type: mRNA  
A:Residues: 1-480 <COF>  
A:Cross-references: UNIPROT:Q01314; UNIPARC:UPI000012E042; EMBL:X61036; NID:9630; PIDN:  
A>Note: this is a revision to the sequence from reference S17999  
R:Coffer, P.J.; Woodgett, J.R.  
Eur. J. Biochem. 205, 1217, 1992  
A:Reference number: S24423; MUID:92249329; PMID:1533586  
A:Contents: erratum  
A:Accession: S24423  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 70-78,'N',80-145 <COW>  
A:Cross-references: UNIPARC:UPI00001725AD; EMBL:X61036  
A>Note: this is a revision to the sequence from reference S17999  
R:Coffer, P.J.; Woodgett, J.R.  
Eur. J. Biochem. 201, 475-481, 1991  
A:Title: Molecular cloning and characterisation of a novel putative protein-serine kina  
A:Reference number: S17999; MUID:92037600; PMID:1718748  
A:Accession: S17999  
A:Molecule type: mRNA  
A:Residues: 1-70,'TPSSAACGSRSSARSTRRRPSGVDHRRHPCGRRRAQAGGDDGLPVGLTRRELGGRGVAGV  
A:Cross-references: UNIPARC:UPI00001725AE; EMBL:X61036  
A>Note: this sequence has been revised in references S62117 and S24423  
C:Function:  
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoni  
A:Pathway: signal transduction pathways regulating various processes  
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C:Keywords: ATP; autophosphorylation; phosphotransferase; proto-oncogen  
F;4-106/Domain: pleckstrin repeat homology <PK>  
F;148-408/Domain: protein kinase homology <KIN>  
F;156-164/Region: protein kinase ATP-binding motif  
F;179/Active site: Lys #status predicted  
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki  
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predict

Query Match 43.2%; Score 845.5; DB 1; Length 480;  
Best Local Similarity 48.3%; Pred. No. 5.6e-33;  
Matches 173; Conservative 58; Mismatches 114; Indels 13; Gaps 7;  
QY 10 SPQPSRANGNINLGPS-ANPNARPT--DFDFLVKVGKNGYKVLAKRKSDGAFYAVKVL 66  
Db 122 SGSPGNSGAEMEVSLSLAKPKHRYTMNEFEYVLLKLGKTFGKVLVKEKATRYAMKIL 181  
QY 67 QKKSILKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGSELPFH 126  
Db 182 KKEVIVAKDEVAHTLTE-NRVLQNSRHPLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
QY 127 RRRERFLEPPRPFYTAEVASAIYGLHS-LNIIYRDLKPNILLDCQGHVLTDFGLCKECV 185  
Db 241 RRRERFSEDRARFYGAIEVSALDYLHSEKNVYRDLKLENMLDKDGHIKITDFGLCKE 300  
QY 186 EPEETTSFTCGTPEYLAPEVLKPEYDRAVDWCLGAVLYEMLHGLPFPFNTDVAQMYEN 245  
Db 301 KDGATMTKTCGTPEYLAPEVLNDYGRAVDWGLGVVYEMWCGRLPFPYQDHEKLFEL 360  
QY 246 ILHQLQIPGGRTVAACDLLOGLLHKDQRL--GSKEDFLDIKNHMFSPINWDDLYHKKR 304  
Db 361 LMBEIRFPRTLGPPEAKSLLSGLLKDPKQRLGGSGSEDAKEIMQHRFFASIVQDVEYK 420  
QY 305 LTPFPNVEGPADLKHDPDPEFTQBAVSKSIGCTPDTVASSSGASSA----FLGFSYA 358  
Db 421 LSPFPKPVQVTSYDTRYFDEEFTAQMITIT--PPQDDDSMEGVDSERRRPHFPQFSYS 475

RESULT 13  
JC2438  
protein kinase (EC 2.7.1.37) akt2 [validated] - rat  
N:Alternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific protei  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004

C;Accession: JC2438  
R;Koniishi, H.; Shinomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.  
Biochem. Biophys. Res. Commun. 205, 817-825, 1994  
A;Title: Molecular cloning of rat RAC protein kinase alpha and beta and their association  
A;Reference number: JC2437; MUID:95091823; PMID:7999118  
A;Accession: JC2438  
A;Molecule type: mRNA  
A;Residues: 1-481 <KON>  
A;Cross-references: UNIPROT:P47197; UNIPARC:UPI000012577E; DDBJ:D30041; NID:9485404; PID  
A;Experimental source: testis  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating various processes including myoblast  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k  
F;4-106/Domain: pleckstrin repeat homology <PLK>  
F;150-409/Domain: protein kinase homology <KIN>  
F;158-166/Region: protein kinase ATP-binding motif  
F;181/Active site: Lys #status predicted

Query Match 42.7%; Score 837; DB 1; Length 481;  
Best Local Similarity 47.2%; Pred. No. 1.4e-32;  
Matches 168; Conservative 57; Mismatches 119; Indels 12; Gaps 5;

QY 10 SPOPSRANGNINLGPS-ANNAPRTDPDFLKVTGKNGYGVLLAKRSDGAFYAVKVLQK 68  
DB 126 SPDSSTSENMVEAVSKARAKVTMNDPYLLKLGKGTGKVLVREKATGRYAMKILRK 185

QY 69 KSLKKNKEQNHMAERNVLLKNVHPVLGRLYSFQTPPEKLYFVLDYVNGELFFHLORE 128  
DB 186 EVIAKDEVAHTVTSRSV-LONTRHPPLTALKYAFQPHDLRCFVMEYANGDFFHLSRE 244

QY 129 RRFLEPRARYTAEVASAIYGLHSLNIIYRDLKPENILLDCQGHVLTDFGLCKECPVEPE 188  
DB 245 RVFTEDRARYGAEIVSALYSLHSTVDVYRDIKLENMLDKDGHKIDTDFGLSKEGISDG 304

QY 189 ETTSTFCGTPEYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLPPFPNTDVAQMYENILH 248  
DB 305 ATKTKTCGTPEYLAPEVLENDYGRAVDMWGLGVWYEMMCGRLFPYQDHERLFELILM 364

QY 249 QPLQIPGGRVTAACDLGLLHKDQORQL-GSKEDFLDIKNHMFSPINWDDLIYHRLTP 307  
DB 365 EIRFPRTLGPEAKSLLAGLKKDKPKQRLGGSPSDAKEVMEHRFFLSINQDVVQKLLP 424

QY 308 PFNPVNEGPADLKHDFPEFTQEAIVSKSIGCTPTDVASSSGA-----SSAFGLGFSYA 358  
DB 425 PFKPQVTSVDVTFYDFDEFT-----AQSIITPDRVDSLGSLDQRTHEPPQFSYS 476

RESULT 14  
A38578  
protein kinase 2 (EC 2.7.1.-) - slime mold (Dictyostelium discoideum)  
C;Species: Dictyostelium discoideum  
C;Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 31-Dec-2004  
C;Accession: A38578  
R;Haribabu, B.; Dottin, R.P.  
Proc. Natl. Acad. Sci. U.S.A. 88, 1115-1119, 1991  
A;Title: Identification of a protein kinase multigene family of Dictyostelium discoideum  
A;Reference number: A38578; MUID:91142122; PMID:1996312  
A;Accession: A38578  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-479 <HAR>  
A;Cross-references: UNIPROT:P28178; UNIPARC:UPI0000131B58; GB:M59744; NID:9167717; PIDN:  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonin  
F;151-407/Domain: protein kinase homology <KIN>  
F;159-167/Region: protein kinase ATP-binding motif

Query Match 42.6%; Score 834; DB 2; Length 479;  
Best Local Similarity 46.3%; Pred. No. 1.9e-32;  
Matches 167; Conservative 65; Mismatches 115; Indels 14; Gaps 5;

QY 10 SPOPSRANGNINLGPSANP-----NARPTDFLKVIGKNGYGVLLAKRSDGA 59

DB 118 SPDSPNGSGNDDDEGPEEVIFSKNKQSATKDDPELLNVIGKSGFGKQVKKKGEDK 177  
QY 60 FYAVKVLQKSKILKNKEQNHMAERNVLLKNVHPFLVGLRYSFQTPPEKLYFVLDYVNGG 119  
DB 178 IFAMKVLKDAIIRAKQVNHKSEKTI-LQCTISHPFIVNLHYAFQTKOKLYMVLDFVNGG 236

QY 120 ELFFHLQRRRRFLEPRARFYTAEVASAIYGLHSLNIIYRDLKPENILLDCQGHVLTDFG 179  
DB 237 ELFFHLKREGRFSEPRVKIYAAIVSALDHLHKQDIVYRDLKPENILLDSEGHICITDFG 296

QY 180 LKCEVPEBETTSFTCGTPEYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLPPFPNTDV 239  
DB 297 LSKK-IETTDGTFTCGTPEYLAPEVLRNGHGHCAVDMWSLGLTLLYEMLTGLPFPYQNV 355

QY 240 AQMYENILHQLQIPGGRVTAACDLGLLHKDQORQLGSKEDFLDIKNHMFSPINWDD 299  
DB 356 STWYQKILNGELKIPYIISPEAKSLLEGLLTREVDRKLGTKGG-EYKQHPWFKNIDWEK 414

QY 300 LVHKRLTPFPNPVNEGPADLKHDFPEFTQEAIVSKSIGCTPTDVASSSGASSAFGLGFSYAQ 359  
DB 415 LDRKEVEVHFKPKVKGSTDISQIDPVTQERPMDSLVET-SALGDANGKDTSPFEGTYVA 473

QY 360 D 360  
DB 474 D 474

RESULT 15  
JS0178  
protein kinase YKR2 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)  
N;Alternate names: protein YM9718.03c; protein YMR104c  
C;Species: Saccharomyces cerevisiae  
C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 05-Oct-2004  
C;Accession: JS0178; S30904; S54565  
R;Kubo, K.; Ohno, S.; Matsumoto, S.; Yahara, I.; Suzuki, K.  
Gene 76, 177-180, 1989  
A;Title: A novel yeast gene coding for a putative protein kinase.  
A;Reference number: JS0178; MUID:89306654; PMID:2663649  
A;Accession: JS0178  
A;Molecule type: DNA  
A;Residues: 1-677 <KUB>  
A;Cross-references: UNIPROT:PI8961; UNIPARC:UPI000013BDFF; EMBL:M24929; NID:9295680; PI:  
R;Chen, P.; Lee, K.S.; Levin, D.E.  
Mol. Gen. Genet. 236, 443-447, 1993  
A;Title: A pair of putative protein kinase genes (YPK1 and YPK2) is required for cell g  
A;Reference number: S30903; MUID:93173125; PMID:8437590  
A;Accession: S30904  
A;Status: nucleic acid sequence not shown; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-677 <CHE>  
A;Cross-references: UNIPARC:UPI000013BDFF  
R;Hunt, S.; Bowman, S.  
submitted to the EMBL Data Library, May 1995  
A;Reference number: S54510  
A;Accession: S54565  
A;Molecule type: DNA  
A;Residues: 1-677 <HUN>  
A;Cross-references: UNIPARC:UPI000013BDFF; EMBL:Z49702; NID:9817859; PIDN:CAA89740.1; P  
A;Experimental source: strain AB972  
C;Genetics:  
A;Gene: SGD:YPK2; YKR2  
A;Cross-references: SGD:S0004710; MIPS:YMR104c  
A;Map position: 13R  
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase  
F;35-57/Region: histidine-rich  
F;342-599/Domain: protein kinase homology <KIN>  
F;350-358/Region: protein kinase ATP-binding motif  
F;351-375/Region: ATP binding #status predicted  
F;466-512/Region: catalytic #status predicted

Query Match 42.5%; Score 833; DB 2; Length 677;  
Best Local Similarity 49.4%; Pred. No. 2.9e-32;

	Matches	174;	Conservative	52;	Mismatches	114;	Indels	12;	Gaps	6;
Qy	15	RANGNINL----	GPSANPNARPTDF	FLKVGKNGYKVL	LAKRSDGAFYAV	KVLQKKS	70			
Db	320	RGYKLNITVDYKPS	KNKPLSIDDFLLK	VIGKSGFKVMQVR	KDQKIYALKAR	KAY	379			
Qy	71	ILKNKEQNHI	MAERNVLLKNVR	HPFLVGLRYS	QTPKLYFVLDY	VNGGELPFHLQ	ERR 130			
Db	380	IVSKCEVTH	TLAERTVLAR-	VDCFFIVPLKFS	QSPKLYLVLA	FINGGELFYHLQ	HEGR 438			
Qy	131	FLEPRARFY	TAEVASAI	GYLHSLNI	IYRDLKPENIL	LDQGHVVLTD	FGLCCKECV	PEET 190		
Db	439	FSLARSRFY	IAELCALDS	LHKLVDIYRDL	KPENILLDY	QGHIALCDF	GLCKLNMKD	NDK 498		
Qy	191	TSTFCGTPE	YLAPEVL	RKPEPYDRA	VDWMCIGAV	LYEMLHGLP	FPFNTDVAQ	MYENILHQP 250		
Db	499	TDTFCGTPE	YLAPEILL	QGQYTKVD	WWTGILLY	EMMTGLP	PYYDENV	VMYKILQOP 558		
Qy	251	LQIPGGR	TVAACDL	LOGLLHKD	ORQLG-S	KEDFLDI	KNHMPSPIN	WDDLYHKRLT	PPF 309	
Db	559	LLFPDGF	DPAAKD	LLIGLSR	DPSPRL	GVNGTD--	EIRNHPF	KDISWKKLL	KGYIPPY 616	
Qy	310	NPVVEG	PADLKH	FDPEFTQ	EAVSKSIG	CTPDTV	VASSSG	ASSAFLG	FSAQDD 361	
Db	617	KPIVKSE	IDTANF	DQBFTKE--	KPIDS	VVDEYLS	AS-IQ	KQFGG	WTYIGDE 664	

Search completed: January 27, 2006, 23:32:04  
Job time : 11.8484 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:08:15 ; Search time 59.7818 Seconds  
(without alignments)  
4331.236 Million cell updates/sec

Title: US-09-868-131A-3

Perfect score: 1959

Sequence: 1 MASSPVGVPSPQPSRANGNI.....ASSAFLGFSYAQDDDDILDS 367

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_05-80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1959	100.0	367	1	SGK2 MOUSE
2	1848	94.3	427	1	SGK2 HUMAN
3	1848	94.3	427	2	Q5H8Y6 HUMAN
4	1846	94.2	367	2	Q5R029_PONPY
5	1841	94.0	367	2	Q5TRZ3_HUMAN
6	1837	93.8	393	2	Q52PK5_HUMAN
7	1832.5	93.5	366	2	Q5H8Z1_HUMAN
8	1615	82.4	302	1	SGK2 RAT
9	1427.5	72.9	350	2	Q4S7Y9_TETNG
10	1423	72.6	285	2	Q5H8Y4_HUMAN
11	1409	71.9	433	2	Q7ZTW4_BRARE
12	1403	71.6	431	2	Q5Q0U5_FUNHE
13	1397	71.3	432	2	Q6U1I9_CHICK
14	1392	71.1	434	2	Q93524_XENLA
15	1391	71.0	418	2	Q5BKX4_XENTR
16	1391	71.0	431	1	SGK1 RABIT
17	1389	70.9	431	2	Q68G05_RAT
18	1389	70.9	434	2	Q6GPN6_XENLA
19	1387	70.8	421	2	Q5TCN4_HUMAN
20	1387	70.8	431	2	Q5TCN3_HUMAN
21	1387	70.8	445	2	Q5TCN2_HUMAN
22	1387	70.8	526	2	Q5V765_HUMAN
23	1385.5	70.7	490	2	Q4RR91_TETNG
24	1385	70.7	431	1	SGK1 MOUSE
25	1385	70.7	519	2	Q6N585_MOUSE
26	1383	70.6	431	1	SGK1 HUMAN
27	1382	70.5	431	2	Q4R633_MACFA
28	1381.5	70.5	534	2	Q73927_SQUAC
29	1380.5	70.5	430	1	SGK1 RAT
30	1377.5	70.3	433	2	Q73926_SQUAC
31	1372	70.0	434	2	Q6GLY8_XENLA

32	1305.5	66.6	429	2	Q8VEK1_MOUSE
33	1305.5	66.6	496	1	SGK3_MOUSE
34	1299.5	66.3	518	2	Q4SFC2_TETNG
35	1297.5	66.2	429	2	Q6FHV7_HUMAN
36	1297.5	66.2	496	1	SGK3_HUMAN
37	1297.5	66.2	496	2	Q53EM6_HUMAN
38	1297.5	66.2	496	2	Q5R7A7_PONPY
39	1292.5	66.0	496	2	Q5H9Q5_HUMAN
40	1287.5	65.7	490	2	Q5ZJQ4_CHICK
41	1186	60.5	1114	2	Q4SYX7_TETNG
42	1034	52.8	316	2	Q4RI65_TETNG
43	1013	51.7	1550	2	Q4SYI0_TETNG
44	982	50.1	423	2	Q613H2_CAEBR
45	981	50.1	422	2	Q94365_CAEBL

#### ALIGNMENTS

#### RESULT 1

ID	SGK2_MOUSE	STANDARD;	PRT;	367 AA.
AC	Q9QZS5; Q8R0P6;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Serine/threonine-protein kinase Sgk2 (EC 2.7.1.37)			
DE	(Serum/glucocorticoid regulated kinase 2).			
GN	Names=Sgk2;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muroidea; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE (ISOFORM 1).			
RX	MEDLINE=20018032; PubMed=10548550; DOI=10.1042/0264-6021:3440189;			
RA	Kobayashi T., Deak M., Morrice N., Cohen P.;			
RT	"Characterization of the structure and regulation of two novel			
RT	isoforms of serum- and glucocorticoid-induced protein kinase.";			
RL	Biochem. J. 344:189-197(1999).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).			
RC	STRAIN=C57BL/6J; TISSUE=Kidney;			
RX	MEDLINE=22354663; PubMed=12466851; DOI=10.1038/nature01266;			
RA	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,			
RA	Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,			
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,			
RA	Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,			
RA	Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,			
RA	Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,			
RA	Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,			
RA	Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,			
RA	Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,			
RA	Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,			
RA	Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,			
RA	Maglott D.R., Malais L., Marchionni L., McKenzie L., Miki H.,			
RA	Nagahama T., Numata K., Okido T., Pavan W.J., Fertea G., Pesole G.,			
RA	Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,			
RA	Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,			
RA	Sandelin A., Schneider C., Sempé C.A., Setou M., Shimada K.,			
RA	Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,			
RA	Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,			
RA	Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L.,			
RA	Yuan Z., Zvolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,			
RA	Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,			
RA	Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,			
RA	Hara A., Hashizume W., Imotani K., Iehi Y., Itoh M., Kagawa I.,			
RA	Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,			
RA	Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,			
RA	Birney E., Hayashizaki Y.;			
RT	"Analysis of the mouse transcriptome based on functional annotation of			
RT	60,770 full-length cDNAs.";			

RL Nature 420:563-573 (2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
 RC TISSUE=Kidney;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Boeak S.A., McSwan P.J., McKernan K.J., Malek J.A., Guaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Whiting J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 CC -!- FUNCTION: Involved in the activation of potassium channels (By  
 similarity).  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q9QZS5-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q9QZS5-2; Sequence=VSP\_004933;  
 CC Note=No experimental confirmation available;  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 CC -!- CAUTION: Not regulated by serum or glucocorticoids.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR ENBL; AFI69033; AAF12756.1; -; mRNA.  
 DR ENBL; AK050009; BAC34031.1; -; mRNA.  
 DR ENBL; BC026549; AAH26549.1; -; mRNA.  
 DR HSSP; P31751; IGZK.  
 DR Ensembl; ENSMUSG00000017868; Mus musculus.  
 DR MGI; MGI:1351318; Sgk2.  
 DR GO; GO:0015459; F:potassium channel regulator activity; ISS.  
 DR GO; GO:0004682; F:protein kinase Ck2 activity; ISS.  
 DR GO; GO:0017080; F:sodium channel regulator activity; ISS.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; ISS.  
 DR InterPro; IPR000961; Pkinase\_C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00069; Pkinase\_1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ST; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 DR PROSITE; PS00109; PROTEIN KINASE ST; 1.  
 KW Alternative splicing; ATP-binding; Kinase; Nucleotide-binding;  
 KW Phosphorylation; Serine/threonine-protein kinase; transferase.  
 FT DOMAIN 35 292 Protein kinase.  
 FT NP\_BIND 41 49 ATP (By similarity).  
 FT MOTIF 68 78 Nuclear localization signal (By  
 similarity).  
 FT ACT\_SITE 159 159 Proton acceptor (By similarity).

FT BINDING 64 64 ATP (By similarity).  
 FT MOD\_RES 193 193 Phosphothreonine (by PDPK1) (By  
 similarity).  
 FT VARSPLIC 171 199 Missing (in isoform 2).  
 FT CONFLICT 77 77 Missing (in Ref. 3).  
 FT SEQUENCE 367 AA; 41359 MW; 668C04B1A1E9E33A CRC64;  
 Query Match 100.0%; Score 1959; DB 1; Length 367;  
 Best Local Similarity 100.0%; Pred. No. 5e-130;  
 Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MASSPVGVSPQPSRANGNINLGPANPNARPTDFELKVIKGNVGVLLAKRKS DGAF 60  
 DB 1 MASSPVGVSPQPSRANGNINLGPANPNARPTDFELKVIKGNVGVLLAKRKS DGAF 60  
 QY 61 YAVKVLQKKSILKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGE 120  
 DB 61 YAVKVLQKKSILKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGE 120  
 QY 121 LFFHLQRRRRFLPRARFYTAESAIGYLHSLNIYYRDLKPENILLDCQGHVLTDFGL 180  
 DB 121 LFFHLQRRRRFLPRARFYTAESAIGYLHSLNIYYRDLKPENILLDCQGHVLTDFGL 180  
 QY 181 CKECVEPEPTTSTFCGTPPEYLAPEVLRKEPYDRAVWVWCLGAVLYEMLHGLPPFNTDVA 240  
 DB 181 CKECVEPEPTTSTFCGTPPEYLAPEVLRKEPYDRAVWVWCLGAVLYEMLHGLPPFNTDVA 240  
 QY 241 QMYENILHQPLOIPGRTVAACDLQLGLLHKDORQLGSKEDFLDIKNHMFSPINWDDL 300  
 DB 241 QMYENILHQPLOIPGRTVAACDLQLGLLHKDORQLGSKEDFLDIKNHMFSPINWDDL 300  
 QY 301 YHKRLTPPPNPNVEGPADLKHDFEFTQEAHSVSKSIGCTPDTVASSSGASSAFILGFSYAQD 360  
 DB 301 YHKRLTPPPNPNVEGPADLKHDFEFTQEAHSVSKSIGCTPDTVASSSGASSAFILGFSYAQD 360  
 QY 361 DDDIILDS 367  
 DB 361 DDDIILDS 367  
 RESULT 2  
 Sgk2\_HUMAN  
 ID Sgk2\_HUMAN STANDARD; PRT; 427 AA.  
 AC Q9HBY8; Q9UKG6;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Serine/threonine-protein kinase Sgk2 (EC 2.7.1.37)  
 DE (Serum/glucocorticoid-regulated kinase 2).  
 GN Name=Sgk2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2), PHOSPHORYLATION SITE THR-253,  
 RP AND MUTAGENESIS OF SER-416.  
 RX MEDLINE=20018032; PubMed=10548550; DOI=10.1042/0264-6021.3440189;  
 RA Kobayashi T., Deak M., Morrice N., Cohen P.;  
 RT "Characterization of the structure and regulation of two novel  
 RT isoforms of serum- and glucocorticoid-induced protein kinase.";  
 RL Biochem. J. 344:189-197 (1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] (ISOFORM 1).  
 RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;  
 RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,  
 RA Bailey J., Barlow K.P., Bates K.N., Bead L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,  
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
RA Hammond D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
RA Harlow S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
RA Lehesvaio M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
RA Marsh V.L., Martin S.L., McConachie L.J., McIay K., McMurray A.A.,  
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,  
RA Stuce C.D., Smyth M.L., Soderlund C., Steward C.A., Sulston J.E.,  
RA Swann R.M., Sytch M., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
RA Rogers J.;  
RT "The DNA sequence and comparative analysis of human chromosome 20.";  
RL Nature 414:865-871(2001).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
RC TISSUE=Brain, and Colon;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,  
RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Capletton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield J.S.N., Krzywinski M.I.J., Skalska U., Smalls D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [4]  
RP FUNCTION.  
RX MEDLINE=22284526; PubMed=12397388; DOI=10.1007/s00424-002-0873-2;  
RA Gamper N., Fillon S., Feng Y., Friedrich B., Lang P.A., Henke G.,  
RA Huber S.M., Kobayashi T., Cohen P., Lang F.;  
RT "K(+) channel activation by all three isoforms of serum- and  
RT glucocorticoid-dependent protein kinase SGK.";  
RL Pflugers Arch. 445:60-66(2002).  
CC -|- FUNCTION: Involved in the activation of potassium channels.  
CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -|- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Names=2; Synonyms=beta;  
CC IsoId=Q9HBY8-1; Sequence=Displayed;  
CC Names=1; Synonyms=alpha;  
CC IsoId=Q9HBY8-2; Sequence=VSP\_004932;  
CC -|- TISSUE SPECIFICITY: Highly expressed in liver, kidney and  
CC pancreas, and at lower levels in brain.  
CC -|- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
CC -|- CAUTION: Not regulated by serum or glucocorticoids.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; AF186470; AAG17012.1; -; mRNA.

DR EMBL; AF169034; AAF12757.2; -; mRNA.  
DR EMBL; Z98752; CAC18509.1; -; Genomic DNA.  
DR EMBL; BC014037; AAH14037.2; ALT SEQ; mRNA.  
DR EMBL; BC065511; AAH65511.1; -; mRNA.  
DR HSSP; P31751; IGZK.  
DR Ensembl; ENSG00000101049; Homo sapiens.  
DR HGNC; HGNC:13900; SGK2.  
DR MIM; 607589; -.  
DR GO; GO:0015459; Fipocassium channel regulator activity; IDA.  
DR GO; GO:0004682; Fiprotein kinase CK2 activity; NAS.  
DR GO; GO:0004674; Fiprotein serine/threonine kinase activity; TAS.  
DR GO; GO:0017080; Fiprotein channel regulator activity; NAS.  
DR GO; GO:0006468; Piprotein amino acid phosphorylation; NAS.  
DR GO; GO:0007243; Piprotein kinase cascade; TAS.  
DR GO; GO:0006979; Presponse to oxidative stress; TAS.  
DR InterPro; IPR000961; Pkinase C.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR Pfam; PF00069; Pkinase; 1.  
DR Pfam; PF00433; Pkinase C; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00133; S-TK\_X; 1.  
DR SMART; SM00220; S-TKC; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
KW Alternative splicing; ATP-binding; Kinase; Nucleotide-binding;  
KW Phosphorylation; Serine/threonine-protein kinase; Transferase.  
FT DOMAIN 95 352 Protein kinase.  
FT NP\_BIND 101 109 ATP (By similarity).  
FT MOTIF 128 138 Nuclear localization signal (By similarity).  
FT ACT\_SITE 219 219 Proton acceptor (By similarity).  
FT BINDING 124 124 ATP (By similarity).  
FT MOD\_RES 253 253 Phosphothreonine (by PDPK1).  
FT VARSPLOC 1 60 Missing (in isoform 1).  
FT MUTAGEN 416 416 S->D: Increased activation.  
FT SEQUENCE 427 AA; 47604 MW; D8F0FAD6F54B1370 CRC64;  
Query Match 94.3%; Score 1848; DB 1; Length 427;  
Best Local Similarity 94.3%; Pred. No. 4.1e-122;  
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;  
QY 1 MASSPVGVSPQPSRANGINILGPSANPNARPTDFLKVIGKNGYKVLAKRKSQDAF 60  
DB 61 MNSSPAGTSPQPSRANGINILGPSANPNARPTDFLKVIGKNGYKVLAKRKSQDAF 120  
QY 61 YAVKVLQKSIILKNKEONHMAERNVLLKNVRHPTLVGLRYSFTQPEKLYFVLVDYNGGE 120  
DB 121 YAVKVLQKSIILKNKEONHMAERNVLLKNVRHPTLVGLRYSFTQPEKLYFVLVDYNGGE 180  
QY 121 LFFHLQRRERFLEPRARFYTAEVASAIYGLHLSNIYRDLKPNILLDCQGHVLTDFGL 180  
DB 181 LFFHLQRRERFLEPRARFYTAEVASAIYGLHLSNIYRDLKPNILLDCQGHVLTDFGL 240  
QY 181 CKECVPEPTTSTFCGTPEYLAPEVLKPEYDRAVDWVCLGAVLYEMLHGLPPFFNTDVA 240  
DB 241 CKECVPEPTTSTFCGTPEYLAPEVLKPEYDRAVDWVCLGAVLYEMLHGLPPFFSQDVS 300  
QY 241 QMVENILHQPLOTGGRTVAACDLLOGLAHKQORQLSGKEDFLDIKNHMFSPINWDDL 300  
DB 301 QMVENILHQPLOTGGRTVAACDLLOGLAHKQORQLSGKEDFLDIKNHMFSPINWDDL 360  
QY 301 YHKRLTPPPNPNVVEGADLKHFDPEFTQBAVSKSIGCTPDVTASSSGASSAFLGFSYAQD 360  
DB 361 YHKRLTPPPNPNVVEGADLKHFDPEFTQBAVSKSIGCTPDVTASSSGASSAFLGFSYAPE 420  
QY 361 DDILD 366  
DB 421 DDILD 426



```
RESULT 3
Q5H8Y6 HUMAN
ID Q5H8Y6_HUMAN PRELIMINARY; PRT; 427 AA.
AC Q5H8Y6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE OTTHUMP0000031703.
GN Names:SGK2; ORFNames=RP1-138B7.2-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Beasley H.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z98752; CAI42312.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
SQ SEQUENCE 427 AA; 47604 MW; D6FOFA6DF54B1370 CRC64;

Query Match 94.3%; Score 1848; DB 2; Length 427;
Best Local Similarity 94.3%; Pred. No. 4.1e-122;
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MASSPVGVSPQPSRANGNINLGPSANPNARPTDFDLKVIKGNVGVLLAKRSDGAF 60
Db 61 MNSSPAGTSPQPSRANGNINLGPSANPNARPTDFDLKVIKGNVGVLLAKRSDGAF 120

Qy 61 YAVKVLQKKSILKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGE 120
Db 121 YAVKVLQKKSILKNKEQNHIAMERSVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGE 180

Qy 121 LFFHLQRERRFLEPRARFYTAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180
Db 181 LFFHLQRERRFLEPRARFYAAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 240

Qy 181 CKCEVEPEETTSTFCGTPPEYLAPEVLRKEPYDRAVDWNCGLGAVLYEMLHGLPPFFNTDVA 240
Db 241 CKEGVEPEETTSTFCGTPPEYLAPEVLRKEPYDRAVDWNCGLGAVLYEMLHGLPPFYSDQVS 300

Qy 241 QMYENILHQPLOIPGGRTVAAACDLLOGLLHKDQORLGSKEPFLDIKNHMFSPINWDDL 300
Db 301 QMYENILHQPLOIPGGRTVAAACDLLOGLLHKDQORLGSKADFLKTNHVFSPINWDDL 360

Qy 301 YHKRLTPPNPNVNEGPAADLKHFDPFTQEAIVSKSIGCTPDTVASSSGASSAFLGFSYAQD 360
Db 361 YHKRLTPPNPNVNTGPAADLKHFDPFTQEAIVSKSIGCTPDTVASSSGASSAFLGFSYAPE 420

Qy 361 DDILD 366
Db 421 DDILD 426

RESULT 4
Q5RDZ9_PONPY PRELIMINARY; PRT; 367 AA.
ID Q5RDZ9_PONPY PRELIMINARY; PRT; 367 AA.
AC Q5RDZ9;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp469N2435.
GN Name=DKFZp469N2435;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RG The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR857741; CAH90008.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Hypothetical protein.
SQ SEQUENCE 367 AA; 41218 MW; 61128B6CC0519B73 CRC64;

Query Match 94.2%; Score 1846; DB 2; Length 367;
Best Local Similarity 94.3%; Pred. No. 4.7e-122;
Matches 345; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MASSPVGVSPQPSRANGNINLGPSANPNARPTDFDLKVIKGNVGVLLAKRSDGAF 60
Db 1 MNSSPAGTSPQPSRANGNINLGPSANPNARPTDFDLKVIKGNVGVLLAKRSDGTF 60

Qy 61 YAVKVLQKKSILKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGE 120
Db 61 YAVKVLQKKSILKNKEQNHIAMERSVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGE 120

Qy 121 LFFHLQRERRFLEPRARFYTAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180
Db 121 LFFHLQRERRFLEPRARFYAAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180

Qy 181 CKCEVEPEETTSTFCGTPPEYLAPEVLRKEPYDRAVDWNCGLGAVLYEMLHGLPPFFNTDVA 240
Db 181 CKEGVEPEETTSTFCGTPPEYLAPEVLRKEPYDRAVDWNCGLGAVLYEMLHGLPPFYSDQVS 240

Qy 241 QMYENILHQPLOIPGGRTVAAACDLLOGLLHKDQORLGSKEPFLDIKNHMFSPINWDDL 300
Db 241 QMYENILHQPLOIPGGRTVAAACDLLOGLLHKDQORLGSKADFLKTNHVFSPINWDDL 300

Qy 301 YHKRLTPPNPNVNEGPAADLKHFDPFTQEAIVSKSIGCTPDTVASSSGASSAFLGFSYAQD 360
Db 301 YHKRLTPPNPNVAGPADLKHFDPFTQEAIVSKSIGCTPDTVASSSGASSAFLGFSYAPE 360

Qy 361 DDILD 366
Db 361 DDILD 366
```



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RESULT 5
Q52R3 HUMAN
AC Q52R3 HUMAN PRELIMINARY; PRT; 367 AA.
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Serum/glucocorticoid regulated kinase 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kalinina N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Pheasant M., Farmer A.;
RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor
vector.";
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT020038; AA028901.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Kinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase_1.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; Tyr_K; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ
SEQUENCE 367 AA; 41233 MW; C91DD892C4C2486B CRC64;

Query Match 94.0%; Score 1841; DB 2; Length 367;
Best Local Similarity 94.0%; Pred. No. 1.1e-121;
Matches 344; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 MASSPVGVSPQSPSRANGINILGPSANPNARPTDFDLKVGKNGYKVKLLAKRKSDFGAF 60
DB 1 MNSSPAGTSPQSPSRANGINILGPSANPNARPTDFDLKVGKNGYKVKLLAKRKSDFGAF 60

QY 61 YAVKVLQKKSILKNKEQNHMAERNVLLKNVRHPLVGLRYSFTPEKLYFVLDYVNGGE 120
DB 61 YAVKVLQKKSILKNKEQSHIMAERSVLLKNVRHPLVGLRYSFTPEKLYFVLDYVNGGE 120

QY 121 LFFHLQRRERFLPRARFYTAEVASAGYLHSLNIYRDLPENILLDCQGHVLTDFGL 180
DB 121 LFFHLQRRERFLPRARFYAAEVASAGYLHSLNIYRDLPENILLDCQGHVLTDFGL 180

QY 181 CKECVPEETSTTFCGTPEYLAPEVLKPEYDRADVWCLGAVLYEMLHGLPFFNTDVA 240
DB 181 CKEGVEPEDTSTTFCGTPEYLAPEVLKPEYDRADVWCLGAVLYEMLHGLPFFYQDVS 240

QY 241 QMYENILHQLQIPGGRTVAACDLQGLLHKDQRLGSKDEFLDIKNHFFSPINWDDL 300
DB 241 QMYENILHQLQIPGGRTVAACDLQGLLHKDQRLGSKADFLDIKNHFFSPINWDDL 300

QY 301 YHKRLTPPNPNVEGADLKHFDPEFTQEAIVSKSIGCTPTDVASSSGASSAFGLGFSYAD 360
DB 301 YHKRLTPPNPNVTGPADLKHFDPEFTQEAIVSKSIGCTPTDVASSSGASSAFGLGFSYAD 360
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QY 361 DDDILD 366
DB 361 DDDILD 366

RESULT 6
Q52PK5 HUMAN
ID Q52PK5 HUMAN PRELIMINARY; PRT; 393 AA.
AC Q52PK5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Serum/glucocorticoid regulated kinase 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Li H., Nong W., Zhou G., Ke R., Shen C., Zhong G., Zheng Z., Liang M.,
RA Xiao W., Lin L., Yang S.;
RT "Direct Submission.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY987010; AAX88805.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase_1.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; Tyr_K; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ
SEQUENCE 393 AA; 43962 MW; B9931E71A8B998D6 CRC64;

Query Match 93.8%; Score 1837; DB 2; Length 393;
Best Local Similarity 93.7%; Pred. No. 2.2e-121;
Matches 343; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 MASSPVGVSPQSPSRANGINILGPSANPNARPTDFDLKVGKNGYKVKLLAKRKSDFGAF 60
DB 27 MNSSPAGTSPQSPSRANGINILGPSANPNARPTDFDLKVGKNGYKVKLLAKRKSDFGAF 86

QY 61 YAVKVLQKKSILKNKEQNHMAERNVLLKNVRHPLVGLRYSFTPEKLYFVLDYVNGGE 120
DB 87 YAVKVLQKKSILKNKEQSHIMAERSVLLKNVRHPLVGLRYSFTPEKLYFVLDYVNGGE 146

QY 121 LFFHLQRRERFLPRARFYTAEVASAGYLHSLNIYRDLPENILLDCQGHVLTDFGL 180
DB 147 LFFHLQRRERFLPRARFYAAEVASAGYLHSLNIYRDLPENILLDCQGHVLTDFGL 206

QY 181 CKECVPEETSTTFCGTPEYLAPEVLKPEYDRADVWCLGAVLYEMLHGLPFFNTDVA 240
DB 207 CKEGVEPEDTSTTFCGTPEYLAPEVLKPEYDRADVWCLGAVLYEMLHGLPFFYQDVS 266

QY 241 QMYENILHQLQIPGGRTVAACDLQGLLHKDQRLGSKDEFLDIKNHFFSPINWDDL 300
DB 267 QMYENILHQLQIPGGRTVAACDLQGLLHKDQRLGSKADFLDIKNHFFSPINWDDL 326

QY 301 YHKRLTPPNPNVEGADLKHFDPEFTQEAIVSKSIGCTPTDVASSSGASSAFGLGFSYAD 360
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Db 327 YHRLTPPPNPNVTGPADLKHDFEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 386  
Qy 361 DDILD 366  
Db 387 DDILD 392

RESULT 7  
Q5H8Z1\_HUMAN  
ID Q5H8Z1\_HUMAN PRELIMINARY; PRT; 366 AA.  
AC Q5H8Z1;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE ORTHUMP00000031706.  
GN Name=SGK2; ORFNames=RPI-138B7.2-006;  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Beasley H.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z98752; CAI42315.1; -; Genomic\_DNA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000961; Kinase C.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR008271; Ser\_Thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_Thr\_pkinase.  
DR InterPro; IPR01245; Tyr\_pkinase.  
DR Pfam; PF00069; Kinase; 1.  
DR Pfam; PF00433; Kinase C; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TK; 1.  
DR SMART; SM00219; TyrKc; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
SQ SEQUENCE 366 AA; 41047 MW; 8BB546894C23571F CRC64;  
  
Query Match 93.5%; Score 1832.5; DB 2; Length 366;  
Best Local Similarity 94.0%; Pred. No. 4.2e-121;  
Matches 344; Conservative 10; Mismatches 11; Indels 1; Gaps 1;  
  
Qy 1 MASSPVGVSPQSRANGINLGPSANPNARPTDFDLKVGKNGYKVLAKRKS DGAF 60  
Db 1 MNSSPATGTPSPQSRANGINLGPSANPNARPTDFDLKVGKNGYKVLAKRKS DGAF 60  
  
Qy 61 YAVKVLQKSIKKNKQNHMAERNVLLKNVRHPLVGLRYSQTPEKLYFVLVDYNGGE 120  
Db 61 YAVKVLQKSIKKNKQNHMAERNVLLKNVRHPLVGLRYSQTPEKLYFVLVDYNGGE 119  
  
Qy 121 LFFHLQRERFLEPRARFYTAEVASAIQVLSLNIYRDLKPNILLDCQGHVLTDFGL 180  
Db 120 LFFHLQRERFLEPRARFYTAEVASAIQVLSLNIYRDLKPNILLDCQGHVLTDFGL 179  
  
Qy 181 CKECVEPEETSTFTCTPEYLAPEVLKGPYDRAVDWCLGAVLYEMLHGLPPFFNTDVA 240  
Db 180 CKEGVEPEETSTFTCTPEYLAPEVLKGPYDRAVDWCLGAVLYEMLHGLPPFYSDVS 239  
  
Qy 241 QMYENILHQLQIPGGRTPVAACDLLOGLLHKQORQLGSKEDFLDIKNHMFSPINWDDL 300  
Db 240 QMYENILHQLQIPGGRTPVAACDLLOGLLHKQORQLGSKADFLDIKNHVFSPINWDDL 299  
  
Qy 301 YHRLTPPPNPNVEGPDALKHDFEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAO 360  
Db 300 YHRLTPPPNPNVTGPADLKHDFEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 359

Qy 361 DDILD 366  
Db 360 DDILD 365  
  
RESULT 8  
SGK2\_RAT  
ID SGK2\_RAT STANDARD; PRT; 302 AA.  
AC Q8RAU9;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Serine/threonine-protein kinase Sgk2 (EC 2.7.1.37)  
DE (Serum/glucocorticoid regulated kinase 2) (Fragment).  
GN Name=Sgk2;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;  
RA Feng Y.X., Huber S.M., Waerntges S., Lang F.;  
RT "SGK2 and SGK3 mRNA expression in rat kidney.";  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Involved in the activation of potassium channels (By similarity).  
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
CC EMBL; AF361756; AAL91351.1; -; mRNA.  
DR HSSP; F31751; IGZK.  
DR Ensembl; ENSRNOG0000033573; Rattus norvegicus.  
DR RGD; 620232; Sgk2.  
DR GO; GO:0015459; F:potassium channel regulator activity; ISS.  
DR GO; GO:0004682; F:protein kinase CK2 activity; ISS.  
DR GO; GO:0017080; F:sodium channel regulator activity; ISS.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; ISS.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR008271; Ser\_Thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_Thr\_pkinase.  
DR Pfam; PF00069; Kinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TK; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
KW ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;  
Serine/threonine-protein kinase; Transferase.  
FT DOMAIN 18 275  
FT NP\_BIND 24 32  
FT MOTIF 51 61  
FT ATP (By similarity).  
FT Nuclear localization signal (By similarity).  
FT Proton acceptor (By similarity).  
FT ATP (By similarity).  
FT Phosphothreonine (by PDPK1) (By similarity).  
FT NON\_TER 1 1  
FT NON\_TER 302 302  
SQ SEQUENCE 302 AA; 34622 MW; A74EE3F424283D66 CRC64;  
  
Query Match 82.4%; Score 1615; DB 1; Length 302;  
Best Local Similarity 99.3%; Pred. No. 7.3e-106;  
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 18 GNINLGSANPNARPTDFDLKVGKGYGVKVLAKRSDGAFYAVKVLQKKSILKNKEQ 77  
 DB 1 GNINLGSANPNARPTDFDLKVGKGYGVKVLAKRSDGAFYAVKVLQKKSILKNKEQ 60  
 QY 78 NHMAERNVLLKNVRHPLVGLRYSFQTPPEKLYFVLVDYVNGGELFFHLQRRRFLPEPR 137  
 DB 61 SHMAERNVLLKNVRHPLVGLRYSFQTPPEKLYFVLVDYVNGGELFFHLQRRRFLPEPR 120  
 QY 138 FYTAEVASAIGYLHSLNIIYRDLPENILLDCQGHVVLTDGFLCKECPVEPEETTSTPCGT 197  
 DB 121 FYTAEVASAIGYLHSLNIIYRDLPENILLDCQGHVVLTDGFLCKECPVEPEETTSTPCGT 180  
 QY 198 PEYLAPVLRKEPYDRAVDWMCGLGAVLYEMLHGLPPFFNTDVAQMYENILHQLQIPGGR 257  
 DB 181 PEYLAPVLRKEPYDRAVDWMCGLGAVLYEMLHGLPPFFNTDVAQMYENILHQLQIPGGR 240  
 QY 258 TVAACDLLOGLLHKDQRLGSKEDFLDIKNHMFPSINWDDLYHKRLTTPFPNPNVGGPA 317  
 DB 241 TVAACDLLOGLLHKDQRLGSKEDFLDIKNHMFPSINWDDLYHKRLTTPFPNPNVGGPA 300  
 QY 318 DL 319  
 DB 301 DL 302

RESULT 9  
 Q4S7Y9 TETNG  
 ID Q4S7Y9 TETNG PRELIMINARY; PRT; 350 AA.  
 AC Q4S7Y9; 2005 (TEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TEMBLrel. 31, Last annotation update)  
 DE Chromosome 9 SCAF14710, whole genome shotgun sequence.  
 DE (Fragment).  
 GN ORFNames=GSTENG00022577001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN NUCLEOTIDE SEQUENCE.  
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 RA Mauceli E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 RA Dasiiva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.;  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 RT the early vertebrate proto-karyotype".  
 RL Nature 431:946-957 (2004).  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RP Genoscope; Whitehead Institute Centre for Genome Research;  
 RG Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 RL -i- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC -i- FUNCTION: Plays a key role in the control of the eukaryotic cell  
 CC cycle. It is required in higher cells for entry into S-phase and  
 CC mitosis. Component of the kinase complex that phosphorylates the  
 CC repetitive C-terminus of RNA polymerase II. Catalytic component of  
 CC MPF (By similarity).  
 CC -i- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in  
 CC mature oocytes (By similarity).  
 CC -i- SIMILARITY: Belongs to the Ser/Thr protein kinase family. IEA.

DR EMBL; CAAE01014710; CAG03243.1; -; Genomic\_DNA.  
 DR InterPro; IPR000961; pkinase C.  
 DR InterPro; IPR000719; prot\_kinase.  
 DR InterPro; IPR008271; Ser\_Thr\_kinase.  
 DR InterPro; IPR002290; Ser\_Thr\_kinase.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF00069; pkinase C.1.  
 DR Pfam; PF00433; pkinase C.1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00220; S\_TK; 1.  
 DR SMART; SM00219; TyrKc; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 KW ATP-binding; Kinase; Nucleotide-binding;  
 KW Serine/threonine-protein kinase; Transferase.  
 FT NON\_TER 1  
 SQ SEQUENCE 350 AA; 39571 MW; 56BF9C5C2889D924 CRC64;

Query Match 72.9%; Score 1427.5; DB 2; Length 350;  
 Best Local Similarity 75.7%; Pred.No. 1.5e-92;  
 Matches 265; Conservative 37; Mismatches 47; Indels 1; Gaps 1;

QY 16 ANGNINLGSANPNARPTDFDLKVGKGYGVKVLAKRSDGAFYAVKVLQKKSILKNK 75  
 DB 2 SHDDVNLGFSANPHARPTDFDLAVIGKGTFGKVLAKHTDSSFYAVKVLQKVKKK 61  
 QY 76 EQNHMAERNVLLKNVRHPLVGLRYSFQTPPEKLYFVLVDYVNGGELFFHLQRRRFLPEPR 135  
 DB 62 EQKNMAERNVLLKSLKHPFLVRLHYLSFQTAELKLYFVLVDYVNGGELFFHLQRRRFLPEPR 121  
 QY 136 AREYTAEVASAIQYLHSLNIIYRDLPENILLDCQGHVVLTDGFLCKECPVEPEETTSTFC 195  
 DB 122 AREYTAEVASAIQYLHSLNIIYRDLPENILLDCQGHVVLTDGFLCKECPVEPEETTSTFC 181  
 QY 196 GTEPYLAPEVLRKEPYDRAVDWMCGLGAVLYEMLHGLPPFFNTDVAQMYENILHQLQIPG 255  
 DB 182 GTEPYLAPEVLRKEPYDRTVDMCGLGAVLYEMLHGLPPFFNTDVAQMYENILHQLQIPG 241  
 QY 256 GRTVAACDLLOGLLHKDQRLGSKEDFLDIKNHMFPSINWDDLYHKRLTTPFPNPNVGG 315  
 DB 242 GRTVAACDLLOGLLHKDQRLGSKEDFLDIKNHMFPSINWDDLYHKRLTTPFPNPNVGG 301  
 QY 316 PADLKHFDPEFTQEAQVSKSGICGTPDVTASSSGASSAFGLGSYAQDDDL 365  
 DB 302 PADTQHIDPEFTREMYSSVSQTPEFTASAS-ASNAFNGFSFVATEDSFL 350

RESULT 10  
 Q5H8Y4 HUMAN  
 ID Q5H8Y4\_HUMAN PRELIMINARY; PRT; 285 AA.  
 AC Q5H8Y4;  
 DT 10-MAY-2005 (TEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TEMBLrel. 30, Last annotation update)  
 DE OTTHUMP00000031704.  
 GN Name=SGK2; ORFNames=RP1-138B7.2-004;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RP Beasley H.;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 CC -i- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -i- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 CC EMBL; Z98752; CAI42314.1; -; Genomic\_DNA.  
 DR DR; GO:0005524; F:ATP binding; IEA.  
 DR DR; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR DR; GO:0004713; F:protein-tyrosine kinase activity; IEA.

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DR GO: 0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_Thr_pkin_AS.
DR InterPro: IPR002290; Ser_Thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TYRKc; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 285 AA; A3493A70IABB4542 CRC64;

Query Match 72.6%; Score 1423; DB 2; Length 285;
Best Local Similarity 94.0%; Pred. No. 2.4e-92;
Matches 267; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 MASSPVGVSPQPSRANGINLGPSANPNARPTDFDLKVGKNGYGVLLAKRKSDGAF 60
DB 1 MNSSPAGTSPQPSRANGINLGPSANPNARPTDFDLKVGKNGYGVLLAKRKSDGAF 60

QY 61 YAVKVLQKKSILKKNQNHIMAEARNVLLKNVRHPELVGLRYSFQTPEKLYFVLDVYNGGE 120
DB 61 YAVKVLQKKSILKKNQNHIMAEARNVLLKNVRHPELVGLRYSFQTPEKLYFVLDVYNGGE 120

QY 121 LFFHLQRRRFLPRARFYTAESAIGYLHSLNIYRDLKPNILLDCQGHVLLDFGL 180
DB 121 LFFHLQRRRFLPRARFYTAESAIGYLHSLNIYRDLKPNILLDCQGHVLLDFGL 180

QY 181 KCEVPEETSTFCGTPEYLADEVLRKEPYDRAVDWVWCLGAVLYEMLHGLPPFFNTDVA 240
DB 181 KCEVPEETSTFCGTPEYLADEVLRKEPYDRAVDWVWCLGAVLYEMLHGLPPFFNTDVA 240

QY 241 QMYENILHQLPIPGGRTVAACDLLOGLLHKDQORLGSKEDPL 284
DB 241 QMYENILHQLPIPGGRTVAACDLLOGLLHKDQORLGSKEDPL 284

RESULT 11
O72TW4 BRARE
ID O72TW4 BRARE PRELIMINARY; PRT; 433 AA.
AC O72TW4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Serum/glucocorticoid regulated kinase.
GN Name=sgk;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney, and Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole body;
RG NIH MGC Project;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RG NIH MGC Project;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (inactive holoenzyme and
CC monomeric catalytic subunit). Translocates into the nucleus
CC (monomeric catalytic subunit) (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC052134; AAH52134.1; -; mRNA.
DR EMBL; BC067618; AAH67618.1; -; mRNA.
DR HSP; P31751; IMRY.
DR Ensembl; ENSDARG0000025522; Danio rerio.
DR ZFIN; ZDB-GENE-030131-2860; sgk.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000961; Pkinase C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_Thr_pkin_AS.
DR InterPro: IPR002290; Ser_Thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase; cAMP.
SQ SEQUENCE 433 AA; 48983 MW; F2AA4771E245FF56 CRC64;

Query Match 71.9%; Score 1409; DB 2; Length 433;
Best Local Similarity 72.5%; Pred. No. 3.8e-91;
Matches 261; Conservative 44; Mismatches 51; Indels 4; Gaps 2;

QY 9 PSPQPSRANGINLGPSANPNARPTDFDLKVGKNGYGVLLAKRKSDGAFYAVKVLQK 68
DB 75 PSPQPSQ-QINLGFSSNPATAKPSDFDLKVGKSGKVLARHRSDEKFAVAVKVLQK 133

QY 69 KSILKKNQNHIMAEARNVLLKNVRHPELVGLRYSFQTPEKLYFVLDVYNGGELFFHLQRE 128
DB 134 KAILKKKEKHIMSERVLLKNVRHPELVGLRYSFQTPEKLYFVLDVYNGGELFFHLQRE 193

QY 129 RFLPEPRARFYTAESAIGYLHSLNIYRDLKPNILLDCQGHVLLDFGLCKECPVE 188
DB 194 RFLPEPRARFYTAESAIGYLHSLNIYRDLKPNILLDCQGHVLLDFGLCKENIEPN 253

QY 189 ETTSTFCGTPEYLADEVLRKEPYDRAVDWVWCLGAVLYEMLHGLPPFFNTDVAQMYENILH 248
DB 254 GTTSTFCGTPEYLADEVLRKEPYDRAVDWVWCLGAVLYEMLHGLPPFFNTDVAQMYENILH 313

QY 249 QPLQIPGGRTVAACDLLOGLLHKDQORLGSKEDFLDIKNHMFPPSPINWDDLHVKRLTTP 308
DB 314 KPLQKPNISNARHLLGLLQKQTKRLGFTDDTFTEIKNHMFPPSPINWDDLHNAKLLTTP 373

QY 309 FNPVVEGPDALKHDPFTTQEA VSKSI GCTPTT---VASSGSSAFAFGFSYAQDDDDIL 365
DB 374 FNPVNTGPNLDRHDFEFTDEPVNSIGCSPPSALVTSITATEAFLGFSYAPAMD SYL 433
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RESULT 12
Q500U5_FUNHE
ID Q500U5_FUNHE PRELIMINARY; PRT; 431 AA.
AC Q500U5;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Serum and glucocorticoid-regulated kinase.
GN Name=SGK;
OS Fundulus heteroclitus (Killifish) (Mummichog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Fundulidae; Fundulus.
OX NCBI_TaxID=8078;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Sato J.D., Clarke C.C., Stanton B.A.;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
EMBL: AY800243; AA080429.1; -; mRNA.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000961; Pfam: P00069; Kinase C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_Thr_pkin_AS.
DR InterPro: IPR002290; Ser_Thr_pkinase.
DR Pfam: PF00069; Kinase C.
DR Pfam: PF00433; Pkinase C; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00219; Tyr_KC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ
SEQUENCE 431 AA; 48870 MW; 91C80821F64B454D CRC64;

Query Match 71.6%; Score 1403; DB 2; Length 431;
Best Local Similarity 71.7%; Pred. No. 1e-90;
Matches 258; Conservative 47; Mismatches 51; Indels 4; Gaps 2;

QY 9 PPSPPSPSQ-QINLGPSSNPANRPTDFDLKLVIGKNGYKVLAKRSDGAFYAVKVLQK 68
DB 73 PPSPPSPSQ-QINLGPSSNPANRPTDFDLKLVIGKNGYKVLAKRSDGAFYAVKVLQK 131
QY 69 KSLKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGELFFHLORE 128
DB 132 KALKKKEKHIMSERVLLKNVKHPLVGLHYSFQTADKLYFVLDYINGGELFYHLORE 191
QY 129 RRFLEPRARYTAESAIGYLHSLNIYRDLKPNILLDCQGHVLTDFGLCKECVEPE 188
DB 192 RCFLEPRARYSAEIASALGYLHSLNIYRDLKPNILLDSQGHILTDFGLCKENIEPN 251
QY 189 ETTSTFCGTPEYLAPEVLKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLN 311
DB 252 GTTSTFCGTPEYLAPEVLKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLN 311
QY 249 QPLQIPGGRVTAACDLQGLLHKDQRLGSKEDFLDKHMFPSPINWDDLYHKRLTTP 308
DB 312 KPLQLKPNITNSARHLEGLLQKDRTKRLGAKEDFTEIKNHVFPSPINWDDLNKKTTP 371
QY 309 FNPVNEGADLKHFDPEFTQEAQVSKSGCTPD---TVASSSGASSAFLGFSYAQDDDL 365
DB 372 FNPVNGPDLRHRDFEFTDEPVSSIGCSFDALATASIKAEAFVGFSPAPSDSYL 431
QY 309 FNPVNEGADLKHFDPEFTQEAQVSKSGCTPDTV---ASSSGASSAFLGFSYAQDDDL 365
DB 373 FNPVNGSPDLRHRDFEFTDEPVSPISIGQSPSILITASVKAAAEAFGFSYAPVDSFL 432

RESULT 13
Q6U119_CHICK
ID Q6U119_CHICK PRELIMINARY; PRT; 432 AA.
AC Q6U119;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Serum and glucocorticoid-induced kinase.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Malkiewicz S.A., Porter T.E.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
EMBL: AY380825; AA08435.1; -; mRNA.
DR HSSP; P05132; IATP.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000961; Pfam: P00069; Kinase C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_Thr_pkin_AS.
DR InterPro: IPR002290; Ser_Thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR Pfam: PF00433; Pkinase C; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00219; Tyr_KC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ
SEQUENCE 432 AA; 48890 MW; 83AB52AFF2609953 CRC64;

Query Match 71.3%; Score 1397; DB 2; Length 432;
Best Local Similarity 71.7%; Pred. No. 2.7e-90;
Matches 258; Conservative 49; Mismatches 49; Indels 4; Gaps 2;

QY 9 PPSPPSRANGINLGPSSNPANRPTDFDLKLVIGKNGYKVLAKRSDGAFYAVKVLQK 68
DB 74 PPSPPSPSQ-QINLGPSSNPANRPTDFDLKLVIGKNGYKVLAKRSDGAFYAVKVLQK 132
QY 69 KSLKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGELFFHLORE 128
DB 133 KALKKKEKHIMSERVLLKNVKHPLVGLHYSFQTADKLYFVLDYINGGELFYHLORE 192
QY 129 RRFLEPRARYTAESAIGYLHSLNIYRDLKPNILLDCQGHVLTDFGLCKECVEPE 188
DB 193 RCFLEPRARYTAESAIGYLHSLNIYRDLKPNILLDSQGHILTDFGLCKENIEHN 252
QY 189 ETTSTFCGTPEYLAPEVLKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLN 248
DB 253 GTTSTFCGTPEYLAPEVLKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLN 312
QY 249 QPLQIPGGRVTAACDLQGLLHKDQRLGSKEDFLDKHMFPSPINWDDLYHKRLTTP 308
DB 313 KPLQLKPNITNSARHLEGLLQKDRTKRLGAKEDFTEIKNHVFPSPINWDDLNKKTTP 372
QY 309 FNPVNEGADLKHFDPEFTQEAQVSKSGCTPDTV---ASSSGASSAFLGFSYAQDDDL 365
DB 373 FNPVNGSPDLRHRDFEFTDEPVSPISIGQSPSILITASVKAAAEAFGFSYAPVDSFL 432

RESULT 14
O93524_XENLA
ID O93524_XENLA PRELIMINARY; PRT; 434 AA.
AC O93524;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
```

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS *Xenopus laevis* (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Renal tubule;  
RP Chen S.-Y., Pearce D.;  
RX MEDLINE=99162637; PubMed=10051674; DOI=10.1073/pnas.96.5.2514;  
RA Chen S.-Y., Bhargava A., Mastroberardino L., Meijer O.C., Wang J.,  
RA Buse P., Firestone G.L., Verrey F., Pearce D.;  
RT "Epithelial sodium channel regulated by aldosterone-induced protein  
sgk.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:2514-2519(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Renal tubule;  
RA Chen S.-Y., Pearce D.;  
RX Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (inactive holoenzyme and  
CC monomeric catalytic subunit). Translocates into the nucleus  
CC (monomeric catalytic subunit) (By similarity).  
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
DR EMBL: AF057138; AAC62398.1; -; mRNA.  
DR HSSP: P31751; 1MRV.  
DR GO: GO:0005524; F:ATP binding; IEA.  
DR GO: GO:0004674; P:protein serine/threonine kinase activity; IEA.  
DR GO: GO:0004674; P:protein amino acid phosphorylation; IEA.  
DR InterPro: IPR000961; Pkinase\_C.  
DR InterPro: IPR000719; Prot\_kinase.  
DR InterPro: IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR Pfam: PF00069; Pkinase\_I.  
DR Pfam: PF00433; Pkinase\_C; 1.  
DR ProDom: PD000001; Prot\_kinase; 1.  
DR SMART: SM00133; S\_TK\_X; 1.  
DR SMART: SM00220; S\_TKC; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Cell cycle; Cell division; Hypothetical protein; Kinase;  
KW Nuclear protein; Nucleotide-binding; Serine/threonine-protein kinase;  
KW Transferase; cAMP.  
SQ SEQUENCE 434 AA; 49130 MW; 4A061E38B6AA6F61 CRC64;  
  
Query Match 71.1%; Score 1392; DB 2; Length 434;  
Best Local Similarity 71.1%; Pred. No. 6.1e-90;  
Matches 251; Conservative 55; Mismatches 41; Indels 6; Gaps 2;  
  
QY 9 PSPQSRANGINLGPANPNARPTDFDLKVIKGNVGVLLAKRSGAFYAVKVLQK 68  
DB PPSPSQ---QINLGSSNHPAKPSDFQFLIKGSGFGKVLARHQSDEKFFAVKVLQK 134  
QY 69 KSILKNQNHMAERNVLLKNVRHPPFLVGLRYSFQTPEKLYFVLDYVANGELFFHFLQRE 128  
DB KILKKKEKHMSERNVLLKNVKHPPFLVGLHFSFQTTSRLYFILDYINGGELFFHFLQRE 194  
QY 129 RRLPRPRPYTAESAIGLHSLNIIYDLKPNILLDCQGHVLTDFGLCKECVEPE 188  
DB RCLEPRPRPYAETIAISALGYSLSNIVYDLKPNILLDSQGHVLTDFGLCKENIEPN 254  
QY 189 ETTSTFCGTPYLAPVLRPEYDRAVDWMLCAVLVEMLHGLPPFPNTDVAQMYENILH 248  
DB GTTSTFCGTPYLAPVLRPEYDRAVDWMLCAVLVEMLHGLPPFPNTDVAQMYENILN 314  
QY 249 QPLQIPGGRVTAACDLGLLHKDQRQRLGSKEDFLDIKNHMPFSPINWDDLHKLTPP 308  
DB KPIQLKPNITNSARNLLEGLQDKRTKRIQAKNDFEIKNHIFFSPINWDDLHKLTPP 374

QY 309 FNPNVGPGADLKHFDPEFTQEAUVSKSIGCTPDTV---ASSSGASSAFLGFSVA 358  
DB 375 FNPNVGPGSDLOHFDPEFTPEPVPNSIGQSPDSILITASIKKAAEAFMGFSVA 427  
  
RESULT 15  
Q5BK4\_XENTR PRELIMINARY; PRT; 418 AA.  
AC Q5BK4;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Hypothetical protein.  
OS *Xenopus tropicalis* (Western clawed frog) (*Silurana tropicalis*).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus; *Silurana*.  
OX NCBI\_TaxID=8364;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Whole body;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Whole body;  
RA Klein S., Gerhard D.S.;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC091042; AAH91042.1; -; mRNA.  
DR GO: GO:0005524; F:ATP binding; IEA.  
DR GO: GO:0004674; P:protein serine/threonine kinase activity; IEA.  
DR GO: GO:0004713; P:protein-tyrosine kinase activity; IEA.  
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro: IPR000961; Pkinase\_C.  
DR InterPro: IPR000719; Prot\_kinase.  
DR InterPro: IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00069; Pkinase; 1.  
DR Pfam: PF00433; Pkinase\_C; 1.  
DR SMART: SM00133; S\_TK\_X; 1.  
DR SMART: SM00220; S\_TKC; 1.  
DR SMART: SM00219; TyrKc; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 418 AA; 47659 MW; B66A29461A54E13F CRC64;  
  
Query Match 71.0%; Score 1391; DB 2; Length 418;  
Best Local Similarity 70.8%; Pred. No. 6.8e-90;  
Matches 250; Conservative 55; Mismatches 42; Indels 6; Gaps 2;

QY 9 PSPQSRANGINLGPANPNARPTDFDLKVIKGNVGVLLAKRSGAFYAVKVLQK 68



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:06:05 ; Search time 76.3566 Seconds  
(without alignments)  
2468.595 Million cell updates/sec

Title: US-09-868-131A-4  
Perfect score: 2269  
Sequence: 1 MALKIPAKRIFGNFDPDFI.....EADDAFVGFSYAPPSDLFL 429

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseq1990s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001s.\*  
5: Geneseq2002s.\*  
6: Geneseq2003as.\*  
7: Geneseq2003bs.\*  
8: Geneseq2004s.\*  
9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2269	100.0	429	3 AAY95278	Aay95278 Human ser
2	2269	100.0	429	7 ADN38798	Adn38798 Cancer/an
3	2269	100.0	429	9 ADY17700	Ady17700 PRO polyp
4	2269	100.0	436	4 AAM40620	Aam40620 Human pol
5	2269	100.0	436	4 AAU87228	Aau87228 Novel cen
6	2269	100.0	436	4 AAU87382	Aau87382 Novel cen
7	2269	100.0	436	8 ADI54543	Adi54543 Novel hum
8	2269	100.0	436	8 ADI54697	Adi54697 Novel hum
9	2269	100.0	436	8 ADQ15046	Adq15046 Human can
10	2263	99.7	436	2 AAW87772	Aaw87772 Human ser
11	2254	99.3	436	4 AAM38834	Aam38834 Human pol
12	2246	99.0	429	3 AAB24114	Aab24114 Human ser
13	2246	99.0	436	8 ADI14041	Adi14041 Human NF-
14	2061	90.8	397	9 ADY18746	Ady18746 PRO polyp
15	2061	90.8	464	4 AAM33732	Aam33732 Human pol
16	2061	90.8	464	8 ADL31662	Adl31662 Human pro
17	1974	87.0	446	4 AAB5616	Aab5616 Novel pro
18	1974	87.0	446	8 ADI29222	Adi29222 Human MAR
19	1699	74.9	322	4 AAB99837	Aab99837 AGC prote
20	1699	74.9	322	8 ADJ38885	Adj38885 SGK3 amin
21	1556.5	68.6	373	8 ABM31102	Abm31102 Human dia
22	1501	66.2	526	6 ADA54293	Ada54293 Human pro
23	1501	66.2	526	7 ADG31710	Adg31710 Human pro
24	1476	65.1	407	7 ADC69794	Adc69794 Human ser

25	1476	65.1	431	2 AAW90139	Aaw90139 Human sgk
26	1476	65.1	431	3 AAB24116	Aab24116 Rat serum
27	1476	65.1	431	3 AAY93530	Aay93530 A rat ser
28	1476	65.1	431	6 ADA10889	Ada10889 Human CDN
29	1476	65.1	431	7 ADG31708	Adg31708 Human pro
30	1476	65.1	431	7 ADC50982	Adk50982 Human NOV
31	1476	65.1	431	7 ADC50984	Adk50984 Human NOV
32	1476	65.1	431	8 ADO55118	Ado55118 Protein #
33	1476	65.1	431	9 ADY14632	Ady14632 PRO polyp
34	1476	65.1	431	9 ADY19878	Ady19878 PRO polyp
35	1476	65.1	431	9 AEA04529	Aea04529 Human pro
36	1476	65.1	442	7 ADG31706	Adg31706 Human pro
37	1476	65.1	445	7 ADC69792	Adc69792 Human pro
38	1474.5	65.0	430	7 ADM95921	Adm95921 Human BEC
39	1472	64.9	431	2 AAW77217	Aaw77217 Human cel
40	1472	64.9	431	3 AAB24115	Aab24115 Human ser
41	1472	64.9	431	4 AAB5613	Aab5613 Novel pro
42	1472	64.9	431	7 ADD14174	Add14174 Human src
43	1472	64.9	431	7 ADE31655	Adi31655 Human 290
44	1472	64.9	431	8 ADI29219	Adi29219 Human MAR
45	1472	64.9	431	8 ADN03773	Adn03773 Antipsori

ALIGNMENTS

RESULT 1  
AAY95278  
ID AAY95278 standard; protein; 429 AA.  
XX  
AC AAY95278;  
XX  
DT 12-SEP-2000 (first entry)  
XX  
DE Human serum and glucocorticoid-induced protein kinase 3.  
XX  
KW Serum and glucocorticoid-induced protein kinase 3; SGK3; human;  
phosphorylation; cancer; diabetes; ischaemia; therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 77  
FT Modified-site /note= "O-phosphorylated"  
FT Modified-site 79  
FT Modified-site /note= "O-phosphorylated"  
XX  
PN WO200035946-A1.  
XX  
PD 22-JUN-2000.  
XX  
PF 14-DEC-1999; 99WO-GB004232.  
PR 14-DEC-1998; 98US-0112217P.  
PR 19-AUG-1999; 99GB-00019676.  
PA (UYDU-) UNIV DUNDEE.  
PI Cohen P, Kobayashi T, Deak M;  
DR WPI; 2000-442364/38.  
DR N-PSDB; AAA27858.  
PT Modulation of serum and glucocorticoid-induced protein kinase (SGK) by  
phosphorylation with 3-phosphoinositide-dependent protein kinase-1 (PDK1)  
or dephosphorylation, useful for treatment of cancer, diabetes and  
ischemic diseases.  
PS Disclosure; Page 7; 127pp; English.  
XX  
CC The present sequence is that of human serum and glucocorticoid-induced  
protein kinase (SGK) isoform 3. SGK (see AAY95279) was initially  
identified as a glucocorticoid and osmotic stress-responsive gene. SGK3

CC is activated by phosphorylation in a similar manner to SGK. The invention  
CC provides methods of activating SGK activity by phosphorylation using 3-  
CC phosphoinositide-dependent protein kinase-1 (PDK1), and of reducing the  
CC activity of SGK by dephosphorylation. The invention also provides a  
CC method of identifying a compound that modulates the activity of SGK. Such  
CC compounds are useful for treating patients requiring modulation of SGK,  
CC such as patients with cancer, diabetes or ischaemic disease  
XX Sequence 429 AA;

Query Match 100.0%; Score 2269; DB 3; Length 429;  
Best Local Similarity 100.0%; Pred. No. 1.4e-214;  
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 60  
DB 1 MALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 60  
QY 61 PSEDEDESSQKLHSTSONINLPGSGNPHAKPTDFDFLKVIGKSGFKVLLAKRKLDGKF 120  
DB 61 PSEDEDESSQKLHSTSONINLPGSGNPHAKPTDFDFLKVIGKSGFKVLLAKRKLDGKF 120  
QY 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDVFNCGE 180  
DB 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDVFNCGE 180  
QY 181 LFFHLQRRSPFPHRARFYAAETASALGYLHSIKIVYRDLKPNILLDSVGHVLTDFGL 240  
DB 181 LFFHLQRRSPFPHRARFYAAETASALGYLHSIKIVYRDLKPNILLDSVGHVLTDFGL 240  
QY 241 CKEGIALSDTTTTCGTPEVLAPEVIRKOPYDNTVDWMCGLGAVLYEMLYCLPFPYCRDVA 300  
DB 241 CKEGIALSDTTTTCGTPEVLAPEVIRKOPYDNTVDWMCGLGAVLYEMLYCLPFPYCRDVA 300  
QY 301 EMYDNILHKPLSLRPGVSLTAWISILBELLEKQNRGLGAKEDFLEIQNHPPFESLSWADL 360  
DB 301 EMYDNILHKPLSLRPGVSLTAWISILBELLEKQNRGLGAKEDFLEIQNHPPFESLSWADL 360  
QY 361 VQKKIPPPNPNVAGPDDIRNFDTAFTEETVPYSVCVSSDYSIVNASVLEADDAFVGFSY 420  
DB 361 VQKKIPPPNPNVAGPDDIRNFDTAFTEETVPYSVCVSSDYSIVNASVLEADDAFVGFSY 420  
QY 421 APPSEDLFL 429  
DB 421 APPSEDLFL 429

RESULT 2  
ADN38798  
ID ADN38798 standard; protein; 429 AA.

XX AC ADN38798;

XX 17-JUN-2004 (first entry)

XX DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:116.

XX KW Human; differential expression; cancer; angiogenic disorder;  
XX KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;  
XX KW inflammatory disease; autoimmune disease;  
XX KW retinal neovascularisation syndrome; scarring; uterine fibroid;  
XX KW detection; diagnosis; prognosis; drug screening; drug targeting;  
XX KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;  
XX KW vulnery; gene therapy; vaccine.

XX OS Homo sapiens.

XX PN WO2003042661-A2.

XX PD 22-MAY-2003.

XX PF 13-NOV-2002; 2002WO-US036810.

XX

PR 13-NOV-2001; 2001US-0350666P.  
PR 21-NOV-2001; 2001US-033464P.  
PR 29-NOV-2001; 2001US-0334393P.  
PR 03-DEC-2001; 2001US-0335394P.  
PR 14-DEC-2001; 2001US-0340376P.  
PR 08-JAN-2002; 2002US-0347211P.  
PR 10-JAN-2002; 2002US-0347349P.  
PR 08-FEB-2002; 2002US-035250P.  
PR 13-FEB-2002; 2002US-0356714P.  
PR 20-FEB-2002; 2002US-0359077P.  
PR 29-MAR-2002; 2002US-036809P.  
PR 04-APR-2002; 2002US-0370110P.  
PR 12-APR-2002; 2002US-037224P.  
PR 05-JUN-2002; 2002US-0386614P.  
PR 16-JUL-2002; 2002US-0396839P.  
PR 22-JUL-2002; 2002US-0397775P.  
PR 22-JUL-2002; 2002US-0397845P.  
PR 09-SEP-2002; 2002US-0409450P.  
XX (EOSB-) EOS BIOTECHNOLOGY INC.  
PA  
XX  
PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;  
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;  
XX  
XX WPI: 2003-468649/44.  
DR N-PSDB; ADN38797.

Determining the presence or absence of a pathological cell in a patient,  
useful for diagnosing, prognosing or treating cancer, comprises detecting  
a nucleic acid in a biological sample.

Claim 12; SEQ ID NO 116; 1385pp; English.

CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)  
CC whose expression is upregulated or downregulated in specific cancers or  
CC other diseases such as angiogenic or fibrotic disorders, and to methods  
CC of determining the presence or absence of a pathological cell in a  
CC patient by detecting a nucleic acid at least 80% identical to those of  
CC the invention or by detecting a polypeptide of the invention. The  
CC invention also relates to expression vectors and host cells comprising a  
CC nucleic acid of the invention; antibodies which specifically bind a  
CC polypeptide of the invention; use of such antibodies for drug targeting;  
CC and methods of screening for modulators of activity or expression of the  
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,  
CC antibodies and methods are useful for diagnosing, prognosing and treating  
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,  
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
CC neovascularisation syndromes, scarring and uterine fibroids. They may  
CC also be useful in wound healing and in contraception. The present  
CC sequence represents a polypeptide of the invention.

XX SQ Sequence 429 AA;

Query Match 100.0%; Score 2269; DB 7; Length 429;  
Best Local Similarity 100.0%; Pred. No. 1.4e-214;  
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 60  
DB 1 MALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 60  
QY 61 PSEDEDESSQKLHSTSONINLPGSGNPHAKPTDFDFLKVIGKSGFKVLLAKRKLDGKF 120  
DB 61 PSEDEDESSQKLHSTSONINLPGSGNPHAKPTDFDFLKVIGKSGFKVLLAKRKLDGKF 120  
QY 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDVFNCGE 180  
DB 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDVFNCGE 180  
QY 181 LFFHLQRRSPFPHRARFYAAETASALGYLHSIKIVYRDLKPNILLDSVGHVLTDFGL 240  
DB 181 LFFHLQRRSPFPHRARFYAAETASALGYLHSIKIVYRDLKPNILLDSVGHVLTDFGL 240

QY 241 CKEGIAISDTTTCGTEPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPPYCRDVA 300  
 DB 241 CKEGIAISDTTTCGTEPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPPYCRDVA 300  
 QY 301 EMDYNIHLKPLSLRPGVSLTAWSLLELLEKORQNLGAKEDFLEIQNHPPFESLSWADL 360  
 DB 301 EMDYNIHLKPLSLRPGVSLTAWSLLELLEKORQNLGAKEDFLEIQNHPPFESLSWADL 360  
 QY 361 VQKKIPPPFNPVAGPDDIRNFDTAFTETVPYSCVSSDYSIIVNASVLEADDAFVGFSY 420  
 DB 361 VQKKIPPPFNPVAGPDDIRNFDTAFTETVPYSCVSSDYSIIVNASVLEADDAFVGFSY 420  
 QY 421 APPSEDLFL 429  
 DB 421 APPSEDLFL 429  
 RESULT 3  
 ADY17700  
 ID ADY17700 standard; protein; 429 AA.  
 AC ADY17700;  
 XX  
 DT 05-MAY-2005 (first entry)  
 DE PRO polypeptide SEQ ID NO 3506.  
 XX  
 KW Antinflammatory; Immune disorder; Dermatological; Immunosuppressive;  
 KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;  
 KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotrophic;  
 KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;  
 KW Antiallergic; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W02005016962-A2.  
 XX  
 PD 24-FEB-2005.  
 XX  
 PF 11-AUG-2004; 2004WO-US026249.  
 XX  
 PR 11-AUG-2003; 2003US-0493546P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;  
 XX  
 DR WPI; 2005-182330/19.  
 XX  
 PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and  
 PT treating an immune related disorder, e.g. systemic lupus erythematosus,  
 PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.  
 XX  
 PS Claim 8; SEQ ID NO 3506; 158pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid encoding a PRO  
 CC polypeptide. The polypeptide, agonist or an antagonist, antibody,  
 CC composition, and method are useful for diagnosing and treating an immune  
 CC related disorder, e.g. systemic lupus erythematosus, rheumatoid  
 CC arthritis. The present sequence represents a PRO polypeptide.  
 XX  
 SQ Sequence 429 AA;  
 Query Match 100.0%; Score 2269; DB 9; Length 429;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-214;  
 Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKQSD 60  
 DB 1 MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKQSD 60  
 QY 61 PSEDEDESSQKLHSTSONINLGPNGPHAKPTDFDLKLVIGKSGFKVLLAKRKLKDKGF 120

DB 61 PSEDEDESSQKLHSTSONINLGPNGPHAKPTDFDLKLVIGKSGFKVLLAKRKLKDKGF 120  
 QY 121 YAVKVLQKKITLVNRKQKHIMAEARNVLLKNVHPFLVGLHVSFOTTEKLYFVLDFVNGGE 180  
 DB 121 YAVKVLQKKITLVNRKQKHIMAEARNVLLKNVHPFLVGLHVSFOTTEKLYFVLDFVNGGE 180  
 QY 181 LFPHLQERSFPEHRAFYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVVLTFDGL 240  
 DB 181 LFPHLQERSFPEHRAFYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVVLTFDGL 240  
 QY 241 CKEGIAISDTTTCGTEPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPPYCRDVA 300  
 DB 241 CKEGIAISDTTTCGTEPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPPYCRDVA 300  
 QY 301 EMDYNIHLKPLSLRPGVSLTAWSLLELLEKORQNLGAKEDFLEIQNHPPFESLSWADL 360  
 DB 301 EMDYNIHLKPLSLRPGVSLTAWSLLELLEKORQNLGAKEDFLEIQNHPPFESLSWADL 360  
 QY 361 VQKKIPPPFNPVAGPDDIRNFDTAFTETVPYSCVSSDYSIIVNASVLEADDAFVGFSY 420  
 DB 361 VQKKIPPPFNPVAGPDDIRNFDTAFTETVPYSCVSSDYSIIVNASVLEADDAFVGFSY 420  
 QY 421 APPSEDLFL 429  
 DB 421 APPSEDLFL 429  
 RESULT 4  
 AAM40620  
 ID AAM40620 standard; protein; 496 AA.  
 XX  
 AC AAM40620;  
 XX  
 DT 22-OCT-2001 (first entry)  
 DE Human polypeptide SEQ ID NO 5551.  
 XX  
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200153312-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 26-DEC-2000; 2000WO-US034263.  
 XX  
 PR 23-DEC-1999; 99US-00471275.  
 PR 21-JAN-2000; 2000US-00488725.  
 PR 25-APR-2000; 2000US-0052317.  
 PR 20-JUN-2000; 2000US-00598042.  
 PR 19-JUL-2000; 2000US-00620312.  
 PR 03-AUG-2000; 2000US-00653450.  
 PR 14-SEP-2000; 2000US-00662191.  
 PR 19-OCT-2000; 2000US-00693036.  
 PR 29-NOV-2000; 2000US-00727344.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
 PI Zhou P, Goodrich R, Drmanac RT;  
 XX  
 DR WPI; 2001-442253/47.  
 DR N-PSDB; AA159776.  
 XX  
 PT Novel nucleic acids and polypeptides, useful for treating disorders such  
 PT as central nervous system injuries.

XX Example 2; SEQ ID NO 5551; 10078pp; English.  
PS The invention relates to human nucleic acids (AA157798-AA161369) and the  
CC encoded polypeptides (AA38642-AA42213) with neurotropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: Immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders. Note: The sequence data for this patent did not form  
CC part of the printed specification  
XX  
SQ Sequence 496 AA;

Query Match 100.0%; Score 2269; DB 4; Length 496;  
Best Local Similarity 100.0%; Pred. No. 1.7e-214;  
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MALKIPAKRIFGDNEDPDRFKQRRAGLNEFIQNLVRYPELYNHPDVRAPLQMDSPKHQSD 60  
DB 68 MALKIPAKRIFGDNEDPDRFKQRRAGLNEFIQNLVRYPELYNHPDVRAPLQMDSPKHQSD 127  
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DB 128 PSEDEDESSQKLHSTSQINILGPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLKGKF 187  
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DB 248 LFPHLORESFPHRARFYAAETASALGYLHSTKIIVYRDLKPENILLDSVGHVVLTDGFL 307  
QY 241 CKEGIAISDTTTFCTGPEYLAPEVIRKQPDYNTVDWMCIGAVLYEMLYGLPFYCRDVA 300  
DB 308 CKEGIAISDTTTFCTGPEYLAPEVIRKQPDYNTVDWMCIGAVLYEMLYGLPFYCRDVA 367  
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DB 368 EMYDNLHKPLSLRPGVSLTAWSIILELLEKQKQNLGAKEDFLEIQNHPPFFESLSWADL 427  
QY 361 VOKKIPPPNPVAGPDDIRNFDTAETETVPYSCVSSDYISVNASVLEADDAFYGFSY 420  
DB 428 VOKKIPPPNPVAGPDDIRNFDTAETETVPYSCVSSDYISVNASVLEADDAFYGFSY 487  
QY 421 APPSEDLFL 429  
DB 488 APPSEDLFL 496

RESULT 5  
AAU87228  
ID AAU87228 standard; protein; 496 AA.  
XX  
AC AAU87228;  
XX  
XX 05-JUN-2002 (first entry)  
XX Novel central nervous system protein #138.  
XX Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;  
XX hyperproliferative disorder; neoplasm; cardiovascular disorder;  
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;  
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;  
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;

KW adenocarcinoma; reproductive system disorder; testicular feminisation;  
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;  
KW respiratory disorder; renal disorder; kidney failure; blood disorder;  
KW myocardial infarction; wound healing; cell proliferation; skin aging;  
KW food additive; food preservative; gene therapy.  
OS Homo sapiens.  
XX  
PN WO200155318-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US001332.  
XX  
XX 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
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PR 07-JUN-2000; 2000US-0209467P.  
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Qy 421 APPSEDLFL 429  
Db 488 APPSEDLFL 496

RESULT 6  
AAU87382  
ID AAU87382 standard; protein; 496 AA.  
XX  
AC AAU87382;  
XX  
DT 05-JUN-2002 (first entry)  
XX  
DE Novel central nervous system protein #292.  
XX  
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;  
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;  
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;  
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;  
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;  
KW adenocarcinoma; reproductive system disorder; testicular feminisation;  
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;  
KW respiratory disorder; renal disorder; kidney failure; blood disorder;  
KW myocardial infarction; wound healing; cell proliferation; skin aging;  
KW food additive; food preservative; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200155318-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US6001332.  
XX  
PR 31-JAN-2000; 2000US-0179065P.  
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 PR 11-DEC-2000; 2000US-0254057P.  
 PR 03-JAN-2001; 2001US-0259678P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Barash SC, Ruben SM;  
 PI  
 XX WPI; 2001-581633/65.  
 DR N-PSDB; ABK43712.  
 XX  
 XX New isolated nucleic acid encoding a protein for diagnosing, preventing,  
 PT treating or ameliorating medical conditions and used as food additives or  
 PT preservatives.  
 PT  
 XX  
 XX Claim 9; SEQ ID NO 900; 837pp; English.  
 PS  
 XX The invention describes an isolated nucleic acid molecule (I) encoding a  
 CC novel central nervous system protein. (I) and polypeptides (II) encoded  
 CC by (I), are used to treat a medical conditions and in diagnosis of a  
 CC pathological condition. Disorders which are diagnosed or treated include  
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and  
 CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses  
 CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders  
 CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,  
 CC adenocarcinomas and irritable bowel syndrome, reproductive system  
 CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes  
 CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.  
 CC leukaemia, disorders involving neovascularisation e.g. malignancies,  
 CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.  
 CC acute kidney failure and blood related disorders e.g. myocardial  
 CC infarction. The polypeptides can also be used to aid wound healing and  
 CC epithelial cell proliferation, to prevent skin aging due to sunburn, to  
 CC maintain organs before transplantation, for supporting cell culture of  
 CC primary tissues, to regenerate tissues and in chemotaxis. The  
 CC polypeptides can also be used as a food additive or preservative to  
 CC increase or decrease storage capabilities, fat content, lipid, protein,  
 CC  
 Query Match 100.0%; Score 2269; DB 4; Length 496;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-214;  
 Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MALKIPAKRIFGNFDDFKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKQSD 60  
 DB 68 MALKIPAKRIFGNFDDFKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKQSD 127  
 QY 61 PSEDEDESSQKLHSTSQNLINLPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLDDKF 120  
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 Db 248 LFFHLQERSFPFHRARFYAAEIASALGYLHSLKIVYRDLPENILLDSVGHVVLTDGFL 307  
 QY 241 CKSGIAISDTTTCGTPPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPPYCRDVA 300  
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 Db 488 APPSEDLFL 496  
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 ID ADI54543 standard; protein; 496 AA.  
 XX  
 AC ADI54543;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Novel human protein seq id 746.  
 XX  
 KW neuroprotective; nootropic; antiparkinsonian; anticonvulsant;  
 KW antidiabetic; antirheumatic; antiarthritic; dermatological;  
 KW antiinflammatory; immunosuppressive; antithyroid; antianemic; vasotropic;  
 KW anti-HIV; hepatotropic; virucide; antibacterial; fungicide;  
 KW antiparasitic; muscular; gynaecological; gastrointestinal; respiratory;  
 KW cardiovascular; antiarteriosclerotic; antiarrhythmic; cardiac;  
 KW nephrotropic; litholytic; cytostatic; gene therapy; neural disorder;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's chorea;  
 KW amyotrophic lateral sclerosis; multiple sclerosis;  
 KW immune system disorder; diabetes; rheumatoid arthritis;  
 KW systemic lupus erythematosus; autoimmune thyroiditis; haemolytic anaemia;  
 KW inflammatory disorder; ischaemia-reperfusion injury;  
 KW inflammatory bowel disease; Crohn's disease; infectious disease;  
 KW HIV infection; hepatitis infection; bacterial infection;  
 KW fungal infection; parasitic infection; muscular disorder;  
 KW reproductive disorder; gastrointestinal disorder; pulmonary disorder;  
 KW cardiovascular disorder; atherosclerosis; arrhythmia; myocarditis;  
 KW renal disorder; acute glomerulonephritis; pyelonephritis;  
 KW renal lithiasis; proliferative disorder; cancerous diseases; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004018969-A1.  
 XX  
 XX 29-JAN-2004.  
 XX  
 XX 17-JAN-2001; 2001US-00764875.  
 PF  
 XX 31-JAN-2000; 2000US-0179065P.  
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PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234397P.  
PR 25-SEP-2000; 2000US-0234398P.  
PR 26-SEP-2000; 2000US-0234584P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 13-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
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PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
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PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
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PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
(ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
XX  
PI Rosen CA, Ruben SM, Barash SC;  
XX  
XX WPI; 2004-122079/12.  
DR N-PSDB; ADI53945.  
XX  
XX New polypeptides and nucleic acid molecules, useful for detecting,  
PT preventing, diagnosing, prognosticating, treating or ameliorating medical  
PT conditions e.g. neural disorders, reproductive disorders or infectious  
PT diseases.  
XX  
XX Claim 11; SEQ ID NO 746; 413pp; English.  
XX  
XX The invention describes an isolated polypeptide comprising an amino acid  
CC



CC sequence at least 90% identical to: a polypeptide fragment, domain,  
 CC epitope, or full-length protein of any one of 607 amino acid sequences  
 CC (i) described in the specification; a polypeptide fragment of (i), or the  
 CC encoded sequence contained in (ii), having biological activity; or a  
 CC variant, allelic variant, or a species homologue of (i). The polypeptides  
 CC and nucleic acid molecules are useful for detecting, preventing,  
 CC diagnosing, prognosticating, treating or ameliorating medical conditions  
 CC such as neural disorders, e.g. Alzheimer's disease, Parkinson's disease,  
 CC Huntington's chorea, amyotrophic lateral sclerosis or multiple sclerosis,  
 CC immune system disorders, e.g. diabetes, rheumatoid arthritis, systemic

Query Match 100.0%; Score 2269; DB 8; Length 496;  
 Best Local Similarity 100.0%; Pred. NO. 1.7e-214;  
 Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MALKIPAKRIFGDNFDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKQSD 60  
 Db |||||||  
 Qy 68 MALKIPAKRIFGDNFDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKQSD 127  
 Db |||||||  
 Qy 61 PSEDEBRSQKLHSTSONINLGPSGNPHAKPTDFDLKVIKGSFGKVLAKRKLKDKF 120  
 Db |||||||  
 Qy 128 PSEDEBRSQKLHSTSONINLGPSGNPHAKPTDFDLKVIKGSFGKVLAKRKLKDKF 187  
 Db |||||||  
 Qy 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSQTTEKLYFVLDFVNGGE 180  
 Db |||||||  
 Qy 188 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSQTTEKLYFVLDFVNGGE 247  
 Db |||||||  
 Qy 181 LFFHLQERSFPFHRARFYAAETASALGYLHSTKIIVYRDLKPNILLDSVGHVLTDFGL 240  
 Db |||||||  
 Qy 248 LFFHLQERSFPFHRARFYAAETASALGYLHSTKIIVYRDLKPNILLDSVGHVLTDFGL 307  
 Db |||||||  
 Qy 241 CKEGIAISDTTTFCTGTPYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVA 300  
 Db |||||||  
 Qy 308 CKEGIAISDTTTFCTGTPYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVA 367  
 Db |||||||  
 Qy 301 EMDYNILHKPLSRPGVSLTAWSLLELLEKQKQNLGAKEDFLEIQNHPPFESLSWADL 360  
 Db |||||||  
 Qy 368 EMDYNILHKPLSRPGVSLTAWSLLELLEKQKQNLGAKEDFLEIQNHPPFESLSWADL 427  
 Db |||||||  
 Qy 361 VQKKIPPPNPVAGDDIRNFDTAFTETVPYVSVCSVDYSIVNASVLEADDAFVGFYSY 420  
 Db |||||||  
 Qy 428 VQKKIPPPNPVAGDDIRNFDTAFTETVPYVSVCSVDYSIVNASVLEADDAFVGFYSY 487  
 Db |||||||  
 Qy 421 APPSEDLFL 429  
 Db |||||||  
 Qy 488 APPSEDLFL 496  
 Db |||||||

## RESULT 8

ADIS4697

ADIS4697 standard; protein; 496 AA.

AC ADIS4697;

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reproductive disorder; gastrointestinal disorder; pulmonary disorder;  
 cardiovascular disorder; atherosclerosis; arrhythmia; myocarditis;  
 renal disorder; acute glomerulonephritis; pyelonephritis;  
 renal lithiasis; proliferative disorder; cancerous diseases; human.

Homo sapiens.

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PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
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PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 13-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249246P.  
PR 17-NOV-2000; 2000US-0249247P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.

PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
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PI Rosen CA, Ruben SM, Barash SC;  
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XX WPI; 2004-122079/12.  
DR N-PSDB; ADI54099.  
XX  
XX  
PT New polypeptides and nucleic acid molecules, useful for detecting, medical  
PT preventing, diagnosing, prognosticating, treating or ameliorating medical  
PT conditions e.g. neural disorders, reproductive disorders or infectious  
PT diseases.  
XX  
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PS Claim 11; SEQ ID NO 900; 413pp; English.  
XX  
CC The invention describes an isolated polypeptide comprising an amino acid  
CC sequence at least 90% identical to: a polypeptide fragment, domain,  
CC epitope, or full-length protein of any one of 607 amino acid sequences  
CC (I) described in the specification; a polypeptide fragment of (I), or the  
CC encoded sequence contained in (II), having biological activity; or a  
CC variant, allelic variant, or a species homologue of (I). The polypeptides  
CC and nucleic acid molecules are useful for detecting, preventing,  
CC diagnosing, prognosticating, treating or ameliorating medical conditions  
CC such as neural disorders, e.g. Alzheimer's disease, Parkinson's disease,  
CC Huntington's chorea, amyotrophic lateral sclerosis or multiple sclerosis,  
CC immune system disorders, e.g. diabetes, rheumatoid arthritis, systemic

Query Match 100.0%; Score 2269; DB 8; Length 496;  
Best Local Similarity 100.0%; Pred. No. 1.7e-214;  
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFQWDSPKHQSD 60  
DB 68 MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFQWDSPKHQSD 127  
QY 61 PSEDEDESSQKLHSTSQNLGSPGNPHAKPTDFDLKVIKGSFGKVLAKRKLDGKF 120  
DB 128 PSEDEDESSQKLHSTSQNLGSPGNPHAKPTDFDLKVIKGSFGKVLAKRKLDGKF 187  
QY 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYHSFQTEKLYFVLDFVNGGE 180  
DB 188 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYHSFQTEKLYFVLDFVNGGE 247  
QY 181 LFFHLQERSFPFHRARFYAAETASALGYLHSIKIVYRDLKPENILLDSVGHVLTDFGL 240  
DB 248 LFFHLQERSFPFHRARFYAAETASALGYLHSIKIVYRDLKPENILLDSVGHVLTDFGL 307  
QY 241 CKEGIAISDTTTFCTPEYLAPEVIRKQPYDNTDWMCLGAVLYEMLYGLPPFYCRDVA 300  
DB 308 CKEGIAISDTTTFCTPEYLAPEVIRKQPYDNTDWMCLGAVLYEMLYGLPPFYCRDVA 367  
QY 301 EMYDNLHKPLSLRPGCVSLTAWSIIEELLEKQRQNLGAKEDPLEIQNHPPFESLSWADL 360  
DB 368 EMYDNLHKPLSLRPGCVSLTAWSIIEELLEKQRQNLGAKEDPLEIQNHPPFESLSWADL 427  
QY 361 VOKKIPPPNPNVAGPDDIRNFDTAFTETVPYSCVSSDYSTVNASVLEADDAFVGFSY 420  
DB 428 VOKKIPPPNPNVAGPDDIRNFDTAFTETVPYSCVSSDYSTVNASVLEADDAFVGFSY 487  
QY 421 APPSEDLFL 429  
DB 488 APPSEDLFL 496

RESULT 9  
ADQ15046  
ID ADQ15046 standard; protein; 496 AA.  
XX

AC ADQ15046;  
XX 07-OCT-2004 (first entry)  
XX Human cancer related polypeptide, 2188.  
XX Cancer; angiogenic disorder; cytostatic; antiangiogenic; gene therapy;  
XX human.  
XX Homo sapiens.  
XX WO2004058153-A2.  
XX 15-JUL-2004.  
XX 16-DEC-2003; 2003WO-US040226.  
XX 20-DEC-2002; 2002US-0435108P.  
XX 23-DEC-2002; 2002US-0436443P.  
XX 07-JAN-2003; 2003US-0438498P.  
XX 31-JAN-2003; 2003US-0444370P.  
XX 06-FEB-2003; 2003US-0446031P.  
XX 11-MAR-2003; 2003US-0453635P.  
XX 25-MAR-2003; 2003US-0457199P.  
XX 10-APR-2003; 2003US-0462458P.  
XX 30-APR-2003; 2003US-0466732P.  
XX 08-MAY-2003; 2003US-0469184P.  
XX 19-MAY-2003; 2003US-0471663P.  
XX 03-JUN-2003; 2003US-0475472P.  
XX 12-JUN-2003; 2003US-0478150P.  
XX 23-JUN-2003; 2003US-0480631P.  
XX 15-JUL-2003; 2003US-0487369P.  
XX 29-JUL-2003; 2003US-0490866P.  
XX 02-SEP-2003; 2003US-0499614P.  
XX 09-OCT-2003; 2003US-0510081P.  
XX 06-NOV-2003; 2003US-0517742P.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX Lightcap ES, Ecsedy JA, Hunter JJ, Macbeth KJ, Nestor MT;  
XX WPI; 2004-525772/50.  
XX N-PSDB; ADQ15045.  
XX Identifying a compound capable of treating cancer or an angiogenic  
XX disorder by combining a compound to be tested with e.g., 15986, 2179 or  
XX 13249 polypeptide and detecting binding of the test compound to the  
XX polypeptide.  
XX Claim 1; SEQ ID NO 4; 576pp; English.  
XX The invention relates to a novel method for identifying a compound  
XX capable of treating cancer or an angiogenic disorder. The method  
XX comprises: combining a compound to be tested with a cancer related  
XX polypeptide; and detecting binding of the test compound to the  
XX polypeptide. The invention further comprises: identifying a subject  
XX having or at risk for developing cancer; and treating a subject having a  
XX cancer or a cancer characterised by aberrant 15986, 2188, 20743, 9148,  
XX 9151, 9791, 44252, 14184, 42461, 8204, 7970, 25552, 21657, 26492, 2411,  
XX 15088, 1905, 28899, 63380, 33935, 10480, 12686, 25501, 17694, 15701,  
XX 53062, 49908, 21612, 38949, 6216, 46863, 9235, 2201, 6985, 9883, 12238,  
XX 18057, 21617, 39228, 49928, 54476, 62113, 64316, 12264, 32362, 58198,  
XX 2887, 3205, 8557, 9600, 9693, 44867, 53058, 55556, 57658, 2208, 10252,  
XX 10302, 14218, 33877, 10317, 10485, 25964, 14815, 1363, 1397, 14827,  
XX 21708, 3801, 64698, 2179 or 13249 cancer related polypeptide activity or  
XX nucleic acid expression. The method and compounds have cytostatic and  
XX antiangiogenic activities. The cancer related genes may be used in gene  
XX therapy to treat disorders. The method is useful in identifying a  
XX compound capable of treating cancer or an angiogenic disorder. This  
XX sequence represents a human cancer related polypeptide used in the method  
XX of the invention.  
XX Sequence 496 AA;

Query Match 100.0%; Score 2269; DB 8; Length 496;  
Best Local Similarity 100.0%; Pred. No. 1.7e-214; Indels 0; Gaps 0;  
Matches 429; Conservative 0; Mismatches 0;  
Qy 1 MALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKQSD 60  
Db 68 MALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKQSD 127  
Qy 61 PSEDEERSOKLHSTSONINLGPSGNPHAKPTDFDLKVIKGSFGKVLAKKLDGKF 120  
Db 128 PSEDEERSOKLHSTSONINLGPSGNPHAKPTDFDLKVIKGSFGKVLAKKLDGKF 187  
Qy 121 YAVKVLQKKIVLNKQKHIMARNVLLKNVKKHPFLVGLHVSFOTTEKLYFVLDFVNGGE 180  
Db 188 YAVKVLQKKIVLNKQKHIMARNVLLKNVKKHPFLVGLHVSFOTTEKLYFVLDFVNGGE 247  
Qy 181 LFFHLQERSFPEHRARFYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVVLTFDGL 240  
Db 248 LFFHLQERSFPEHRARFYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVVLTFDGL 307  
Qy 241 CKEGIALSDTTTTFCGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFCRDVA 300  
Db 308 CKEGIALSDTTTTFCGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFCRDVA 367  
Qy 301 EMYDNLHKPLSLRPGVSLTAWSIILBELLEKQNRILGAKEDFLEIQNHHPFFESLSWADL 360  
Db 368 EMYDNLHKPLSLRPGVSLTAWSIILBELLEKQNRILGAKEDFLEIQNHHPFFESLSWADL 427  
Qy 361 VQKKIPPPNPVAGPDDIRNPDFTAFTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 420  
Db 428 VQKKIPPPNPVAGPDDIRNPDFTAFTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 487  
Qy 421 APPESEDLFL 429  
Db 488 APPESEDLFL 496  
RESULT 10  
AAW87772  
ID AAW87772 standard; protein; 496 AA.  
XX AC AAW87772;  
XX AC AAW87772;  
XX 17-MAR-1999 (first entry)  
XX DE Human serum glucocorticoid-regulated kinase (H-SGK2) polypeptide.  
XX KW Serum glucocorticoid-regulated kinase; H-SGK2; human; gene therapy;  
XX KW serine/threonine protein kinase; inflammation; rheumatoid arthritis;  
XX KW septicemia; autoimmune disease; inflammatory bowel disease; psoriasis;  
XX KW transplant rejection; infection; stroke; ischaemia; renal disorder;  
XX KW restenosis; brain injury; acquired immune deficiency syndrome; AIDS;  
XX KW metabolic; bone; osteoporosis; lymphoproliferation; atherosclerosis;  
XX KW Alzheimer's disease; cancer.  
XX OS Homo sapiens.  
XX PN EP889127-A1.  
XX PD 07-JAN-1999.  
XX PF 18-JUN-1998; 98EP-00304830.  
XX PR 01-JUL-1997; 97US-0051446P.  
XX PR 23-DEC-1997; 97US-00997212.  
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.  
XX PI Kumar S, Zou C;  
XX WPI; 1999-062658/06.  
XX N-PSDB; AAV99653.

XX New nucleic acid encoding human H-SGK2 poly-peptide(s) - useful for  
PT diagnosis, treatment and prevention of e.g. arthritis, infections,  
PT cancer, Alzheimer's disease.  
XX  
PS  
PS  
XX Claim 11; Page 8; 27pp; English.  
XX  
XX This represents a human serum glucocorticoid-regulated kinase (H-SGK2)  
CC polypeptide, a novel member of the serine/threonine protein kinase  
CC family. A host cell transfected or transformed with an expression system  
CC comprising the H-SGK2 nucleic acid can be used for the recombinant  
CC production of the protein. The H-SGK2 polypeptide is useful for treating  
CC a subject who require enhanced/reduced activity or expression/inhibition  
CC of the polypeptide. Recombinant H-SGK2 is used to raise antibodies; in  
CC vaccines; in drug screens; and to identify soluble or membrane-bound  
CC receptors. The H-SGK2 polypeptides are useful for treating inflammation  
CC (rheumatoid arthritis); septicemia; autoimmune disease (inflammatory  
CC bowel disease or psoriasis); transplant rejection; infection; stroke;  
CC leukaemia; renal disorders; restenosis; brain injury; acquired immune  
CC deficiency syndrome; metabolic and other bone diseases (osteoporosis);  
CC cancer (e.g. lymphoproliferation); atherosclerosis and Alzheimer's  
XX disease. The H-SGK2 nucleic acids can be used in gene therapy  
XX  
SQ Sequence 496 AA;

Query Match 99.7%; Score 2263; DB 2; Length 496;  
Best Local Similarity 99.8%; Pred. No. 6.7e-214;  
Matches 428; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALKIPAKRIFGDNFDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 60  
DB 68 MALKIPAKRIFGDNFDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 127  
QY 61 PSEDEDESSQKLHSTSQNLGPGSGNPHAKPTDFDLKVIKGSFGKVLAKRKLDDGKF 120  
DB 128 PSEDEDESSQKLHSTSQNLGPGSGNPHAKPTDFDLKVIKGSFGKVLAKRKLDDGKF 187  
QY 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVKHPFLVGLHYSFQTTEKLYFVLDVNGGE 180  
DB 188 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVKHPFLVGLHYSFQTTEKLYFVLDVNGGE 247  
QY 181 LFFHLQERSFPPHRAFYAAETASALGYLHSIKIVYRDLKPNILLDSVGHVLLTDFGL 240  
DB 248 LFFHLQERSFPPHRAFYAAETASALGYLHSIKIVYRDLKPNILLDSVGHVLLTDFGL 307  
QY 241 CKEGIAISDTTTFCTGPEYLAPEVIRKQPYDNTVDWCLGAVLYEMLYGLPPFYCRDVA 300  
DB 308 CKEGIAISDTTTFCTGPEYLAPEVIRKQPYDNTVDWCLGAVLYEMLYGLPPFYCRDVA 367  
QY 301 EMDYDNLHKPLSLRPGVSLTAWSLBELLEKQKQNLGAKEDPLEIQNHPPFFESLSWADL 360  
DB 368 EMDYDNLHKPLSLRPGVSLTAWSLBELLEKQKQNLGAKEDPLEIQNHPPFFESLSWADL 427  
QY 361 VQKKIPPPNPVAGPDDIRNFDTAETFTVPYVCVSDYSIVNASVLEADDAFVGFSY 420  
DB 428 VQKKIPPPNPVAGPDDIRNFDTAETFTVPYVCVSDYSIVNASVLEADDAFVGFSY 487  
QY 421 APPSEDLFL 429  
DB 488 APPSEDLFL 496

RESULT 11  
AAM38834  
ID AAM38834 standard; protein; 496 AA.

XX  
AC AAM38834;

XX 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 1979.

XX Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;

KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
XX  
XX Homo sapiens.  
XX WO200153312-A1.  
XX 26-JUL-2001.  
XX  
XX 26-DEC-2000; 2000WO-US034263.  
XX  
XX 23-DEC-1999; 99US-00471275.  
PR 21-JAN-2000; 2000US-00488725.  
PR 25-APR-2000; 2000US-00552317.  
PR 20-JUN-2000; 2000US-00598042.  
PR 19-JUL-2000; 2000US-00620312.  
PR 03-AUG-2000; 2000US-00653450.  
PR 14-SEP-2000; 2000US-00662191.  
PR 19-OCT-2000; 2000US-00693036.  
PR 29-NOV-2000; 2000US-00727344.  
XX  
XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou P, Goodrich R, Drmanac RT;  
XX  
XX WPI; 2001-442253/47.  
DR N-PSDB; AAI57990.

XX Novel nucleic acids and polypeptides, useful for treating disorders such  
PT as central nervous system injuries.  
XX  
XX Example 3; SEQ ID NO 1979; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the  
CC encoded polypeptides (AAM38642-AAM42213) with neurotropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: Immune system suppression.  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemia and  
CC C.N.S disorders. Note: The sequence data for this patent did not form  
CC part of the printed specification

XX Sequence 496 AA;

Query Match 99.3%; Score 2254; DB 4; Length 496;  
Best Local Similarity 99.5%; Pred. No. 5.1e-213;  
Matches 427; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MALKIPAKRIFGDNFDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 60  
DB 68 MALKIPAKRIFGDNFDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 127  
QY 61 PSEDEDESSQKLHSTSQNLGPGSGNPHAKPTDFDLKVIKGSFGKVLAKRKLDDGKF 120  
DB 128 PSEDEDESSQKLHSTSQNLGPGSGNPHAKPTDFDLKVIKGSFGKVLAKRKLDDGKF 187  
QY 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVKHPFLVGLHYSFQTTEKLYFVLDVNGGE 180  
DB 188 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVKHPFLVGLHYSFQTTEKLYFVLDVNGGE 247  
QY 181 LFFHLQERSFPPHRAFYAAETASALGYLHSIKIVYRDLKPNILLDSVGHVLLTDFGL 240

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Db      248  LFFHLQERSFPEHRAFYAAETASALGYLHSIKIVYRDLKPENILSDSGHVVLDTDFGL 307
Qy      241  CKEGIAISDTTTCGTPPEYLAPEVIRKQPDYDNTVDWCLGAVLYEMLYGLPPFYCRDVA 300
Db      308  CKEGIAISDTTTCGTPPEYLAPEVIRKQPDYDNTVDWCLGAVLYEMLYGLPPFYCRDVA 367
Qy      301  EMDYDNLHKPLSLRPGVSLTAWSLLELLEKQDNRLGAKEDFLEIQNHPPFFESLSWADL 360
Db      368  EMDYDNLHKPLSLRPGVSLTAWSLLELLEKQDNRLGAKEDFLEIQNHPPFFESLSWADL 427
Qy      361  VQKKIPPPFNPNVAGPDDIRNEDTAFTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 420
Db      428  VQKKIPPPFNPNVAGPDDIRNEDTAFTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 487
Qy      421  APPSEDLFL 429
Db      488  APPSEDLFL 496

RESULT 12
AAB24114
ID AAB24114 standard; protein; 429 AA.
AC AAB24114;
XX
XX 29-JAN-2001 (first entry)
XX Human serine threonine kinase STK3 protein sequence SEQ ID NO:4.
XX Human; STK3; serine threonine kinase; HSGK; RSGK;
KW serum and glucocorticoid regulated kinase.
XX Homo sapiens.
XX CN1259573-A.
XX 12-JUL-2000.
XX 29-OCT-1998; 98CN-00123822.
XX 29-OCT-1998; 98CN-00123822.
XX (UYFU-) UNIV FUDAN.
XX Yu L, Fu Q, Zhao Y;
XX WPI; 2000-587991/56.
DR N-PSDB; AAA99248.
XX New human serine threonine protein kinase, its code sequence,
PT preparation, and use.
XX Claim 4; Page 19; 29pp; Chinese.
XX
XX The present invention describes human serine threonine kinase STK3, which
CC is a new member of the serine/threonine protein kinase family. Human STK3
CC shares homology with human serum and glucocorticoid regulated kinase
CC (HSGK) and rat SGK (RSGK). The present sequence represents the human STK3
CC protein from the present invention
XX
SQ Sequence 429 AA;

Query Match 99.0%; Score 2246; DB 3; Length 429;
Best Local Similarity 99.1%; Pred. No. 2.6e-212;
Matches 425; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1  MALKIPAKRIFGNFDFIKQRRAGINEFIONLVRYPELYNHPDVRAFLQWDSPKHQSD 60
Db      1  MALKIPAKRIFGNFDFIKQRRAGINEFIONLVRYPELYNHPDVRAFLQWDSPKHQSG 60
Qy      61  PSEDEDESSQKLHSTSQNINLGPSGNPHAKPTDFDLKVIKGSFGKVLAKRKLDGKF 120

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Db      61  PSEDEDESSQKLHSTSQNINLGPSGNPHAKPTDFDLKVIKGSFGKVLAKRKLDGKV 120
Qy      121  YAVKVLQKKIVLNRKQKHIMAEARNVLLKNVXHPFLVGLHYHSQTTEKLYFVLDFVNGGE 180
Db      121  YAVKVLQKKIVLNRKQKHIMAEARNVLLKNVXHPFLVGLHYHSQTTEKLYFVLDFVNGGE 180
Qy      181  LFFHLQERSFPEHRAFYAAETASALGYLHSIKIVYRDLKPENILSDSGHVVLDTDFGL 240
Db      181  LFFHLQERSFPEHRAFYAAETASALGYLHSIKIVYRDLKPENILSDSGHVVLDTDFGL 240
Qy      241  CKEGIAISDTTTCGTPPEYLAPEVIRKQPDYDNTVDWCLGAVLYEMLYGLPPFYCRDVA 300
Db      241  CKEGIAISDTTTCGTPPEYLAPEVIRKQPDYDNTVDWCLGAVLYEMLYGLPPFYCRDVA 300
Qy      301  EMDYDNLHKPLSLRPGVSLTAWSLLELLEKQDNRLGAKEDFLEIQNHPPFFESLSWADL 360
Db      301  EMDYDNLHKPLSLRPGVSLTAWSLLELLEKQDNRLGAKEDFLEIQNHPPFFESLSWADL 360
Qy      361  VQKKIPPPFNPNVAGPDDIRNEDTAFTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 420
Db      361  VQKKIPPPFNPNVAGPDDIRNEDTAFTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 420
Qy      421  APPSEDLFL 429
Db      421  APPSEDLFL 429

RESULT 13
ADRI4041
ID ADRI4041 standard; protein; 496 AA.
AC ADRI4041;
XX
XX 21-OCT-2004 (first entry)
XX Human NF-kappaB pathway-associated protein SeqID42.
XX
KW NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
KW immunosuppressive; vulnery; gene therapy; immune disorder;
KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
KW hyper-IGM syndrome; hypohidrotic ectodermal dysplasia;
KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
KW viral replication; host cell survival; evasion of immune response;
KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
KW autoimmune disorder; hyper immune activity;
KW aberrant acute phase response; hypercongenital condition; birth defect;
KW necrotic lesion; wound; organ transplant rejection;
KW aberrant signal transduction; proliferating disorder; cancer;
KW HIV propagation; human.
XX
XX Homo sapiens.
XX WO2004065577-A2.
XX 05-AUG-2004.
XX 13-JAN-2004; 2004WO-US0000798.
XX 14-JAN-2003; 2003US-0440068P.
PR 12-MAY-2003; 2003US-0469757P.
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX Nadler SG, Neubauer MG, Feder JN, Carman J;
PI WPI; 2004-562168/54.
XX DR N-PSDB; ADRI4040.
XX

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PT New isolated polynucleotides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or diseases associated with NF-kappaB pathway.

PS Claim 6; SEQ ID NO 42; 237pp; English.

XX This invention relates to the novel association of protein sequences (and CC the genes which encode them) to the NF-kappaB pathway. The invention may CC be useful for the production of compounds with an anti-inflammatory, CC cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic, CC gastrointestinal-Gen, antiasthmatic, antiarthritic, antirheumatic, CC immunomodulatory, cerebroprotective, vasotropic, immunosuppressive or CC vulnary activity or for gene therapy. The proteins and nucleotides are CC useful for diagnosing, preventing, treating, or ameliorating conditions CC or diseases associated with the NF-kappaB pathway. The condition is an CC immune disorder, an inflammatory disorder, an inflammatory disorder CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis, CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM CC syndromes, hypohidrotic ectodermal dysplasia X-linked anhidrotic CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1, CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick CC syndrome, stroke, BAE, autoimmune disorders, disorders related to hyper CC immune activity, disorders related to aberrant acute phase responses, CC hypercongenital conditions, birth defects, necrotic lesions, wounds, CC organ transplant rejection, conditions related to organ transplant CC rejection, disorders related to aberrant signal transduction, CC proliferating disorders, cancers and HIV propagation in cells infected CC with other viruses. The present sequence is that of a human protein which CC is subject to the novel association with the NF-kappaB pathway of the CC invention. Note: This sequence does not appear in the specification but CC was obtained by the indexer from Genbank.

XX SQ Sequence 496 AA;

Query Match 99.0%; Score 2246; DB 8; Length 496;  
Best Local Similarity 99.1%; Pred. No. 3.2e-212;  
Matches 425; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 60  
DB 68 MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSG 127  
QY 61 PSEDEDESSQKLHSTSQNLGPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLDGKF 120  
DB 128 PSEDEDESSQKLHSTSQNLGPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLDGKV 187  
QY 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGE 180  
DB 188 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGE 247  
QY 181 LFFHLQERSFPFHRARFYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVLTDFGL 240  
DB 248 LFFHLQERSFPFHRARFYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVLTDFGL 307  
QY 241 CKEGIAISDTTTCGTPEYLAPEVIRKQPDYNTVDWMCGLGAVLYEMLYGLPFPYCRDVA 300  
DB 308 CKEGIAISDTTTCGTPEYLAPEVIRKQPDYNTVDWMCGLGAVLYEMLYGLPFPYCRDVA 367  
QY 301 EMYDNLHKPLSLRPGVSLTAWSIILEELKQRNLGAKEDFLEIQNHPPFFESLSWADL 360  
DB 368 EMYDNLHKPLSLRPGVSLTAWSIILEELKQRNLGAKEDFLEIQNHPPFFESLSWADL 427  
QY 361 VQKKIPPPNPNVAGPDIDRFNFTAFTEETVPYSCVSSDYISVNASVLEADDAFVGFSY 420  
DB 428 VQKKIPPPNPNVAGPDIDRFNFTAFTEETVPYSCVSSDYISVNASVLEADDAFVGFSY 487  
QY 421 APPSEDLFL 429  
DB 488 APPSEDLFL 496

RESULT 14  
ADY18746

ID ADY18746 standard; protein; 397 AA.

XX AC ADY18746;

XX DT 05-MAY-2005 (first entry)

XX DE PRO polypeptide SEQ ID NO 4552.

XX Antinflammatory; Immune disorder; Dermatological; Immunosuppressive;  
KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;  
KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;  
KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;  
KW Antiallergic; diagnosis.

XX OS Homo sapiens.

XX PN WO2005016962-A2.

XX PD 24-FEB-2005.

XX PF 11-AUG-2004; 2004WO-US026249.

XX PR 11-AUG-2003; 2003US-0493546P.

XX PA (GETH ) GENENTECH INC.

XX PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

XX DR WPI; 2005-182330/19.

XX PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and  
PT treating an immune related disorder, e.g. systemic lupus erythematosus,  
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

XX PS Claim 8; SEQ ID NO 4552; 158pp; English.

XX CC The invention relates to an isolated nucleic acid encoding a PRO  
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,  
CC composition, and method are useful for diagnosing and treating an immune  
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid  
CC arthritis. The present sequence represents a PRO polypeptide.

XX SQ Sequence 397 AA;

Query Match 90.8%; Score 2061; DB 9; Length 397;  
Best Local Similarity 92.5%; Pred. No. 4.2e-194;  
Matches 397; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 60  
DB 1 MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 60  
QY 61 PSEDEDESSQKLHSTSQNLGPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLDGKF 120  
DB 61 PSEDEDESSQKLHSTSQNLGPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLDGKF 120  
QY 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGE 180  
DB 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGE 180  
QY 181 LFFHLQERSFPFHRARFYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVLTDFGL 240  
DB 181 LFFHLQERSFPFHRARFYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVLTDFGL 240  
QY 241 CKEGIAISDTTTCGTPEYLAPEVIRKQPDYNTVDWMCGLGAVLYEMLYGLPFPYCRDVA 300  
DB 241 CKEGIAISDTTTCGTPEYLAPEVIRKQPDYNTVDWMCGLGAVLYEMLYGLPFPYCRDVA 268  
QY 301 EMYDNLHKPLSLRPGVSLTAWSIILEELKQRNLGAKEDFLEIQNHPPFFESLSWADL 360  
DB 269 EMYDNLHKPLSLRPGVSLTAWSIILEELKQRNLGAKEDFLEIQNHPPFFESLSWADL 328

Qy	361	VQKKIPPPNPNVAGDDDIRNPDFTAFTBETVPYSCVSSDYSIYNASVLEADDAFVGFSY	420
Db	329	VQKKIPPPNPNVAGDDDIRNPDFTAFTBETVPYSCVSSDYSIYNASVLEADDAFVGFSY	388
Qy	421	APPESEDLFL	429
Db	389	APPESEDLFL	397

RESULT 15

AAM93732  
ID AAM93732 standard; protein; 464 AA.

XX

AC AAM93732;

DT 06-NOV-2001 (first entry)

XXI

DE Human polypep

XX

KW Human; full

XX

OS Homo sapiens.

XX

PN EP1130094-A2.

XX

PD 05-SEP-2001.

XX

PF 07-JUL-2000: 2000EP-

XXX  
XXX  
0007  
0007  
0007  
0007  
0007  
0007

08-JUL-1999; 99JP-00194486.  
PR  
11-JAN-2000; 2000JP-00118774.  
PR

[illegible]

(HELI-) HELIX RES INST.  
Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
Wakamatsu A., Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
WPI; 2001-524355/58.  
DR N-PSDB; AAK94684.

Sequence 464 AA;

Query Match	90.8%	Score 2061;	DB 4;	Length 464;
Best Local Similarity	92.5%	Pred. No. 5.2e-194;		
Matches 397;	Conservative	0;	Mismatches 0;	Indels 32;
				Gaps 1;

QV 1 MALKIPAKRIEFGDNFDPDEFIKORRAGLNEEFIONLVRYPELYNHPPDVRAFIOMDSPKHOSD 60

27  
1 FFAAIAAGUATTCGNTTCTDCTTNGKGGGNETIQNEVAKIFETNNHFDVNARLQMDSFNQSD 80

Db 68 MALKIPAKRIFGDNFDPDFIKORRAGLNEFIONLVRYPELVNHPDVRAFLOMDSPKHOSD 127

**THE UNIVERSITY OF CHICAGO**

Qy	121	YAVKVLQKKIIVLNRKEQKHIAERNVLLKNVKHPFLVGLHYSFQTEKLYFVLDVFNGGE	180
Db	188	YAVKVLQKKIIVLNRKEQKHIAERNVLLKNVKHPFLVGLHYSFQTEKLYFVLDVFNGGE	247
Qy	181	LFFHLQERSPPPEARFYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVLTDFGL	240
Db	248	LFFHLQERSPPPEARFYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVLTDFGL	307
Qy	241	CKEGIATSDTTTTCGTPPEYLAPVIRKQPDYNTVDWCLGANVLYEMLYGLPPFYCRDVA	300
Db	308	CKEGIATSDTTTTCGTPPE-----PPFYCRDVA	335
Qy	301	EMYDNIHLKPLSLRPGVSLTAWLSILELLEKDRQNLGAKEDFLEIQNHPPFESLWADL	360
Db	336	EMYDNIHLKPLSLRPGVSLTAWLSILELLEKDRQNLGAKEDFLEIQNHPPFESLWADL	395
Qy	361	VQKKIPPPPNPNVAGPDDIRNFDFTAETTPYPSVCVSSDYSIVNASVLEADDAFVGFSY	420
Db	396	VQKKIPPPPNPNVAGPDDIRNFDFTAETTPYPSVCVSSDYSIVNASVLEADDAFVGFSY	455
Qy	421	APPSDDLFL	429
Db	456	APPSDDLFL	464

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Job time : 80.3566 sec

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:21:11 ; Search time 20.2358 Seconds  
(without alignments)  
1752.724 Million cell updates/sec

Title: US-09-868-131A-4  
Perfect score: 2269  
Sequence: 1 MALKIPAKRIFGDNFDPDFI.....EADDAFVGFSYAPPSIDLFL 429

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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- 2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1476	65.1	407	2	US-10-067-977-4
2	1476	65.1	445	2	US-10-067-977-2
3	1472	64.9	431	2	US-09-031-295-2
4	1472	64.9	431	2	US-10-000-039-2
5	1468	64.7	431	1	US-08-712-709-5
6	1468	64.7	431	2	US-09-111-444-5
7	1468	64.7	431	2	US-09-541-228-5
8	1458.5	64.3	430	1	US-08-712-709-9
9	1458.5	64.3	430	2	US-09-111-444-9
10	1458.5	64.3	430	2	US-09-541-228-9
11	870	38.3	465	2	US-09-526-043-2
12	866.5	38.2	479	2	US-09-771-161A-246
13	866.5	38.2	479	2	US-09-771-161A-247
14	866.5	38.2	479	2	US-09-771-161A-248
15	860.5	37.9	454	2	US-09-526-043-17
16	844.5	37.2	480	2	US-09-526-043-13
17	844.5	37.2	481	2	US-09-538-092-1054
18	818.5	36.1	480	2	US-09-590-740-6
19	818.5	36.1	726	2	US-09-417-197-71
20	816.5	36.0	480	2	US-09-091-058-2
21	816.5	36.0	480	2	US-09-590-740-2
22	816.5	36.0	480	2	US-09-538-092-1053
23	816.5	36.0	480	2	US-09-526-043-14
24	816.5	36.0	480	2	US-09-771-161A-223
25	816.5	36.0	727	2	US-09-417-197-139
26	803.5	35.4	587	1	US-08-313-274-2
27	803.5	35.4	655	2	US-09-949-016-11676

28	792	34.9	417	2	US-09-530-740-4	Sequence 4, Appli
29	790.5	34.8	737	2	US-09-772-647-4	Sequence 4, Appli
30	790.5	34.8	737	2	US-10-228-931-4	Sequence 4, Appli
31	789	34.8	525	1	US-08-749-902-7	Sequence 7, Appli
32	789	34.8	525	1	US-08-749-902-8	Sequence 8, Appli
33	789	34.8	525	2	US-09-430-564-16	Sequence 16, Appli
34	789	34.8	525	2	US-09-762-258-4	Sequence 4, Appli
35	788.5	34.8	480	2	US-09-205-658-157	Sequence 157, App
36	787.5	34.7	502	2	US-09-538-092-996	Sequence 996, App
37	786	34.6	482	2	US-09-430-564-2	Sequence 2, Appli
38	786	34.6	495	2	US-09-430-564-3	Sequence 3, Appli
39	786	34.6	495	2	US-09-762-258-2	Sequence 2, Appli
40	784	34.6	470	2	US-09-248-796A-18482	Sequence 18482, A
41	779.5	34.4	737	2	US-09-771-161A-195	Sequence 195, App
42	763	33.6	672	2	US-10-092-138A-27	Sequence 27, Appl
43	763	33.6	672	2	US-09-538-092-943	Sequence 943, App
44	763	33.6	672	2	US-08-681-219A-27	Sequence 27, Appl
45	760.5	33.5	546	2	US-09-205-658-155	Sequence 155, App

ALIGNMENTS

RESULT 1  
US-10-067-977-4  
; Sequence 4, Application US/10067977  
; Patent No. 6830911  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Chunhua and KE, Zhaoxi  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CLO01313  
; CURRENT APPLICATION NUMBER: US/10/067,977  
; CURRENT FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 407  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-067-977-4

Query Match	65.1%	Score 1476;	DB 2;	Length 407;
Best Local Similarity	67.5%	Pred. No. 3.9e-134;		
Matches	280;	Conservative	52;	Mismatches 69;
			Indels	14;
			Gaps	3;
Qy	19	FIKRRAGLNEFTQNLVRYPELYNHPDVRFLQMDSPKH----	QSDPSEDESSQKLH	74
Db	3	FMKQRMGLNDFIQKIANNYSACKHPEVQSIKISQBPPELMNANPSPPP-----	53	
Qy	75	STSQNTNLGFSGNPHAKPTDFPLKVIKGSFGKVLAKRKLKGKFAVKVLOKKIVLNR	134	
Db	54	SPSQINLGFSSNPHAKPSDFHFLKVIKGSFGKVLAKRKLKGKFAVKVLOKKIATKK	113	
Qy	135	KEQKHIMARNVLLKNVHPGLVGLHVSQTTEKLYFVLDFVNGGELFEHLQERSPEH	194	
Db	114	KEKHIMSRNVLNKNVHPGLVGLHVSQTADKLYFVLDFVNGGELFEHLQERCELEP	173	
Qy	195	RARFYAAETASALGYLHSIKIVYRDLPENILDSVGHVLTDFGLCKEGIAISDTTTF	254	
Db	174	RARFYAAETASALGYLHSINIVYRDLPENILDSQGHIVLTDGFLCKENIENSTSTP	233	
Qy	255	CGTPEYLAPEVIRKQPDYNTVDMWCLGAVLYEMLYGLPPYPCRDVAEMYNILHKPLSLR	314	
Db	234	CGTPEYLAPEVLHKQPDYRTVDWMLGAVLYEMLYGLPPYPCRDVAEMYNILKNKPLQLK	293	
Qy	315	PGVSLTAMSIIEELLEKQRNRLGAKEDFLEIQNHFFESLSWADLVOKKIPPEFNPVA	374	
Db	294	FNITTSARHLLEGLLQKDRKRLGAKDDFMEIKSHVFFSLINWDDLLINKKITPPFPNPVS	353	
Qy	375	GPDDIRNFOTAFTEETVPYSCVSSDYISVNASVLEADDAFVGFSYAPPSDDLFL	429	



COUNTRY: U.S.A.  
 ZIP: 20007-5109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 FILING DATE: 04-Dec-2001  
 APPLICATION NUMBER: US/10/000,039  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/031,295  
 FILING DATE: 26-FEB-1998  
 APPLICATION NUMBER: DE 197-08-173.8  
 FILING DATE: 28-FEB-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sandercock, Colin G.  
 REGISTRATION NUMBER: 31,298  
 REFERENCE/DOCKET NUMBER: 058315/0123  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 672-5300  
 TELEFAX: (202) 672-5399  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 431 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-10-000-039-2

Query Match 64.9%; Score 1472; DB 2; Length 431;  
 Best Local Similarity 67.2%; Pred. No. 1e-133;  
 Matches 279; Conservative 53; Mismatches 69; Indels 14; Gaps 3;

QY 19 FIKQRAGLNEFTQNLVRYPELVNHPDVRAFLQMDSPKH----QSDPSEDEDRSSQKLH 74  
 Db 27 FMKQRRMGLNDFIQKIANNYSACKHPEVQSILKISQBPPELMNANPSPPP----- 77

QY 75 STSQNLGPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLKDKGYAVKVLQKIVLNR 134  
 Db 78 SPSSQNLGPGSNPHAKPSDFHFLKVIKGSFGKVLAKRKLKDKGYAVKVLQKIVLNR 137

QY 135 KEQKHIMSERVLLKNNKHPFLVGLHVSFTQTEKLYFVLDVFNGLFHLQERGFPEH 194  
 Db 138 KEKHIMSERVLLKNNKHPFLVGLHVSFTQTEKLYFVLDVFNGLFHLQERGFPEH 197

QY 195 RARFYAAEIASALGYLHSLKIVYRDLPENILDSVGHVLTDFGLCKEGIAISDTTTF 254  
 Db 198 RARFYAAEIASALGYLHSLNIVYRDLPENILDSVGHVLTDFGLCKEGIAISDTTTF 257

QY 255 CGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPYCRDVAEMVDNILHKLPLSR 314  
 Db 258 CGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPYCRDVAEMVDNILHKLPLSR 317

QY 315 PGVSLTAWSLTELEKQRLGAKEDFLEIQNHPPFESLSWADLVOKKI PPPFNPVA 374  
 Db 318 PNITNSARHLLEGLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNVS 377

QY 375 GPDDIRNFDTAFTEETVPYSCVSSDYISVNAEADDAFVGFSYAPPT-DSFL 429  
 Db 378 GPNELRHFDPEETPEEPVNSIGKSPDSVLVTASVKEAEAFVGFSYAPPT-DSFL 431

RESULT 5  
 US-08-712-709-5  
 ; Sequence 5, Application US/08712709  
 ; Patent No. 5863780  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Au-Young, Janice  
 ; APPLICANT: Guegler, Karl J.  
 ; APPLICANT: Hawkins, Phillip R.

TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: U.S.  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/712,709  
 FILING DATE: Filed Herewith  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PF-0118 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-4166  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 431 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 IMMEDIATE SOURCE:  
 LIBRARY: Consensus  
 CLONE: 712-709-5  
 US-08-712-709-5

Query Match 64.7%; Score 1468; DB 1; Length 431;  
 Best Local Similarity 67.2%; Pred. No. 2.5e-133;  
 Matches 279; Conservative 52; Mismatches 70; Indels 14; Gaps 3;

QY 19 FIKQRAGLNEFTQNLVRYPELVNHPDVRAFLQMDSPKH----QSDPSEDEDRSSQKLH 74  
 Db 27 FMKQRRMGLNDFIQKIANNYSACKHPEVQSILKISQBPPELMNANPSPPP----- 77

QY 75 STSQNLGPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLKDKGYAVKVLQKIVLNR 134  
 Db 78 SPSSQNLGPGSNPHAKPSDFHFLKVIKGSFGKVLAKRKLKDKGYAVKVLQKIVLNR 137

QY 135 KEQKHIMSERVLLKNNKHPFLVGLHVSFTQTEKLYFVLDVFNGLFHLQERGFPEH 194  
 Db 138 KEKHIMSERVLLKNNKHPFLVGLHVSFTQTEKLYFVLDVFNGLFHLQERGFPEH 197

QY 195 RARFYAAEIASALGYLHSLKIVYRDLPENILDSVGHVLTDFGLCKEGIAISDTTTF 254  
 Db 198 RARFYAAEIASALGYLHSLNIVYRDLPENILDSVGHVLTDFGLCKEGIAISDTTTF 257

QY 255 CGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPYCRDVAEMVDNILHKLPLSR 314  
 Db 258 CGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPYCRDVAEMVDNILHKLPLSR 317

QY 315 PGVSLTAWSLTELEKQRLGAKEDFLEIQNHPPFESLSWADLVOKKI PPPFNPVA 374  
 Db 318 PNITNSARHLLEGLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNVS 377

QY 375 GPDDIRNFDTAFTEETVPYSCVSSDYISVNAEADDAFVGFSYAPPT-DSFL 429  
 Db 378 GPNELRHFDPEETPEEPVNSIGKSPDSVLVTASVKEAEAFVGFSYAPPT-DSFL 431

RESULT 6  
 US-09-111-444-5  
 ; Sequence 5, Application US/09111444  
 ; Patent No. 6045792



Qy	315	PGVSLTAMSLIELLEKORQNRNLGAKEDFLBIQNHPPFSELSNADIWQKKIPPPFNPNVA	374
Db	318	PNITTSARHLLEGLQKQRTKRLGAKDMEIKSHVFFSLINMDDLINKKITPPFNPNVS	377
Qy	375	GPDDIRNFDTATETVPYSCVCSDSYSIVNASVLEADDAFVGFSYAPPSSEDLFL	429
Db	378	GNDLRHFDPETEPSPVNSICKSPDSVLVVTASVKEAAEAFLGFSYAPPT - DSEFL	431

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; RESULT 8
; US-08-712-709-9
; Sequence 9, Application US/08712709
; Patent No. 5863780
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
;

```

[illegible][illegible]

RESULT 9  
 US-09-111-444-9  
 ; Sequence 9, Application US/09111444  
 ; Patent No. 6045792  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Au-Young, Janice  
 ; APPLICANT: Hawgler, Karl J.  
 ; APPLICANT: Hawkins, Phillip R.  
 ; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: U.S.  
 ; ZIP: 94304

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Query Match      64.3%; Score 1458.5; DB 2; Length 430;
Best Local Similarity 67.5%; Pred. No. 2.le-132;
Matches 280; Conservative 50; Mismatches 70; Indels 15; Gaps 4

QY 19 FTKQRAGLNEFIQNLVYPPELVNHPDRAFLQMDSPKH----QSDPSDEDESSOKLH 74
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Db 27 FMKQRRLMGDLDFIQLANNSYACKHPQVQSYLKISQPELNMVANSPP- 77

QY 75 STSQNLNLPSPGNPHAKPTDFDLKVIKGSGFKVLLAKRKLGGKTFYAVKVLOKKIVLNR 134
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 78 SFSDQNLNLPSSNPHAKPSDFHFLKVIKGSGFGKVLILARHAKBAEAFYAVKVLOKKAILKK 137
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 248  
; LENGTH: 479  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-771-161A-248

Query Match 38.2%; Score 866.5; DB 2; Length 479;  
Best Local Similarity 43.7%; Pred. No. 4.5e-75;  
Matches 184; Conservative 65; Mismatches 145; Indels 27; Gaps 7;

QY 20 IKORRAGLNEFTONLVRYPELYNHPDVRAFLQWDSPKHQSDPSE-----DEDER 68  
Db 62 MKTERPKPNTFIIRCLQWTV-----IERTFHVDTPEREEREWEATQAVADRRLQROEER 116  
QY 69 SSQKLHSTQNINLG-----PSGNPHAKPT--DPDFLKVIGKSGFKVLLAKRKLQDKEY 121  
Db 117 --MNCSPTSQIDNIGSEEMDASTTHHKRKTMDFDYLLKLGKTFGKVLVREKASGKY 174  
QY 122 AVKVLQKKIVLNRKQKHMAERNVLLKNVGHFPLVGLHYSFQTTTEKLYFVLDFVNGGEL 181  
Db 175 AMKILKKEVIIAKDEVAHTLTESRV-LKNTRHPFLTSLKYSFQTKDRLCFVMEYVNGGEL 233  
QY 182 FFHLQERSFPPEHRARFYAAEIASALGYLHSIKIVYRDLKPNILDSVGHVVLTDGFLC 241  
Db 234 FFHLRSRVFSEDRTRFYGAIEVSALDYLSHSGKIVYRDLKLENMLDKDGHKIKITDFGLC 293  
QY 242 KEGIALSDTTTTCGTPPEYLAPVIRKQPDYNTVDWMLCGAVLYEMLYGLPPFYCRDVAE 301  
Db 294 KEGITDAATMKTFCGTPPEYLAPVLENDNDYGRAVDWMLGVVYEMMCGRLPFYNQDHEK 353  
QY 302 MYDNILHKPLSLRPGVSLTAWSIIEELLEKDRQNL-GAKEDFLEIQNHPPFPESLSWADL 360  
Db 354 LPELILMEDIKPPTLSSDAKSLLSGLLIKDPNKRLLGGGPDPAKEIMRHSFFSGVNWQDV 413  
QY 361 VQKIPPPNPNVAGPDDIRNFTAFTEETVPSYVCSSDYSIVNASVLEADDAFVGFSY 420  
Db 414 YDKKLVPFPKPOVTSETDTRYFDEEFTAQITITTPPEKYDEGDMCDMNERRPHFPQFSY 473  
QY 421 A 421  
Db 474 S 474

RESULT 15  
US-09-526-043-17  
; Sequence 17, Application US/09526043  
; Patent No. 6881555  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Kun  
; APPLICANT: Pagnoni, Marco  
; APPLICANT: Clark, Kenneth  
; APPLICANT: Ivashchenko, Yuri  
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF  
; FILE REFERENCE: A3278A-US  
; CURRENT APPLICATION NUMBER: US/09/526,043  
; CURRENT FILING DATE: 2000-03-14  
; EARLIER APPLICATION NUMBER: 60/125,108  
; EARLIER FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 454  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer  
US-09-526-043-17

Query Match 37.9%; Score 860.5; DB 2; Length 454;  
Best Local Similarity 45.5%; Pred. No. 1.6e-74;  
Matches 178; Conservative 61; Mismatches 125; Indels 27; Gaps 7;  
QY 20 IKORRAGLNEFTONLVRYPELYNHPDVRAFLQWDSPKHQSDPSE-----DEDER 68  
Db 62 MKTERPKPNTFIIRCLQWTV-----IERTFHVDTPEREEREWEATQAVADRRLQROEER 116  
QY 69 SSQKLHSTQNINLG-----PSGNPHAKPT--DPDFLKVIGKSGFKVLLAKRKLQDKEY 121  
Db 117 --MNCSPTSQIDNIGSEEMDASTTHHKRKTMDFDYLLKLGKTFGKVLVREKASGKY 174  
QY 122 AVKVLQKKIVLNRKQKHMAERNVLLKNVGHFPLVGLHYSFQTTTEKLYFVLDFVNGGEL 181  
Db 175 AMKILKKEVIIAKDEVAHTLTESRV-LKNTRHPFLTSLKYSFQTKDRLCFVMEYVNGGEL 233  
QY 182 FFHLQERSFPPEHRARFYAAEIASALGYLHSIKIVYRDLKPNILDSVGHVVLTDGFLC 241  
Db 234 FFHLRSRVFSEDRTRFYGAIEVSALDYLSHSGKIVYRDLKLENMLDKDGHKIKITDFGLC 293  
QY 242 KEGIALSDTTTTCGTPPEYLAPVIRKQPDYNTVDWMLCGAVLYEMLYGLPPFYCRDVAE 301  
Db 294 KEGITDAATMKTFCGTPPEYLAPVLENDNDYGRAVDWMLGVVYEMMCGRLPFYNQDHEK 353  
QY 302 MYDNILHKPLSLRPGVSLTAWSIIEELLEKDRQNL-GAKEDFLEIQNHPPFPESLSWADL 360  
Db 354 LPELILMEDIKPPTLSSDAKSLLSGLLIKDPNKRLLGGGPDPAKEIMRHSFFSGVNWQDV 413  
QY 361 VQKIPPPNPNVAGPDDIRNFTAFTEETV 391  
Db 414 YDKKLVPFPKPOVTSETDTRYFDEEFTAQTI 444

Search completed: January 27, 2006, 23:33:31  
Job time : 21.2358 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2006, 23:31:20 ; Search time 75.2774 Seconds  
(without alignments)  
2381.178 Million cell updates/sec

Title: US-09-868-131A-4  
Perfect score: 2269  
Sequence: 1 MALKIPAKRIFGNFDPDFI.....EADDAFVGFSYAPPSDFL 429

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_Main:  
1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2269	100.0	429	4	US-10-295-027-116
2	2269	100.0	496	3	US-09-764-875-746
3	2269	100.0	496	3	US-09-764-875-900
4	2269	100.0	496	5	US-10-737-450-4
5	2263	99.7	496	3	US-09-784-249-2
6	2246	99.0	496	4	US-10-755-889-42
7	1501	66.2	526	4	US-10-094-749-1861
8	1476	65.1	407	4	US-10-067-977-4
9	1476	65.1	407	4	US-10-827-272-4
10	1476	65.1	431	3	US-09-981-353-7
11	1476	65.1	431	4	US-10-403-161-2
12	1476	65.1	431	4	US-10-403-161-4
13	1476	65.1	445	4	US-10-067-977-2
14	1476	65.1	445	4	US-10-827-272-2
15	1472	64.9	431	4	US-10-000-039-2
16	1472	64.9	431	4	US-10-353-690-12
17	1472	64.9	431	5	US-10-756-149-5279
18	1472	64.9	431	6	US-11-044-570-2
19	1468	64.7	431	3	US-09-810-808-5
20	1458.5	64.3	430	3	US-09-810-808-9
21	1447	63.8	594	5	US-10-732-923-10768
22	1415	62.4	388	4	US-10-131-410-104
23	1414	62.3	433	5	US-10-732-923-10767
24	1346.5	59.3	340	4	US-10-217-574-17
25	1346.5	59.3	340	4	US-10-217-555-17
26	1338	59.0	276	3	US-09-764-868-669
27	1338	59.0	276	3	US-09-764-875-1176

28	1329.5	58.6	382	4	US-10-296-115-1109
29	1329	58.6	396	5	US-10-926-543-83
30	1328.5	58.6	427	5	US-10-753-267-126
31	1323.5	58.3	367	3	US-09-971-118-2
32	1323.5	58.3	367	4	US-10-291-172-256
33	1323.5	58.3	367	4	US-10-429-160-52
34	1323.5	58.3	367	4	US-10-221-278-256
35	1323.5	58.3	367	4	US-10-380-235-6
36	1187.5	52.3	308	4	US-10-664-421-85
37	1187.5	52.3	308	5	US-10-941-635-85
38	1171	51.6	398	4	US-10-262-511-140
39	1047	46.1	194	3	US-09-784-249-4
40	1019.5	44.9	422	4	US-10-369-493-7027
41	976	43.0	276	3	US-09-764-868-811
42	976	43.0	276	3	US-09-764-875-1050
43	870	38.3	465	3	US-09-526-043-2
44	870	38.3	465	4	US-10-394-568-2
45	870	38.3	465	4	US-10-394-568-12

ALIGNMENTS

RESULT 1

US-10-295-027-116  
; Sequence 116, Application US/10295027  
; Publication No. US20030232350A1  
; GENERAL INFORMATION:  
; APPLICANT: Afar, Daniel  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Ginsberg, Wendy M.  
; APPLICANT: Gish, Kurt C.  
; APPLICANT: Glynn, Richard  
; APPLICANT: Hevez, Peter A.  
; APPLICANT: Mack, David H.  
; APPLICANT: Murray, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer  
; FILE REFERENCE: 018501-012500US  
; CURRENT APPLICATION NUMBER: US/10/295,027  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: US 09/663,733  
; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: US 60/350,666  
; PRIOR FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 60/335,394  
; PRIOR FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: US 60/332,464  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: US 60/334,393  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: US 60/340,376  
; PRIOR FILING DATE: 2001-12-14  
; PRIOR APPLICATION NUMBER: US 60/347,211  
; PRIOR FILING DATE: 2002-01-08  
; PRIOR APPLICATION NUMBER: US 60/347,349  
; PRIOR FILING DATE: 2002-01-10  
; PRIOR APPLICATION NUMBER: US 60/355,250  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 60/356,714  
; PRIOR FILING DATE: 2002-02-13  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1386  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 116  
; LENGTH: 429  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-295-027-116

Query Match 100.0%; Score 2269; DB 4; Length 429;



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RESULT 4
US-10-737-450-4
; Sequence 4, Application US/10737450
; Publication No. US20040235071A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Ecsedy, Jeffrey A.
; APPLICANT: Hunter, John Joseph
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Tighe Nescor, Michelle
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 15986, 2188, 20743, 9148, 9151, 9791, 44252,
; TITLE OF INVENTION: 14184, 8204, 7970, 25552, 21657, 26492, 2411, 15088,
; TITLE OF INVENTION: 1905, 28899, 63380, 33935, 10480, 12686, 25501, 17694,
; TITLE OF INVENTION: 15701, 53062, 49908, 21612, 38949, 6216, 46863, 9235, 2201,
; TITLE OF INVENTION: 6985, 9883, 12238, 18057, 21617, 39228, 49928, 54476, 62113,
; TITLE OF INVENTION: 64316, 12264, 32362, 58198, 2887, 3205, 8557, 9600, 9693,
; TITLE OF INVENTION: 44867, 53058, 55556, 57658, 2208, 10252, 10302, 14218,
; TITLE OF INVENTION: 33877, 10317, 10485, 25964, 14815, 1363, 1397, 14827, 21708,
; FILE REFERENCE: MP102-207P1RNMNM
; CURRENT APPLICATION NUMBER: US/10737,450
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/435,108
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/436,443
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/438,498
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/444,370
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/446,031
; PRIOR FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: US 60/453,635
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/457,199
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/462,458
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 60/466,732
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/469,184
; PRIOR FILING DATE: 2003-05-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-737-450-4

Query Match 100.0%; Score 2269; DB 5; Length 496;
Best Local Similarity 100.0%; Pred. No. 4.1e-172;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 60
Db 68 MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 127

QY 61 PSEDEDESSQKLHSTSONINLPGSGNPHAKPTDFDLKVIKGSGFKVLLAKRKLDGKF 120
Db 128 PSEDEDESSQKLHSTSONINLPGSGNPHAKPTDFDLKVIKGSGFKVLLAKRKLDGKF 187

QY 121 YAVKVLQKKIIVLNKREQKHMAERNVLLKNVHPFLVGLHYSQTTEKLYFVLDVFNNGE 180
Db 188 YAVKVLQKKIIVLNKREQKHMAERNVLLKNVHPFLVGLHYSQTTEKLYFVLDVFNNGE 247

QY 181 LFFHLQERSFPFHRARFYAAETASALGYLHSIKIIVYRDLKPNILLDSVGHVVLDTDFGL 240
Db 248 LFFHLQERSFPFHRARFYAAETASALGYLHSIKIIVYRDLKPNILLDSVGHVVLDTDFGL 307

QY 241 CKEGIAISDTTTCGTPEYLAPEVIRKOPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVA 300
Db 308 CKEGIAISDTTTCGTPEYLAPEVIRKOPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVA 367

QY 301 EMYDNILHKPLSLRPGVSLTAMWSILBELLEKQRNLGAKEDFLEIQNHPPFFESLSWADL 360
Db 368 EMYDNILHKPLSLRPGVSLTAMWSILBELLEKQRNLGAKEDFLEIQNHPPFFESLSWADL 427

QY 361 VQKKI PPPPNVAGPDDIRNFDTAFTETVPYSCVSSDYSIVNASVLEADDAFVGFSY 420
Db 428 VQKKI PPPPNVAGPDDIRNFDTAFTETVPYSCVSSDYSIVNASVLEADDAFVGFSY 487

US-09-784-249-2
; Sequence 2, Application US/09784249
; Patent No. US20010027184A1
; GENERAL INFORMATION:
; APPLICANT: Sanjay Kumar
; APPLICANT: Cheng Zou
; TITLE OF INVENTION: SERINE/THREONINE PROTEIN KINASE (H-SGK2)
; FILE REFERENCE: GH-70124-C1
; CURRENT APPLICATION NUMBER: US/09/784,249
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 08/997,212
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/051,446
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-784-249-2

Query Match 99.7%; Score 2263; DB 3; Length 496;
Best Local Similarity 99.8%; Pred. No. 1.2e-171;
Matches 428; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 60
Db 68 MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 127

QY 61 PSEDEDESSQKLHSTSONINLPGSGNPHAKPTDFDLKVIKGSGFKVLLAKRKLDGKF 120
Db 128 PSEDEDESSQKLHSTSONINLPGSGNPHAKPTDFDLKVIKGSGFKVLLAKRKLDGKF 187

QY 121 YAVKVLQKKIIVLNKREQKHMAERNVLLKNVHPFLVGLHYSQTTEKLYFVLDVFNNGE 180
Db 188 YAVKVLQKKIIVLNKREQKHMAERNVLLKNVHPFLVGLHYSQTTEKLYFVLDVFNNGE 247

QY 181 LFFHLQERSFPFHRARFYAAETASALGYLHSIKIIVYRDLKPNILLDSVGHVVLDTDFGL 240
Db 248 LFFHLQERSFPFHRARFYAAETASALGYLHSIKIIVYRDLKPNILLDSVGHVVLDTDFGL 307

QY 241 CKEGIAISDTTTCGTPEYLAPEVIRKOPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVA 300
Db 308 CKEGIAISDTTTCGTPEYLAPEVIRKOPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVA 367

QY 301 EMYDNILHKPLSLRPGVSLTAMWSILBELLEKQRNLGAKEDFLEIQNHPPFFESLSWADL 360
Db 368 EMYDNILHKPLSLRPGVSLTAMWSILBELLEKQRNLGAKEDFLEIQNHPPFFESLSWADL 427

QY 361 VQKKI PPPPNVAGPDDIRNFDTAFTETVPYSCVSSDYSIVNASVLEADDAFVGFSY 420
Db 428 VQKKI PPPPNVAGPDDIRNFDTAFTETVPYSCVSSDYSIVNASVLEADDAFVGFSY 487
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QY 421 APPSEDLFL 429
DB 488 APPSEDLFL 496

RESULT 6
US-10-755-889-42
; Sequence 42, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-42

Query Match 99.0%; Score 2246; DB 4; Length 496;
Best Local Similarity 99.1%; Pred. No. 2.8e-170;
Matches 425; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MALKIPAKRIFGDNFDPDFIKORRAGINEFIQNLVRYPELYNHPDVRAFLQMDSPKQSD 60
DB 68 MALKIPAKRIFGDNFDPDFIKORRAGINEFIQNLVRYPELYNHPDVRAFLQMDSPKQSG 127
QY 61 PSDEDESSQKLHSTSQNLINLGPSSGNPHAKPTDFDLKVIKGSFGKVLAKRKLKGKF 120
DB 128 PSDEDESSQKLHSTSQNLINLGPSSGNPHAKPTDFDLKVIKGSFGKVLAKRKLKGKV 187
QY 121 YAVKVLQKKILVLRKQKHIMAEARNVLLKNVHPFLVGLHYSFOTTEKLYFVLDFVNGGE 180
DB 188 YAVKVLQKKILVLRKQKHIMAEARNVLLKNVHPFLVGLHYSFOTTEKLYFVLDFVNGGE 247
QY 181 LFPHLQERSFPFHRARFYAAETASALGYLHSIKIVYRDLKPNILLDSVGHVLTDFGL 240
DB 248 LFPHLQERSFPFHRARFYAAETASALGYLHSIKIVYRDLKPNILLDSVGHVLTDFGL 307
QY 241 CKEGIAISDTTTFCTGTPPEYLAPEVIRKQPDYNTVDWCLGAVLYEMLYGLPPFYCRDVA 300
DB 308 CKEGIAISDTTTFCTGTPPEYLAPEVIRKQPDYNTVDWCLGAVLYEMLYGLPPFYCRDVA 367
QY 301 EMDYNTILHKPLSRPGVSLTAWLSILBELLEKQRNLRGAKEDFLEIQNHPPFESLSWADL 360
DB 368 EMDYNTILHKPLSRPGVSLTAWLSILBELLEKQRNLRGAKEDFLEIQNHPPFESLSWADL 427
QY 361 VQKKIPPPNPVAGPDDIRNFDTAFTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 420
DB 428 VQKKIPPPNPVAGPDDIRNFDTAFTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 487
QY 421 APPSEDLFL 429
DB 488 APPSEDLFL 496

RESULT 7
US-10-094-749-1861
; Sequence 1861, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
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; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1861
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-1861

Query Match 66.2%; Score 1501; DB 4; Length 526;
Best Local Similarity 66.8%; Pred. No. 6.6e-111;
Matches 286; Conservative 52; Mismatches 76; Indels 14; Gaps 3;

QY 6 PAKRIFGDNFDPDFIKORRAGINEFIQNLVRYPELYNHPDVRAFLQMDSPKH---QSDP 61
DB 109 PDRFTFTWDDPAFMKQRRMGLNDFIQTIANNYSYACKHPVEQSILKISQPEPELMNANP 168
QY 62 SDEDESSQKLHSTSQNLINLGPSSGNPHAKPTDFDLKVIKGSFGKVLAKRKLKGKF 121
DB 169 SPPP-----SPSQINLGPSSGNPHAKPSDFHFLKVIKGSFGKVLAKRKAEEVFY 219
QY 122 AVKVLQKKILVLRKQKHIMAEARNVLLKNVHPFLVGLHYSFOTTEKLYFVLDFVNGGEL 181
DB 220 AVKVLQKKAILKKBEKHIMSERNVLLKNVHPFLVGLHFSFQTADKLYFVLDIYINGGEL 279
QY 182 FPHLQERSFPFHRARFYAAETASALGYLHSIKIVYRDLKPNILLDSVGHVLTDFGLC 241
DB 280 FYHLQERBCFLEPRARFYAAETASALGYLHSIKIVYRDLKPNILLDSVGHVLTDFGLC 339
QY 242 KEGIAISDTTTFCTGTPPEYLAPEVIRKQPDYNTVDWCLGAVLYEMLYGLPPFYCRDVAE 301
DB 340 KENIEHNSTSTFCGTPPEYLAPEVIRKQPDYNTVDWCLGAVLYEMLYGLPPFYSRNTAE 399
QY 302 MYDNTILHKPLSRPGVSLTAWLSILBELLEKQRNLRGAKEDFLEIQNHPPFESLSWADLV 361
DB 400 MYDNTILNKPLQLKPNITNSARHLLGGLQKDRTKRLGAKDDFMEIKSHVFFSLINWDDLI 459
QY 362 OKKIPPPNPVAGPDDIRNFDTAFTEETVPYSCVSSDYSIVNASVLEADDAFVGFSYA 421
DB 460 NKKITPPFPNPVSGPNDLRHFDPEFTEEPVPSIGKSPDSVLTASVKAAEAFLGFSYA 519
QY 422 PPSEDLFL 429
DB 520 PPT-DSFL 526

RESULT 8
US-10-067-977-4
; Sequence 4, Application US/10067977
; Publication No. US20030157679A1
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; GENERAL INFORMATION:  
 ; APPLICANT: YAN, Chunhua and KE, Zhaoxi  
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
 ; TITLE OF INVENTION: THEREOF  
 ; FILE REFERENCE: CL001313  
 ; CURRENT APPLICATION NUMBER: US/10/067,977  
 ; CURRENT FILING DATE: 2002-02-08  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 407  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-067-977-4

Query Match 65.1%; Score 1476; DB 4; Length 407;  
 Best Local Similarity 67.5%; Pred. No. 4.7e-109;  
 Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;  
 QY 19 FIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQWDSPKH---QSDPSEDEDESSQKLH 74  
 DB 3 FIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQWDSPKH---QSDPSEDEDESSQKLH 53  
 QY 75 STSQINILGPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLKDGKFAVAVKVLQKIVLNR 134  
 DB 54 SPSQOINLGPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLKDGKFAVAVKVLQKIVLNR 113  
 QY 135 KEQKHMAERNVLLKNVHPFLVGLHYSFQTEKLYFVLDVFNNGELFFHQLQERSPEH 194  
 DB 114 KEEKHIMSERVLLKNVHPFLVGLHYSFQTEKLYFVLDVFNNGELFFHQLQERSPEH 173  
 QY 195 RARFYAAETASALGYLHSLNIVRDLPENILDSVGHVLTDFGLCKEGIAISDTTTF 254  
 DB 174 RARFYAAETASALGYLHSLNIVRDLPENILDSVGHVLTDFGLCKEGIAISDTTTF 233  
 QY 255 CGTPEYLAPEVIRKQPDYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMYNILHKPLSLR 314  
 DB 234 CGTPEYLAPEVIRKQPDYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMYNILHKPLSLR 293  
 QY 315 PGVSLTAWSLLELLEKDRQNRIGAKEDFLEIQNHPPFESLSWADLVQKKIPPPFNVA 374  
 DB 294 PNITNSARHLLEGLLQKDRKRLGAKDDFMEIKSHVFFSLINWDDLKINKITPPFPNVS 353  
 QY 375 GPDIRNFDFTAETETPVYSCVSSDYSIYNASVLEADDAFVGFSYAPPSDELFL 429  
 DB 354 GPNDLRHFDPEFTEEPVNSIGKSPSVLVTASVKEAAEAPLGFSYAPPT-DSFL 407

RESULT 9  
 US-10-827-272-4  
 ; Sequence 4, Application US/10827272  
 ; Publication No. US20040203127A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KE, Zhaoxi  
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
 ; TITLE OF INVENTION: THEREOF  
 ; FILE REFERENCE: CL001313-DIV  
 ; CURRENT APPLICATION NUMBER: US/10/827,272  
 ; CURRENT FILING DATE: 2004-04-20  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 407  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-827-272-4

Query Match 65.1%; Score 1476; DB 4; Length 407;  
 Best Local Similarity 67.5%; Pred. No. 4.7e-109;  
 Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;

QY 19 FIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQWDSPKH---QSDPSEDEDESSQKLH 74  
 DB 3 FIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQWDSPKH---QSDPSEDEDESSQKLH 53  
 QY 75 STSQINILGPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLKDGKFAVAVKVLQKIVLNR 134  
 DB 54 SPSQOINLGPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLKDGKFAVAVKVLQKIVLNR 113  
 QY 135 KEQKHMAERNVLLKNVHPFLVGLHYSFQTEKLYFVLDVFNNGELFFHQLQERSPEH 194  
 DB 114 KEEKHIMSERVLLKNVHPFLVGLHYSFQTEKLYFVLDVFNNGELFFHQLQERSPEH 173  
 QY 195 RARFYAAETASALGYLHSLNIVRDLPENILDSVGHVLTDFGLCKEGIAISDTTTF 254  
 DB 174 RARFYAAETASALGYLHSLNIVRDLPENILDSVGHVLTDFGLCKEGIAISDTTTF 233  
 QY 255 CGTPEYLAPEVIRKQPDYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMYNILHKPLSLR 314  
 DB 234 CGTPEYLAPEVIRKQPDYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMYNILHKPLSLR 293  
 QY 315 PGVSLTAWSLLELLEKDRQNRIGAKEDFLEIQNHPPFESLSWADLVQKKIPPPFNVA 374  
 DB 294 PNITNSARHLLEGLLQKDRKRLGAKDDFMEIKSHVFFSLINWDDLKINKITPPFPNVS 353  
 QY 375 GPDIRNFDFTAETETPVYSCVSSDYSIYNASVLEADDAFVGFSYAPPSDELFL 429  
 DB 354 GPNDLRHFDPEFTEEPVNSIGKSPSVLVTASVKEAAEAPLGFSYAPPT-DSFL 407

RESULT 10  
 US-09-981-353-7  
 ; Sequence 7, Application US/09981353  
 ; Patent No. US20020160382A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Laeek, Amy W.  
 ; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER  
 ; FILE REFERENCE: PA-0038 US  
 ; CURRENT APPLICATION NUMBER: US/09/981,353  
 ; CURRENT FILING DATE: 2001-10-11  
 ; NUMBER OF SEQ ID NOS: 194  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 7  
 ; LENGTH: 431  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No. US20020160382A1 3819039CD1  
 US-09-981-353-7

Query Match 65.1%; Score 1476; DB 3; Length 431;  
 Best Local Similarity 67.5%; Pred. No. 5.1e-109;  
 Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;  
 QY 19 FIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQWDSPKH---QSDPSEDEDESSQKLH 74  
 DB 27 FIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQWDSPKH---QSDPSEDEDESSQKLH 77  
 QY 75 STSQINILGPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLKDGKFAVAVKVLQKIVLNR 134  
 DB 78 SPSQOINLGPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLKDGKFAVAVKVLQKIVLNR 137  
 QY 135 KEQKHMAERNVLLKNVHPFLVGLHYSFQTEKLYFVLDVFNNGELFFHQLQERSPEH 194  
 DB 138 KEEKHIMSERVLLKNVHPFLVGLHYSFQTEKLYFVLDVFNNGELFFHQLQERSPEH 197  
 QY 195 RARFYAAETASALGYLHSLNIVRDLPENILDSVGHVLTDFGLCKEGIAISDTTTF 254  
 DB 198 RARFYAAETASALGYLHSLNIVRDLPENILDSVGHVLTDFGLCKEGIAISDTTTF 257  
 QY 255 CGTPEYLAPEVIRKQPDYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMYNILHKPLSLR 314

Db 258 CGTPEYLAPEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMVDNINLKPLQLK 317  
QY 315 PGVSLTAMWILBELLEKRONRLGAKEDFLEIQNHPPFFESLSWADLVQKKIPPPNPVA 374  
Db 318 PNITNSARHLLEGLLQKRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNPVS 377  
QY 375 GPDDIRNFDTAFTTEETVPYSCVSSDYSIVNASVLEADDAFVGFSYAPPSDELFL 429  
Db 378 GPNDLRHFDPEFTTEEPVPNSIGKSPDSVLVTASVKEAAEAFUGFSYAPPT-DSFL 431

RESULT 11  
US-10-403-161-2  
; Sequence 2, Application US/10403161  
; Publication No. US20040043930A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, David et al.  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-573C  
; CURRENT APPLICATION NUMBER: US/10/403,161  
; CURRENT FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: 60/370349  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 60/384543  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: 60/370969  
; PRIOR FILING DATE: 2002-04-08  
; PRIOR APPLICATION NUMBER: 60/403748  
; PRIOR FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: 60/372019  
; PRIOR FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: 60/374379  
; PRIOR FILING DATE: 2002-04-22  
; PRIOR APPLICATION NUMBER: 09/779679  
; PRIOR FILING DATE: 2001-02-08  
; PRIOR APPLICATION NUMBER: 60/181045  
; PRIOR FILING DATE: 2000-02-08  
; PRIOR APPLICATION NUMBER: 10/055877  
; PRIOR FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: 60/262892  
; PRIOR FILING DATE: 2001-01-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 173  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 2  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-403-161-2

Query Match 65.1%; Score 1476; DB 4; Length 431;  
Best Local Similarity 67.5%; Pred. No. 5.1e-109;  
Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;  
QY 19 FIKORRAGLNERIQNLVRYPELVNHPDVRFAFLQMDSPKH----QSDPSEDEDESSQKLH 74  
Db 27 FMKQRMGLNDFIQKIANNYSACKPEVQSILKISQPEPELMNANPSPPP----- 77  
QY 75 STSQINILGPSGNPHAKPTDFDLKVIKGSFGKVLAKRKLKDKFYAVKVLQKKIVLNR 134  
Db 78 SPQQOINLGPSSNPHAKPSDFHLKVIKGSFGKVLARHKAEEVFYAVKVLQKKAILKK 137  
QY 135 KEQKHMAERNVLLKNVGHPLVGLHYSFQTTKLYFVLDLVNNGGELFFHLQERSFPPEH 194  
Db 138 KEEKHIMSERNVLLKNVGHPLVGLHYSFQTTADKLYFVLDYINGGELFFHLQERCFCLEP 197  
QY 195 RARFYAAEIASALGYLHSLIKIVYRDLKPENILLDSVGHVVLTDFGLCKEGIAISDTTTF 254  
Db 198 RARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTDFGLCKENIEHNTSTTF 257  
QY 255 CGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMVDNINLKPLSLR 314  
Db 258 CGTPEYLAPEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMVDNINLKPLQLK 317

QY 315 PGVSLTAMWILBELLEKRONRLGAKEDFLEIQNHPPFFESLSWADLVQKKIPPPNPVA 374  
Db 318 PNITNSARHLLEGLLQKRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNPVS 377  
QY 375 GPDDIRNFDTAFTTEETVPYSCVSSDYSIVNASVLEADDAFVGFSYAPPSDELFL 429  
Db 378 GPNDLRHFDPEFTTEEPVPNSIGKSPDSVLVTASVKEAAEAFUGFSYAPPT-DSFL 431

RESULT 12  
US-10-403-161-4  
; Sequence 4, Application US/10403161  
; Publication No. US20040043930A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, David et al.  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-573C  
; CURRENT APPLICATION NUMBER: US/10/403,161  
; CURRENT FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: 60/370349  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 60/384543  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: 60/370969  
; PRIOR FILING DATE: 2002-04-08  
; PRIOR APPLICATION NUMBER: 60/403748  
; PRIOR FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: 60/372019  
; PRIOR FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: 60/374379  
; PRIOR FILING DATE: 2002-04-22  
; PRIOR APPLICATION NUMBER: 09/779679  
; PRIOR FILING DATE: 2001-02-08  
; PRIOR APPLICATION NUMBER: 60/181045  
; PRIOR FILING DATE: 2000-02-08  
; PRIOR APPLICATION NUMBER: 10/055877  
; PRIOR FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: 60/262892  
; PRIOR FILING DATE: 2001-01-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 173  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 4  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-403-161-4

Query Match 65.1%; Score 1476; DB 4; Length 431;  
Best Local Similarity 67.5%; Pred. No. 5.1e-109;  
Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;  
QY 19 FIKORRAGLNERIQNLVRYPELVNHPDVRFAFLQMDSPKH----QSDPSEDEDESSQKLH 74  
Db 27 FMKQRMGLNDFIQKIANNYSACKPEVQSILKISQPEPELMNANPSPPP----- 77  
QY 75 STSQINILGPSGNPHAKPTDFDLKVIKGSFGKVLAKRKLKDKFYAVKVLQKKIVLNR 134  
Db 78 SPQQOINLGPSSNPHAKPSDFHLKVIKGSFGKVLARHKAEEVFYAVKVLQKKAILKK 137  
QY 135 KEQKHMAERNVLLKNVGHPLVGLHYSFQTTKLYFVLDLVNNGGELFFHLQERSFPPEH 194  
Db 138 KEEKHIMSERNVLLKNVGHPLVGLHYSFQTTADKLYFVLDYINGGELFFHLQERCFCLEP 197  
QY 195 RARFYAAEIASALGYLHSLIKIVYRDLKPENILLDSVGHVVLTDFGLCKEGIAISDTTTF 254  
Db 198 RARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTDFGLCKENIEHNTSTTF 257  
QY 255 CGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMVDNINLKPLSLR 314  
Db 258 CGTPEYLAPEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMVDNINLKPLQLK 317

QY 315 PGVSLTAWSLLELEKDRQNRILGAKEDFLBQNHPPFESLSWADLVQKKIPPPFNVA 374  
Db 318 PNITNSARHLLEGLQKDRKRLGAKODFMEIKSHVFFSLINWDLINKKITPPFPNVS 377  
QY 375 GPDIRNFDTAFTETVPYSCVSSDIYNVNSLEADDAFVGFSYAPPSDELFL 429  
Db 378 GPNDLRHFDPEFTPEEPVNSIGKSPDSVLVTASVKEAAEFLGFSYAPPT-DSFL 431

## RESULT 13

US-10-067-977-2  
; Sequence 2, Application US/10067977  
; Publication No. US20030157679A1  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Chunhua and KE, Zhaoxi  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001313  
; CURRENT APPLICATION NUMBER: US/10/067,977  
; CURRENT FILING DATE: 2002-02-08  
; SOFTWARE: FastSeq for Windows Version 4.0  
; NUMBER OF SEQ ID NOS: 4  
; SEQ ID NO 2  
; LENGTH: 445  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-067-977-2

Query Match 65.1%; Score 1476; DB 4; Length 445;  
Best Local Similarity 67.5%; Pred. No. 5.3e-109;  
Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;

QY 19 FIKQRAGLNEFTQNLVRYPELVNHPDVRAPFLQWDSPKH---QSDPSEDESSQKLH 74  
Db 41 FMKQRRMGLNDFLOKTNANSYACKHPEVQSILKISQPEPELMNANSPPPP----- 91  
QY 75 STSQNLGPGSNPHAKPTDFDLKLVIGKSGFGKVLAKRKLGDGFYAVKVLQKKIVLNR 134  
Db 92 SPQQINLGPSNPHAKPSDFHLKLVIGKSGFGKVLAKRKLGDGFYAVKVLQKKAILKK 151  
QY 135 KEQKHIMARNVLLKNVHPFLVGLHYSPOTTLEKLVFVLDVNGGELFFHLQERSFPEH 194  
Db 152 KEEKHIMSERVLLKNVHPFLVGLHFSFQTDKLYFVLDYINGGELFFHLQERCFLP 211  
QY 195 RARFYAAETASALGYLHSIKIVYRDLKPNILLDSQGHIVLTDGFLCKENIENSTTSTF 254  
Db 212 RARFYAAETASALGYLHSINIVYRDLKPNILLDSQGHIVLTDGFLCKENIENSTTSTF 271  
QY 255 CGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMVDNILHKPLSLR 314  
Db 272 CGTPEYLAPEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPYSRNTAEMVDNILNKPLQLK 331  
QY 315 PGVSLTAWSLLELEKDRQNRILGAKEDFLBQNHPPFESLSWADLVQKKIPPPFNVA 374  
Db 332 PNITNSARHLLEGLQKDRKRLGAKODFMEIKSHVFFSLINWDLINKKITPPFPNVS 391  
QY 375 GPDIRNFDTAFTETVPYSCVSSDIYNVNSLEADDAFVGFSYAPPSDELFL 429  
Db 392 GPNDLRHFDPEFTPEEPVNSIGKSPDSVLVTASVKEAAEFLGFSYAPPT-DSFL 445

## RESULT 14

US-10-827-272-2  
; Sequence 2, Application US/10827272  
; Publication No. US20040203127A1  
; GENERAL INFORMATION:  
; APPLICANT: KE, Zhaoxi  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001313-DIV  
; CURRENT APPLICATION NUMBER: US/10/827,272

; CURRENT FILING DATE: 2004-04-20  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 445  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-827-272-2

Query Match 65.1%; Score 1476; DB 4; Length 445;  
Best Local Similarity 67.5%; Pred. No. 5.3e-109;  
Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;

QY 19 FIKQRAGLNEFTQNLVRYPELVNHPDVRAPFLQWDSPKH---QSDPSEDESSQKLH 74  
Db 41 FMKQRRMGLNDFLOKTNANSYACKHPEVQSILKISQPEPELMNANSPPPP----- 91  
QY 75 STSQNLGPGSNPHAKPTDFDLKLVIGKSGFGKVLAKRKLGDGFYAVKVLQKKIVLNR 134  
Db 92 SPQQINLGPSNPHAKPSDFHLKLVIGKSGFGKVLAKRKLGDGFYAVKVLQKKAILKK 151  
QY 135 KEQKHIMARNVLLKNVHPFLVGLHYSPOTTLEKLVFVLDVNGGELFFHLQERSFPEH 194  
Db 152 KEEKHIMSERVLLKNVHPFLVGLHFSFQTDKLYFVLDYINGGELFFHLQERCFLP 211  
QY 195 RARFYAAETASALGYLHSIKIVYRDLKPNILLDSQGHIVLTDGFLCKENIENSTTSTF 254  
Db 212 RARFYAAETASALGYLHSINIVYRDLKPNILLDSQGHIVLTDGFLCKENIENSTTSTF 271  
QY 255 CGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMVDNILHKPLSLR 314  
Db 272 CGTPEYLAPEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPYSRNTAEMVDNILNKPLQLK 331  
QY 315 PGVSLTAWSLLELEKDRQNRILGAKEDFLBQNHPPFESLSWADLVQKKIPPPFNVA 374  
Db 332 PNITNSARHLLEGLQKDRKRLGAKODFMEIKSHVFFSLINWDLINKKITPPFPNVS 391  
QY 375 GPDIRNFDTAFTETVPYSCVSSDIYNVNSLEADDAFVGFSYAPPSDELFL 429  
Db 392 GPNDLRHFDPEFTPEEPVNSIGKSPDSVLVTASVKEAAEFLGFSYAPPT-DSFL 445

## RESULT 15

US-10-000-039-2  
; Sequence 2, Application US/10000039  
; Publication No. US20030003559A1  
; GENERAL INFORMATION:  
; APPLICANT: LANG, Florian  
; TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: 3000 K Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/000,039  
; FILING DATE: 04-Dec-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/031,295  
; FILING DATE: 26-FEB-1998  
; APPLICATION NUMBER: DE 197-08-173.8  
; FILING DATE: 28-FEB-1997  
; ATTORNEY/AGENT INFORMATION:





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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:32:16 ; Search time 11.0623 Seconds  
(without alignments)  
419.957 Million cell updates/sec

Title: US-09-868-131A-4

Perfect score: 2269

Sequence: 1 MALKIPAKRIFGDNFDPDFI.....EADDAVFGFSYAPPSDLFL 429

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1501	66.2	543	6	US-10-821-234-1158
2	816.5	36.0	480	7	US-11-109-156-18
3	786	34.6	495	6	US-10-770-726-81
4	779.5	34.4	737	7	US-11-152-366-28
5	708	31.2	740	6	US-10-878-556A-129
6	686.5	30.3	705	6	US-10-995-561-856
7	686.5	30.3	706	6	US-10-995-561-855
8	686.5	30.3	706	6	US-11-099-958-1
9	684.5	30.2	351	7	US-11-099-958-2
10	684	30.1	942	6	US-10-770-726-76
11	657.5	29.0	398	7	US-11-132-142-7
12	654.5	28.8	341	7	US-11-092-168-4
13	650	28.6	351	7	US-11-132-142-13
14	649	28.6	381	7	US-11-132-142-9
15	647.5	28.5	351	7	US-11-132-142-14
16	647	28.5	343	7	US-11-092-168-3
17	642	28.3	480	7	US-11-132-142-6
18	641.5	28.3	515	7	US-11-132-142-8
19	637.5	28.1	462	7	US-11-132-142-10
20	635.5	28.0	350	6	US-10-497-767-4
21	632	27.9	395	7	US-11-132-142-12
22	626.5	27.6	353	7	US-11-132-142-11
23	624.5	27.5	548	7	US-11-132-142-5
24	543	23.9	1732	6	US-10-055-877-147
25	534	23.5	1590	6	US-10-055-877-146

26	533	23.5	1613	6	US-10-055-877-145	Sequence 145, App
27	533	23.5	1637	6	US-10-055-877-144	Sequence 144, App
28	532	23.4	637	7	US-11-113-837-4	Sequence 4, Appli
29	531	23.4	635	7	US-11-113-837-16	Sequence 16, Appli
30	529	23.3	256	6	US-10-877-346-72	Sequence 72, Appl
31	529	23.3	256	7	US-11-113-424-183	Sequence 183, App
32	526	23.2	1197	6	US-10-055-877-8	Sequence 8, Appli
33	526	23.2	1247	6	US-10-055-877-10	Sequence 10, Appl
34	524	23.1	1663	6	US-10-055-877-148	Sequence 148, App
35	516.5	22.8	756	7	US-11-113-837-20	Sequence 20, Appl
36	503.5	22.2	639	7	US-11-113-837-21	Sequence 21, Appl
37	498	21.9	668	7	US-11-113-424-12	Sequence 12, Appl
38	494	21.8	689	7	US-11-113-424-47	Sequence 47, Appl
39	492.5	21.7	598	7	US-11-113-837-18	Sequence 18, Appl
40	491	21.6	689	7	US-11-113-424-46	Sequence 46, Appl
41	488	21.5	688	7	US-11-113-424-45	Sequence 45, Appl
42	485.5	21.4	396	7	US-11-125-295-11	Sequence 11, Appl
43	485.5	21.4	407	7	US-11-125-295-9	Sequence 9, Appli
44	485	21.4	688	7	US-11-113-424-48	Sequence 48, Appl
45	484	21.3	665	7	US-11-113-837-19	Sequence 19, Appl

## ALIGNMENTS

### RESULT 1

US-10-821-234-1158  
; Sequence 1158, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; PRIOR FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pc\_seq\_genes Version 1.0  
; SEQ ID NO 1158  
; LENGTH: 543  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1158

Query Match	66.2%	Score 1501;	DB 6;	Length 543;
Best Local Similarity	66.8%	Pred. No. 1.4e-126;		
Matches	286;	Conservative	52;	Mismatches 76;
				Indels 14;
				Gaps 3;
QY	6	PAKRIFGDNFDPDFIKORAGLNEFTQNLVRYPELVNHPDVFRAFLQWDSPKH----	QSDP	61
Db	126	PDPRTEWTDPAFMQKRMGLNDFIQKIANNYSACKHPEVQSIKISQBPPELMANP	185	
QY	62	SEDEDRSSQKLHSTQNLNIGPSGNPHAKPTDFDLKVIKGSFGKVLAKRLDKGFY	121	
Db	186	SPPP-----SPSQINLGPSSNPHAKPSDFHLKVIKGSFGKVLARHAKAEVFY	236	
QY	122	AVKLQKIVLNKKEOKHMAERNVLLKNVHPFLVGLHVSFOTTEKLYFVLDPVNGGEL	181	
Db	237	AVKLQKAILKKEKHIMERNVLLKNVHPFLVGLHVSFOTADKLYFVLDPVNGGEL	296	
QY	182	FPHLQERSFPFHRARFYAAETASALGYLHSIKIVYRDLKPNENILDSVGHVVLTDGLC	241	
Db	297	FYHLQERCFLEPRARFYAAETASALGYLHSINIVYRDLKPNENILDSQGHVLTDFGLC	356	
QY	242	KGIALSDTTTTTCGTPPEYLAPEVTRKQYDNTVDMWCLGAVLYEMLYGLPPYCRDVAE	301	
Db	357	KENIEHNSTSTTCGTPPEYLAPEVTRKQYDNTVDMWCLGAVLYEMLYGLPPYCRDVAE	416	
QY	302	MYDNILHKLPLSLRPGVSLTAWSLTELELLEKDRQNLGAKEDFLEIQNHPPFESLSWADLV	361	

Db 417 MYNINLKPQLKPNTNSARHLEGLQKDRYRGLGAKDDFWELKSHVFFSLINWDDLI 476  
Qy 362 QKKIPFPNPNVAGPDDIRNFDTAFTETVPYGVCVSSDYSIYNASVLEADDAFVGFSYA 421  
Db 477 NKKITPFPNPNVSGPNDLRHFDPEFTTEPVPNSIGKSPDSVLVTASVKEAAEAFLGFSYA 536

Qy 422 PPSDELFL 429  
Db 537 PPT-DSFL 543

RESULT 2  
US-11-109-156-18  
; Sequence 18, Application US/11109156  
; Publication No. US20050250144A1  
; GENERAL INFORMATION:  
; APPLICANT: Toshio Ota  
; APPLICANT: Takao Ieogai  
; APPLICANT: Tetsuo Nishikawa  
; APPLICANT: Koji Hayashi  
; APPLICANT: Kaoru Otsuka  
; APPLICANT: Jun-Ichi Yamamoto  
; APPLICANT: Shizuko Ishii  
; APPLICANT: Tomoyasu Sugiyama  
; APPLICANT: Ai Wakamatsu  
; APPLICANT: Keiichi Nagai  
; APPLICANT: Tetsuji Otsuki  
; APPLICANT: Shin-Ichi Funahashi  
; APPLICANT: Chiaki Senoo  
; APPLICANT: Jun-Ichi Nezu  
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN  
; TITLE OF INVENTION: PHOSPHATASE  
; FILE REFERENCE: 06501-099002  
; CURRENT APPLICATION NUMBER: US/11/109,156  
; CURRENT FILING DATE: 2005-04-19  
; PRIOR APPLICATION NUMBER: US/10/060,065  
; PRIOR FILING DATE: 2002-01-29  
; PRIOR APPLICATION NUMBER: PCT/JP00/05061  
; PRIOR FILING DATE: 2000-07-28  
; PRIOR APPLICATION NUMBER: US 60/159,590  
; PRIOR FILING DATE: 1999-10-18  
; PRIOR APPLICATION NUMBER: US 60/183,322  
; PRIOR FILING DATE: 2000-02-17  
; PRIOR APPLICATION NUMBER: JP 11-248036  
; PRIOR FILING DATE: 1999-07-29  
; PRIOR APPLICATION NUMBER: JP 2000-118776  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: JP 2000-183767  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: JP 2000-241899  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 480  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-109-156-18

Query Match 36.0%; Score 816.5; DB 7; Length 480;  
Best Local Similarity 41.0%; Pred. No. 1.9e-65;  
Matches 185; Conservative 63; Mismatches 146; Indels 57; Gaps 12;  
Qy 17 PDFIKORRAGINEFIQNLVRYPELY--NHPDVRAFL-----QMDSPKHQSDPSEDED 66  
Db 42 PQVDQREAPLNNF---SVAQCQLMKTERPRNTPFIIRCLQWTTVIERTFHVETPEERE 98  
Qy 67 ERS-----QKLHSTSONILG-PSGNPH-----AKP-----TDFPLKVIK 103  
Db 99 WTTAIQTVDGLKKQEEEMDFRSGSPDSNGAEEMEVSLAKPKHRVTWNEFEYLKLGK 158  
Qy 104 GSGFKVLLAKRLDGKFAVKVLQKKIVLNRKQKHMAERNVLLKNVHPFLVGLHYSF 163

Db 159 GTFGKVLVKEATGRYAMKILKKEVIIVAKDEVATLTTE-NRVLQNSRHPPFTALXYSP 217  
Qy 164 QTTEKLYFVLDVFNVGSELFPHLQRRSFPEHRARFYAAEIASALGYLHSHK-IYVRDLKP 222  
Db 218 QTHDRLCFVMEYANGSELFPHLSRERVFSEDRARFYGAELVSALDYLVHSEKNVVRDLKL 277  
Qy 223 ENILLDSVGHVLTDFGLCKEGIAISDTTTTTCGTPEYLAPFVIRKQPDYNTVDWVCLGA 282  
Db 278 ENMLDKDGHIIKITDFGLCKEGIKDGAATWKTTCGTPEYLAPFVLEDDNDYGRAVDWVGLGV 337  
Qy 283 VLYEMLYGLPPFYCRDVAEMYNILHKPLSLRPGVSLTAWLSILEELLEKDRQNL-CAKE 341  
Db 338 VMYEMMCGRLPPFYNQDHEKLFELILWEEIRFPRTLGPEAKSLLSGLLKDKPKORLGGSE 397  
Qy 342 DFLEIQNHPPFESLSWADLVQKKIPFPNPNVAGPDDIRNFDTAFTETVPYS----- 394  
Db 398 DAKIEMQHRFFAGIVQHVVEKKLSPPKFPQVTSETDTRVDFDEFTAQMITITPPDQDDS 457  
Qy 395 -VCVSSDYSIVNASVLEADDAFVGFSYAPPS 424  
Db 458 MECVDS-----ERRPFPQFSYSASS 478

RESULT 3  
US-10-770-726-81  
; Sequence 81, Application US/10770726  
; Publication No. US20050266409A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Brown, Eugene  
; APPLICANT: Liu, Wei  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATIN  
; TITLE OF INVENTION: CANCERS  
; FILE REFERENCE: AM101079 (031896-010000)  
; CURRENT APPLICATION NUMBER: US/10/770,726  
; CURRENT FILING DATE: 2004-02-04  
; NUMBER OF SEQ ID NOS: 48640  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 81  
; LENGTH: 495  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-770-726-81  
Query Match 34.6%; Score 786; DB 6; Length 495;  
Best Local Similarity 42.1%; Pred. No. 1.1e-62;  
Matches 170; Conservative 70; Mismatches 124; Indels 40; Gaps 11;  
Qy 48 AFLQWDSPKHQSDPSEDEDESS-----QKLHSTSONILGSPG- 86  
Db 16 AVFDLDLETEGSEGEPELSPADACPLAELRAAGLEPVGHYEVELTETSVNVGPERI 75  
Qy 87 NPHAKPTDFDLKVIKSGSFGKVLAKRKLD---GKFYAVKVLQK-KIVLNRKEQKHIM 141  
Db 76 GPFC-----FELLRLVGKGGYGVQV-RKVGQTNLGIYAMKVLRAKIVRNAKDTAHR 130  
Qy 142 AERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDVFNVGSELFPHLQRRSFPEHRARFYAA 201  
Db 131 ASRNI-LESVKHPFVELAYAFQTGKLYLLECLSGGSELFTHLEREGIFLEDTACFYLA 189  
Qy 202 ETASALGYLHSHKIVYRDLKPNILLDSVGHVLTDFGLCKEGIALSDTTTTTCGTPEYL 261  
Db 190 EITLALGHLSGIIYRDLKPNINILSSQGHKLTDFGLCKESIHEGAVTHTCGTIEYM 249  
Qy 262 APEVIRKQPDYNTVDWVCLGAVLYEMLYGLPPFYCRDVAEMYNILHKPLSLRPGVSLTA 321  
Db 250 ABEILVRSRHNRAVDWWSLGALMYDMLTGSPPFTAENRKKTKMDKIIRGLKALPFLTPDA 309  
Qy 322 WSILEELLBKDRNRU-GAKEDFLEIQNHPPFESLSWADLVQKKIPFPNPNVAGPDDIR 380  
Db 310 RDLVKKFLKRNPSQRIGGGGGAADVQRHPFFRHHNMWDLALAWRVDPFPRPCLQSBEDVS 369

QY 381 NFDTAFTTEVPYVCVSSDYISVNASVLEADAFVGFVSAPPS 424  
||| ||| : | : : : : : : : : : : : : : : : : :  
Db 370 QFDTRFTRQT-PVD---SPDDTALSES---ANOAFGLGFTTVAPS 406

## RESULT 4

US-11-152-366-28

; Sequence 28, Application US/11152366  
; Publication No. US20060014184A1  
; GENERAL INFORMATION:  
; APPLICANT: Bvys, Reginald  
; APPLICANT: Vandeghinste, Nick  
; APPLICANT: Tomme, Peter H. M.  
; TITLE OF INVENTION: Methods For Identification, And Compounds Useful For The  
; TITLE OF INVENTION: Treatment Of Degenerative & Inflammatory Diseases  
; FILE REFERENCE: P27,880-A USA  
; CURRENT APPLICATION NUMBER: US/11/152,366  
; CURRENT FILING DATE: 2005-06-14  
; PRIOR APPLICATION NUMBER: 60/579,307  
; PRIOR FILING DATE: 2004-06-14  
; NUMBER OF SEQ ID NOS: 295  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 28  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-152-366-28

Query Match 34.4%; Score 779.5; DB 7; Length 737;

Best Local Similarity 39.7%; Pred. No. 7.1e-62; Mismatches 122; Indels 59; Gaps 9;

Matches 167; Conservative 73

QY 53 DSPKHQSDPSEDEDESSOKLHSTQNTN-----SOKLHSTQNTN-----L 82

Db 328 ESPQASGSSPSEDESKSAPSPCQOEIKELENNIRKALSFNRRGEHRAASSPDGQLM 387

QY 83 GPSGNPHAKP-----TDFDLKVGKSGFGKVLAKKLDGKFYAVKVLQKIVLNR 134

Db 388 SPGENGEVRQGAQKRLGLDEFNFIKVLGKSGFGKWLAEKLGKDEYVAVKVLKQVILQD 447

QY 135 KEQKHIMAEENVLLKNVQHPFLVGLHYSFQTTKLYFLVDFVNGGELFFHLQERSFPEH 194

Db 448 DDVDCVTMTKRIILARKHPYLTQLYCCFQTKRLFFWMEYVNGGDLMFQIORSKRFDEP 507

QY 195 RARFYAAETASALGYLHSIKIVYRDLKPNILDSVGHVVLTDPLGCKEGIAISDTITTF 254

Db 508 RSRFYAAEVTSALMFLHQGVITRDLKDLNLLDAEGHCKLADFGMCKEGLNGVITTF 567

QY 255 CGTPEYLAPEVIRKQPDYNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMYNILHKLPSLR 314

Db 568 CGTPDYIAPEILQLEVEYGPSVDWALGVLMYEMWAGOPPEADNEDDLFESILHDDVLYP 627

QY 315 PGVSLTAWSLLELEKDRQNRIGA-----KEPFLQIHPFPESISWADLVOKKIPPPF 369

Db 628 VWLSKEAVSILKAFMTKNPKHRLGCVASONGED--AIKQHPFPEKEDWVLEOKKIKPPF 685

QY 370 NPNVAGPDDIRNFDTAFT--EETPYSCVSSDYISVNASVLEA--DDAFVGFVSAPPS 426

Db 686 KPRIKTRDVNNFDQDFTREEPV-----LTLVDEAIVKQINQOEFPKGFYSF--GED 734

QY 427 L 427

Db 735 L 735

## RESULT 5

US-10-878-556A-129

; Sequence 129, Application US/10878556A  
; Publication No. US20050266399A1  
; GENERAL INFORMATION:  
; APPLICANT: Hoffmann La-Roche Inc.  
; TITLE OF INVENTION: HCV regulated protein expression  
; FILE REFERENCE: 21762

Query Match 30.3%; Score 686.5; DB 6; Length 705;  
Best Local Similarity 39.6%; Pred. No. 1.4e-53;  
Matches 148; Conservative 68; Mismatches 131; Indels 27; Gaps 7;QY 51 QMDSPKHQSDPSEDEDESSOKLHSTQNTNINLPGSGNPHAKPTDFDLKVGKSGFGKVL 110  
||| ||| : | : : : : : : : : : : : : : : : : :  
Db 351 EVDKMCMLPEPELNKERPISLQ-----IKL-----KIEDFILHMKLKGSGFGKVF 394

; CURRENT APPLICATION NUMBER: US/10/878,556A

; CURRENT FILING DATE: 2004-06-28

; NUMBER OF SEQ ID NOS: 199

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 129

; LENGTH: 740

; TYPE: PRT

; ORGANISM: Homo sapiens

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: sw\_hum/k6a3\_human

; DATABASE ENTRY DATE: 1996-10-01

US-10-878-556A-129

Query Match 31.2%; Score 708; DB 6; Length 740;  
Best Local Similarity 40.7%; Pred. No. 1.8e-55;  
Matches 157; Conservative 63; Mismatches 134; Indels 32; Gaps 8;QY 52 MDSPKHQSDPSEDEDESSOKLHSTQNTNINLPGSGNPHAKPTDFDLKVGKSGFGKVL 111  
||| ||| : | : : : : : : : : : : : : : : : : :  
Db 29 MDEPMGEERINPQTEEVSVIKEIAITHH---VKEGHEKADPSQFELLKVLGQSGFGKVF 84

QY 112 AKKELDG---KPYAVKVLQKIVLNKKEQKHIMAEENVLLKNVQHPFLVGLHYSFQTT 167

Db 85 VK-KISGSARQLYAMKVL-KKATLKVRDRVTRTMRDILVE-VNHFIVKLHYAFQTEG 141

QY 168 KLYFVLDVNGGELFFHLQERSFPEHRAFYAAETASALGYLHSIKIVYRDLKPNILL 227

Db 142 KLYLILDFLGGDLFTRLSKVMTBEDVKFYLAELALDLHLHSLGIIYRDLKPNILL 201

QY 228 DSVGHVVLTDPLGCKEGIAISDTITTFCTGPEYLAPEVIRKQPDYNTVDMWCLGAVLY 287

Db 202 DEEGHKLKLDGKLSKESIDHEKKAYSFCGTVEYMAPEVNVNRGHTQSADWWSFGVLMFEM 261

QY 288 LYLPLPFYCRDVAEMYNILHKLPSLRPGVSLTAWSLLELEKDRQNLGAKEDFL-EI 346

Db 262 LGTLFPQGRKDRKETMTMLKAKLGMPOFLSPQAQSLRLMLFKRNPNRNLGAGPDGVVEI 321

QY 347 QNHPPFESISWADLVOKKIPPPNPNVAGPDDIRNFDTAFTET-----VPYSCVSSD 400

Db 322 KRHSFFSTIDWNKLYRREIHPKPKATGRPEDTFYFDPEFTAKTPKDSPIPPSA----- 376

QY 401 YSIVNASVLEADDAFVGFVSAPPS 426

Db 377 -----NAHQLPFGSFAITSD 393

## RESULT 6

US-10-995-561-856

; Sequence 856, Application US/10995561

; Publication No. US20050272054A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; TITLE OF INVENTION: DETECTION AND USES THEREOF

; FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995,561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 856

; LENGTH: 705

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-995-561-856



```
; Publication No. US20060003431A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Zhang Bao
; APPLICANT: Olland, Stephanie
; APPLICANT: Wolfstrom, Scott
; APPLICANT: Malakian, Karl
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; APPLICANT: Lee, Julie
; APPLICANT: Fitz, Lori
; APPLICANT: Greco, Rita
; APPLICANT: Chaudhary, Divya
; APPLICANT: Somers, William Stuart
; APPLICANT: Mosyak, Lidia
; TITLE OF INVENTION: STRUCTURE OF PROTEIN KINASE C THETA
; FILE REFERENCE: 16163-018001
; CURRENT APPLICATION NUMBER: US/11/099,958
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US 60/560,441
; PRIOR FILING DATE: 2004-04-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-099-958-2

Query Match      30.2%; Score 684.5; DB 7; Length 351;
Best Local Similarity 41.9%; Pred. No. 7.8e-54;
Matches 143; Conservative 62; Mismatches 125; Indels 11; Gaps 5;

QY 84 PSGNPHAKPTDFDLKLVIGKSGFQKVLAKKLDGKFAVAVKLVKQKIVLNKKEQKHTMAE 143
DB 8 PSQIKLIKIEDFILHRMLKGGSPGVFLAEFKTNQNFALKALKKQVLMDDDDVECTMVE 67

QY 144 RNVLKNVHPFLVGLHYSTQTEKLYFVLDFVNGGELFFHLQERSFPPHRAFYAAEI 203
DB 68 KRVLSLAWHPFLTHMCTFQTKENLFFVMEYLNGLDMYHIQSKHFDLSRATFYAAEI 127

QY 204 ASALGYLHSIKIVYRDLPENILLDSVGHVLTDFGLCKEGIAISDTTTCGTPPEYLAP 263
DB 128 ILGLQFLHSGIVYRDLPENILLDSVGHVLTDFGLCKEGIAISDTTTCGTPPEYLAP 187

QY 264 EVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMVDNI-LHKPLSLRPGVSLTAW 322
DB 188 EILGQKYNHSDVMSFGVLLYEMLYGLQSPFHGQDEBELFHSIRMDNPFYPR-WLEKEAK 246

QY 323 SILLELEKRONRLGAKEDFLEIQNHPPFESLWADLVQKIPPPFNPNVAGPDDIRNF 382
DB 247 DLLVKLFVREPEKELVGRGD--LRQHPLEINWEELERKEIDPPRPVKVSPFDCSNF 303

QY 383 DTAFTETVPYVCVSSDYISVNASVLEADDAFVGFSYAPP 423
DB 304 DKEFLNEKPLRSF---ADRALINSM---DQNMFRNFSFMNP 338

RESULT 10
US-10-770-726-76
; Sequence 76, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76

; Publication No. US20060003431A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Zhang Bao
; APPLICANT: Olland, Stephanie
; APPLICANT: Wolfstrom, Scott
; APPLICANT: Malakian, Karl
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; APPLICANT: Lee, Julie
; APPLICANT: Fitz, Lori
; APPLICANT: Greco, Rita
; APPLICANT: Chaudhary, Divya
; APPLICANT: Somers, William Stuart
; APPLICANT: Mosyak, Lidia
; TITLE OF INVENTION: STRUCTURE OF PROTEIN KINASE C THETA
; FILE REFERENCE: 16163-018001
; CURRENT APPLICATION NUMBER: US/11/099,958
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US 60/560,441
; PRIOR FILING DATE: 2004-04-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-099-958-2

Query Match      30.2%; Score 684.5; DB 7; Length 351;
Best Local Similarity 41.9%; Pred. No. 7.8e-54;
Matches 143; Conservative 62; Mismatches 125; Indels 11; Gaps 5;

QY 84 PSGNPHAKPTDFDLKLVIGKSGFQKVLAKKLDGKFAVAVKLVKQKIVLNKKEQKHTMAE 143
DB 8 PSQIKLIKIEDFILHRMLKGGSPGVFLAEFKTNQNFALKALKKQVLMDDDDVECTMVE 67

QY 144 RNVLKNVHPFLVGLHYSTQTEKLYFVLDFVNGGELFFHLQERSFPPHRAFYAAEI 203
DB 68 KRVLSLAWHPFLTHMCTFQTKENLFFVMEYLNGLDMYHIQSKHFDLSRATFYAAEI 127

QY 204 ASALGYLHSIKIVYRDLPENILLDSVGHVLTDFGLCKEGIAISDTTTCGTPPEYLAP 263
DB 128 ILGLQFLHSGIVYRDLPENILLDSVGHVLTDFGLCKEGIAISDTTTCGTPPEYLAP 187

QY 264 EVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMVDNI-LHKPLSLRPGVSLTAW 322
DB 188 EILGQKYNHSDVMSFGVLLYEMLYGLQSPFHGQDEBELFHSIRMDNPFYPR-WLEKEAK 246

QY 323 SILLELEKRONRLGAKEDFLEIQNHPPFESLWADLVQKIPPPFNPNVAGPDDIRNF 382
DB 247 DLLVKLFVREPEKELVGRGD--LRQHPLEINWEELERKEIDPPRPVKVSPFDCSNF 303

QY 383 DTAFTETVPYVCVSSDYISVNASVLEADDAFVGFSYAPP 423
DB 304 DKEFLNEKPLRSF---ADRALINSM---DQNMFRNFSFMNP 338

RESULT 11
US-11-132-142-7
; Sequence 7, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; TITLE OF INVENTION: CYCLIC-AMP-DEPENDENT KINASE AND A TARGET FOR SARS THERAPY
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Saccharomyces sp.
US-11-132-142-7

Query Match      29.0%; Score 657.5; DB 7; Length 398;
Best Local Similarity 41.6%; Pred. No. 2.4e-51;
Matches 127; Conservative 64; Mismatches 107; Indels 7; Gaps 5;

QY 93 TDFDLKLVIGKSGFQKVLAKKLDGKFAVAVKLVKQKIVLNKKEQKHIAMERNVLLKNVK 152
DB 86 SDFQILRTLTGTSFGVRLIRSNHNGRFAVKLTKKHTIVKLVKQVEHNDERR-MLSIVS 144

QY 153 HPFLVGLHYSTQTEKLYFVLDFVNGGELFFHLQERSFPPHRAFYAAIASALGYLHS 212
DB 145 HPFLIRMGWTFQDSQQFVWMDYIEGELFSLRKQSFENPVAKFYAAEVCLEVLHS 204

QY 213 IKIVYRDLPENILLDSVGHVLTDFGLCKEGIAISDTTTCGTPPEYLAPVIRKOPYD 272
DB 205 KDIIVYRDLPENILLDSVGHVLTDFGLCKEGIAISDTTTCGTPPEYLAPVIRKOPYD 261
```





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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:12:00 ; Search time 12.6811 Seconds  
(without alignments)  
3254.993 Million cell updates/sec

Title: US-09-868-131A-4

Perfect score: 2269

Sequence: 1 MALKIPAKRIFGDNFDPDFI.....EADDAVGFVSAPPSEDLFL 429

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_80.\*

1: PIR1.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1476	65.1	431	2 A48094	serum and glucocor
2	1019.5	44.9	422	2 T26334	hypothetical prote
3	870	38.3	462	1 T17287	protein kinase (EC
4	866.5	38.2	479	1 A59380	protein kinase (EC
5	860.5	37.9	454	1 JC4345	protein kinase (EC
6	850.5	37.5	611	1 A55888	protein kinase (EC
7	844.5	37.2	481	1 A46288	protein kinase (EC
8	839	37.0	479	2 A38578	protein kinase 2 (
9	834.5	36.8	481	1 JC2438	protein kinase (EC
10	820.5	36.2	480	1 JC2437	protein kinase (EC
11	818.5	36.1	480	1 S33364	protein kinase (EC
12	818.5	36.1	763	1 A40831	gag-akt polypepti
13	816.5	36.0	480	1 A39360	protein kinase (EC
14	810	35.7	586	2 A37358	protein kinase (EC
15	804.5	35.5	480	1 S62117	protein kinase (EC
16	804	35.4	680	2 S37955	protein kinase ypk
17	803.5	35.4	587	2 A49509	protein kinase C (
18	800	35.3	677	2 JS0178	protein kinase YKR
19	795.5	35.1	569	2 T50414	probable prolifera
20	790.5	34.8	737	1 KIMSCE	protein kinase C (
21	790	34.8	634	1 B32392	protein kinase C (
22	789	34.8	525	1 A41687	ribosomal protein
23	789	34.8	525	1 S12906	probable ribosomal
24	786.5	34.7	481	2 JE0377	p70 S6 kinase (EC
25	785	34.6	736	1 KIRBCE	protein kinase C (
26	780	34.4	525	1 TVRTK6	ribosomal protein
27	779.5	34.4	737	1 S28942	protein kinase C (
28	777	34.2	547	2 T22856	hypothetical prote
29	774	34.1	707	1 A53530	protein kinase C (

## ALIGNMENTS

### RESULT 1

A48094

serum and glucocorticoid-regulated kinase - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 31-Dec-2004

C;Accession: A48094

R;Webster, M.K.; Goya, L.; Ge, Y.; Maiyar, A.C.; Firestone, G.L.

Mol. Cell. Biol. 13, 2031-2040, 1993

A;Title: Characterization of sgk, a novel member of the serine/threonine protein kinase

A;Reference number: A48094; MUID:93204949; PMID:8455596

A;Accession: A48094

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-431 <WEB>

A;Cross-references: UNIPARC:UPI000017A3B8

A;Experimental source: Con8.hdb mammary epithelial tumor cells

A;Note: sequence extracted from NCBI backbone (NCBIN:127618, NCBIP:127619)

C;Keywords: ATP

F;96-355/Domain: protein kinase homology <KIN>

F;104-112/Region: protein kinase ATP-binding motif

Query Match 65.1%; Score 1476; DB 2; Length 431;  
Best Local Similarity 67.7%; Pred. No. 6.2e-63;  
Matches 281; Conservative 50; Mismatches 70; Indels 14; Gaps 3;

Qy	19	FIKRRAGLNEFTQNLVRYPDELNHPDRAFLQMDSPKH-----OSDPSEDEKSSQKLH	74
Db	27	FMKQRRMGLNDFIQKLANNYSACKHPEVQSYLKISQPEPELMNANSPPP-----	77
Qy	75	STSQNLGPGSNPHAKPTDFDKVIGKSGFGKLLAKRKLQKGFYAVKVLQKIVLNR	134
Db	78	SPSQQLNGSPSNPHAKPSDFHFLKVGSGFGKLLARHKAEEAFYAVKVLQKALKKK	137
Qy	135	KEQKHMAERNVLLKNVKKHFFLVGLHYSFQTTKLYFVLDVANGGELFFHQLQRSFPFH	194
Db	138	KEEKHIMSERVLLKNVKKHFFLVGLHFSFQTKLYFVLDYINGGELFYHLQRCFLEP	197
Qy	195	RARFYAAETASALGYLHSIKIVYRDLPENILDSVGHVLTDFGLCKEGIAISDTTTF	254
Db	198	RARFYAAETASALGYLHSLNIVYRDLPENILDSQGHIVLTDFGLCKENIEHNGTSTF	257
Qy	255	CGTPEVLAPRVIKQYDNTVDWMLGAVLYEMLYGLPPFYCDVASMVNIHLKPLSLR	314
Db	258	CGTPEVLAPRVLHKQYDRTVDWMLGAVLYEMLYGLPPFYSRNTAEYNIHLNKPQLK	317
Qy	315	PGVSLTAWSLIEELLEKDRNLGAKEDFLEIQNHPPFESLSWADLVQKKIPPPFNVA	374
Db	318	PNITNSARHLEGLLQKORTKRLGAKDDFNEIKSHIFFSLINWDDLINKKITPPFNVS	377
Qy	375	GPDDIRNFDFTAFTEETVPYSCVSSYIVNASVLEADDAFVGFSYAPPSEDLFL	429
Db	378	GPSDLRHDFEFTPEEPVSSIGRSPDSILVTASVKEAAEAFLGFSYAPPW-DSFL	431



A;Residues: 1-479 <MAS>  
A;Cross-references: UNIPARC:UPI00000335E8; GB:CAB53537; NID:G5804886; PTDN:CAB53537.1  
C;Genetics:  
A;Gene: GDB:AKT3; PKBG: PRKBG; RAC-gamma  
A;Cross-references: GDB:9954867  
A;Map position: 1q44-1q44  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating various processes  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene  
F;7-108/Domain: pleckstrin repeat homology <PLK>  
F;149-408/Domain: protein kinase homology <KIN>  
F;157-165/Region: protein kinase ATP-binding motif  
F;177/Active site: Lys #status predicted  
F;305/Binding site: phosphate (Thr) (covalent) #status predicted  
F;474/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 38.2%; Score 866.5; DB 1; Length 479;  
Best Local Similarity 43.7%; Pred. No. 3.3e-34;  
Matches 184; Conservative 65; Mismatches 145; Indels 27; Gaps 7;

QY 20 IKORRAGLNFQNLVRYPELYNHPDVRAFLOMSPKHQSPSE-----DDED 68  
Db 62 MKTERPKPTFIIRCLQWTV-----IERTFVDVTPEREWEITAQVADRLOQBEER 116  
QY 69 SSQKLHSTQINILG-----PSGNPHAKPT--DFDLKVIKGSFGKVLAKRKLKGKFY 121  
Db 117 --MNCSPSTQIDNIGEBEMDASTTHHKRTKWNDFYLLKLGKGTGKVLVREKASGY 174  
QY 122 AVKVLQKKIVLNKKEQKHMAERNVLLKNVHPPLVGLHYSFQTEKLYFVLDVFNNGEL 181  
Db 175 AMKILKEVIIAKDEVAHTLTESRV-LKNTRHPPLTSLKYSFQTKDLRCFVMEYVNGEL 233  
QY 182 FFHLQRRSPPEHRARYFAAIAAGLGHISIKIVYRDLPENILLDSVGHVLTDFGLC 241  
Db 234 FFHLRSRVFSEDRTRFYGAIEVSALDYLHSGKIVYRDLPENILLDSVGHVLTDFGLC 293  
QY 242 KEGIAISDTTTCGTPPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFCRDVAE 301  
Db 294 KEGITDAATKTKTCGTPPEYLAPEVLENDYGRAVDMWGLGVVMYEMCGRLPFYNQDHEK 353  
QY 302 MYDNILHKPLSLRPGVSLTAWSLLELEKDRQNL--GAKEDFLEIQNHPPFESLSWADL 360  
Db 354 LFELILMEDIKFPRTLLSSDAKSLGILLKDPNKRLLGGPGDPAKEIMRHSFFSGVNWQDV 413  
QY 361 VQKIPPPNPNVAGPDDIRNFTAFTEETVPYSVCVSSYIVNASVLEADAFVGFYSY 420  
Db 414 YDKKLVPFPKPQVTSSETDTRYDFDEEFTAQTITTPPEKYDEGDMCDMERNRPHFPQFSY 473  
QY 421 A 421  
Db 474 S 474

RESULT 5  
JC4345  
protein kinase (EC 2.7.1.37) akt3 [validated] - rat  
N;Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific prote  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C;Accession: JC4345  
R;Konishi, H.; Kuroda, S.; Tanaka, M.; Matsuzaki, H.; Ono, Y.; Kameyama, K.; Haga, T.; K  
Biochem. Biophys. Res. Commun. 216, 526-534, 1995  
A;Title: Molecular cloning and characterization of a new member of the RAC protein kinase  
e C subtypes and beta gamma subunits of G proteins.  
A;Reference number: JC4345; MUID:96063640; PMID:7488143  
A;Accession: JC4345  
A;Molecule type: mRNA  
A;Residues: 1-454 <KON>  
A;Cross-references: UNIPROT:Q63484; UNIPARC:UPI000012577F; DBJ:D49836; NID:g1136777; PT  
A;Experimental source: brain  
C;Function:

A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating various processes  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein  
F;4-105/Domain: pleckstrin repeat homology <PLK>  
F;146-405/Domain: protein kinase homology <KIN>  
F;154-162/Region: protein kinase ATP-binding motif  
F;177/Active site: Lys #status predicted

Query Match 37.9%; Score 860.5; DB 1; Length 454;  
Best Local Similarity 45.5%; Pred. No. 5.9e-34;  
Matches 178; Conservative 61; Mismatches 125; Indels 27; Gaps 7;

QY 20 IKORRAGLNFQNLVRYPELYNHPDVRAFLOMSPKHQSPSE-----DDED 68  
Db 62 MKTERPKPTFIIRCLQWTV-----IERTFVDVTPEREWEITAQVADRLOQBEER 116  
QY 69 SSQKLHSTQINILG-----PSGNPHAKPT--DFDLKVIKGSFGKVLAKRKLKGKFY 121  
Db 117 --MNCSPSTQIDNIGEBEMDASTTHHKRTKWNDFYLLKLGKGTGKVLVREKASGY 174  
QY 122 AVKVLQKKIVLNKKEQKHMAERNVLLKNVHPPLVGLHYSFQTEKLYFVLDVFNNGEL 181  
Db 175 AMKILKEVIIAKDEVAHTLTESRV-LKNTRHPPLTSLKYSFQTKDLRCFVMEYVNGEL 233  
QY 182 FFHLQRRSPPEHRARYFAAIAAGLGHISIKIVYRDLPENILLDSVGHVLTDFGLC 241  
Db 234 FFHLRSRVFSEDRTRFYGAIEVSALDYLHSGKIVYRDLPENILLDSVGHVLTDFGLC 293  
QY 242 KEGIAISDTTTCGTPPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFCRDVAE 301  
Db 294 KEGITDAATKTKTCGTPPEYLAPEVLENDYGRAVDMWGLGVVMYEMCGRLPFYNQDHEK 353  
QY 302 MYDNILHKPLSLRPGVSLTAWSLLELEKDRQNL--GAKEDFLEIQNHPPFESLSWADL 360  
Db 354 LFELILMEDIKFPRTLLSSDAKSLGILLKDPNKRLLGGPGDPAKEIMRHSFFSGVNWQDV 413  
QY 361 VQKIPPPNPNVAGPDDIRNFTAFTEETVPYSVCVSSYIVNASVLEADAFVGFYSY 391  
Db 414 YDKKLVPFPKPQVTSSETDTRYDFDEEFTAQTITTPPEKYDEGDMCDMERNRPHFPQFSY 444

RESULT 6  
A55888  
protein kinase (EC 2.7.1.37) akt [similarity] - fruit fly (Drosophila melanogaster)  
N;Alternate names: protein kinase B; RAC-PK; serine/threonine-specific protein kinase  
C;Species: Drosophila melanogaster  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Aug-2004  
C;Accession: A55888  
R;Andjelkovic, M.; Jones, P.F.; Grosniklaus, U.; Cron, P.; Schier, A.F.; Dick, M.; Bil  
J. Biol. Chem. 270, 4066-4075, 1995  
A;Title: Developmental regulation of expression and activity of multiple forms of the D  
A;Reference number: A55888; MUID:95181376; PMID:7876156  
A;Accession: A55888  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-611 <AND>  
A;Cross-references: UNIPROT:Q24469; UNIPARC:UPI00000866BE; GB:X83510  
C;Genetics:  
A;Gene: FlyBase:RacPK  
A;Cross-references: FlyBase:FBgn0013324  
A;Start codon: ACG  
A;Introns: 261/3; 327/3; 457/3; 535/3; 584/3  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating various processes  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threon  
F;105-209/Domain: pleckstrin repeat homology <PLK>  
F;264-523/Domain: protein kinase homology <KIN>  
F;272-280/Region: protein kinase ATP-binding motif  
F;295/Active site: Lys #status predicted  
F;423/Binding site: phosphate (Thr) (covalent) #status predicted

F;596/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted									
Query Match 37.5%; Score 850.5; DB 1; Length 611;									
Best Local Similarity 49.9%; Pred. No. 2.3e-33;									
Matches 172; Conservative 47; Mismatches 115; Indels 11; Gaps 4;									
QY	54	SPKHQDPSE-----DEDESSQKLHSTSONINLPGSGNPHAKPTDFDLKVIKGSFG	107						
DB	222	TPSEQDMDTDVDMATIAEDLSQ---FSVOGTTCSNNGVKKVLTENFEFLKVLGKGTG	278						
QY	108	KVLLAKRKLDGKFYAVKVLQKTIVLNRKEQKHMAERNVLLKNVKGPFVLGLHYSFQTTE	167						
DB	279	KVILCREKATAKYAIKILKEVLIQDEVAHVLTSRV-LKSTNHPFLISLKYSFQTN	337						
QY	168	KLVFVLDFVNGBELFPHLQERSFPFHRARFYAAEIASALGYLHSIKIVYRDLKPNILL	227						
DB	338	RLCFVMQYVNGGELFWHLSHERIFTEDRTRYGAEIISALGYLHSOGIIVYRDLKLENLL	397						
QY	228	DSVGHVVLDFGLCKEGIAISDITTTTCGTPPEYLAPEVIRKQPYDNTDWMCLGAVLYEM	287						
DB	398	KDGHKIKVADFGLCKEDITVYGRITKTFCGTPPEYLAPEVLDDNDYGOAVDMWGTGVMYEM	457						
QY	288	LYGLPFYPCRDVAEMVDNIIHLKPLSRPGVSLTAWGILBELLEKDRQNR-L-GAKEDFLEI	346						
DB	458	ICGRLEFYNRDHVDVLTLLVEEVKFPNITDEAKNLLAGLLAKDPKRLGGGKDDVKEI	517						
QY	347	QNHPPFESWADLVQKKIPPPNPNVAGPDDIRNFDTAFTETV	391						
DB	518	QAHPPFASINWTDLVLKIPPPKPVQTSDDTRYFDKFTGTSV	562						
RESULT 7									
A46288									
N;protein kinase (EC 2.7.1.37) akt2 - human									
C;Species: Homo sapiens (man)									
C;Date: 22-Sep-1993 #sequence_revision 12-May-1994 #text_change 16-Aug-2004									
C;Accession: A46288									
R;Cheng, J.Q.; Godwin, A.K.; Bellacosa, A.; Taguchi, T.; Franke, T.F.; Hamilton, T.C.; T									
Proc. Natl. Acad. Sci. U.S.A. 89, 9267-9271, 1992									
A;Title: AKT2, a putative oncogene encoding a member of a subfamily of protein-serine/th									
A;Reference number: A46288; MUID:93028445; PMID:1409633									
A;Accession: A46288									
A;Molecule type: mRNA									
A;Residues: 1-481 <CHE>									
A;Cross-references: UNIPROT:P31751; UNIPARC:UPI0000049EDB; GB:M95936; NID:gl78325; PIDN:									
A;Note: sequence extracted from NCBI backbone (NCBIP:115859)									
C;Comment: This protein is amplified in some pancreatic, ovarian, and other carcinomas.									
C;Genetics:									
A;Gene: GDB:AKT2									
A;Cross-references: GDB:l35660; OMIM:164731									
A;Map position: 19q13.2-19q13.2									
C;Function:									
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin									
A;Pathway: signal transduction pathways regulating various processes									
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein									
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k									
F;4-106/Domain: pleckstrin repeat homology <PLK>									
F;150-409/Domain: protein kinase homology <KIN>									
F;158-166/Region: protein kinase ATP-binding motif									
F;181/Active site: Lys #status predicted									
Query Match 37.2%; Score 844.5; DB 1; Length 481;									
Best Local Similarity 42.3%; Pred. No. 3.5e-33;									
Matches 181; Conservative 76; Mismatches 148; Indels 23; Gaps 9;									
QY	13	DNF---DPDPIKORRAGLEFIQNLVRYPEL-----YNHPD-----VRAFLQWDSFKQ	58						
DB	53	NNFSVAECQLMKTERPRNPNTFVIRCLQWTVIERTFHVDSPREBWMRAIQWVNSLKQ	112						
QY	59	SDPSED--EDERSQKLHSTSONINLPGSGNPHAKPT--DFDFLKVIKGSFGKVLAKR	114						
DB	113	RAGEDPMDYKCGSPSDSSSTTEMEVAVS-KARAKVTMDFYLLKLGKGTGFKVLVRE	171						

QY	115	KLDGKFYAVKVLQKKIIVLNKREKQKHMAERNVLLKNVKGPFVLGLHYSFQTTEKLYFVLD	174						
DB	172	KATGRYYAMKILRKEVIIIAKDEVAHTVTESRV-LQNRHPEFLTALYAFQTHDRLCFVME	230						
QY	175	FVNGGELFPHLQERSFPFHRARFYAAEIASALGYLHSIKIVYRDLKPNILLDSVGHVV	234						
DB	231	YANGGELFPHLSRERVFTTEARFYGAELVSALEYLHSDVDVYRDIKLENMLDKDGHK	290						
QY	235	LTDFGLCKEGIAISDITTTTCGTPPEYLAPEVIRKQPYDNTDWMCLGAVLYEMLYGLPPF	294						
DB	291	ITDFGLCKEGISDGAETMTKTCGTPPEYLAPEVLDDNDYGRAVDWGLGVVYEMMCGRLPF	350						
QY	295	YCRDVAEMVDNIIHLKPLSRPGVSLTAWGILBELLEKDRQNR-L-GAKEDFLEIQNHPPFE	353						
DB	351	YNQDHERLPELIMEEIRFPRTLSPKASLLAGLLKPKQRLGGGSPDAKMEYHRRFEL	410						
QY	354	SLSWADLVQKKIPPPNPNVAGPDDIRNFDTAFTETVPYSCVSSDYSIVNASVLEADD	413						
DB	411	SINQDVVQKULPPFPKQVTSVDTRYDDEFTAQSI--TITPPRYDSLGLLELDQRT	468						
QY	414	AFVGFSYA	421						
DB	469	HFPOFSYS	476						
RESULT 8									
A38578									
C;Species: Dictyostelium discoideum									
C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 31-Dec-2004									
C;Accession: A38578									
R;Haribabu, B.; Dottin, R.P.									
Proc. Natl. Acad. Sci. U.S.A. 88, 1115-1119, 1991									
A;Title: Identification of a protein kinase multigene family of Dictyostelium discoideu									
A;Reference number: A38578; MUID:91142122; PMID:1996312									
A;Accession: A38578									
A;Status: preliminary									
A;Molecule type: DNA									
A;Residues: 1-479 <HAR>									
A;Cross-references: UNIPROT:P28178; UNIPARC:UPI0000131B58; GB:M59744; NID:gl67717; PIDN:									
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threon.									
F;151-407/Domain: protein kinase homology <KIN>									
F;159-167/Region: protein kinase ATP-binding motif									
Query Match 37.0%; Score 839; DB 2; Length 479;									
Best Local Similarity 47.1%; Pred. No. 6.4e-33;									
Matches 177; Conservative 57; Mismatches 118; Indels 24; Gaps 7;									
QY	53	DSPKQSDPSEDEDESSQKLHSTSONINLPGSGNPHAKPTDFDFLKVIKGSFGKVLVA	112						
DB	120	DSPNGSGNGNDDDEGPEEVIFSKNQ-----SATKDDFELLNVITKGSFGKVMQV	170						
QY	113	KEKLDGKFYAVKVLQKKIIVLNKREKQKHMAERNVLLKNVKGPFVLGLHYSFQTTEKLYFV	172						
DB	171	KKGEDKIPAMVKLRDAIARQVNHKSEKII-LQCISHFPIVNLHAFQTKDKLYMV	229						
QY	173	LDFVNGGELFPHLQERSFPFHRARFYAAEIASALGYLHSIKIVYRDLKPNILLDSVGH	232						
DB	230	LDFVNGGELFPHLKGREGSEPRVKIYAAEIVSALDHLHKQDIVYRDLKPNILLDSEGH	289						
QY	233	VVLTFGLCKEGIAISDITTTTCGTPPEYLAPEVIRKQPYDNTDWMCLGAVLYEMLYGLP	292						
DB	290	ICITDFGLSKK-IETTDGTFTCGTPPEYLAPEVLNGHGHGCAVDMWSLGTLLYEMLTGUP	348						
QY	293	PYCRDVAEMVDNIIHLKPLSRPGVSLTAWGILBELLEKDRQNR-L-GAKEDFLEIQNHPPF	352						
DB	349	PYISQVSTWYQKILNGELKIPITYISPEAKSLLEGLLTREVDRKLTGKGG-EVKQHPWF	407						
QY	353	ESLSWADLVQKKIPPPNPNVAGPDDIRNFDTAFTETVPYSCVSSDYSIVNASVLE---	409						
DB	408	KNIDWEKLDKREVEVHFVKPKVSGTDSIQIDPVFTQER-PMD-----SLVETSALGDA	459						



A;Molecule type: mRNA  
A;Residues: 1-480 <BEL>  
A;Cross-references: UNIPROT:P31750; UNIPARC:UPI0000001726; EMBL:X65687; NID:g287806; PID  
C;Genetics:  
A;Gene: MGI:Akt  
A;Cross-references: MGI:87986  
A;Map position: 12  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating various processes  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene  
F;4-106/Domain: pleckstrin repeat homology <PLK>  
F;148-408/Domain: protein kinase homology <KIN>  
F;156-164/Region: protein kinase ATP-binding motif  
F;179/Active site: Lys #status predicted  
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki  
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 36.1%; Score 818.5; DB 1; Length 480;  
Best Local Similarity 40.8%; Pred. No. 5.9e-32;  
Matches 183; Conservative 63; Mismatches 145; Indels 57; Gaps 11;

QY 17 PDFIKORRAGLNEFIQNLVRYPELY--NHPDVRAFL-----QMDSPKHQSDPSEDED 66  
DB 42 PQDVQDRESPLNNF---SVAQCQLMKTERPRNTFIIRCLQWTTVTIERTFHVETPEEREE 98

QY 67 -----ERSSQKLHSTSQNLNLGPS-----GNPHAKPT--DFDFLKVIQK 103  
DB 99 WATAIQTVADGLKROEETMDFRSGSPSDNSGAEMEVSIAKPKHRVTWNEFEYLLKLGK 158

QY 104 GSFGKVLAKRKLDGKFYAVKVLQKKIVLNLRKEQKHMAERNVLLKNVXHPFLVGLHYSF 163  
DB 159 GTFGKVLVKEKATGRYYAMKILKEVIVAKDEVAHTLTE--NRVLQNSRHPFLTALKYSF 217

QY 164 QTTEKLYFVLDPVNGGELFFHLQRRSPPEHRRARYAABTASALGYLHSLIK-IVYRDLKP 222  
DB 218 QTHDRLCFVMEYANGGELFFHLRSRVSFSDRARFYGAIEVSALDYLSHSEKNVYVRDLKL 277

QY 223 ENILDSVGHVLTDFGLCKEGIAISDTTTFCTGTPYLAPEVIRKQPDNTVDMWCLGA 282  
DB 278 ENLMLDKOGHIKITDFGLCKEGIKDGNATMKTFCGTPYLAPEVLENDYGRAVDWMLGLV 337

QY 283 VLYEMLYGLPPFYCRDVAEMYDNILHKPLSLRPGVSLTAWSIIEELLEKDRQNL--GAKE 341  
DB 338 VMYEMMCGRLPFYFNQDHEKLFELILMEIRFPRTLGPPEAKSLSLGLLKKDPTQRLGGSGE 397

QY 342 DFLEIQNHPPFESLSWADLVQKKIPPPENPNVAGPDDIRNFDTAFTTEETVPYS----- 394  
DB 398 DAKIEWQHRFFANIVMQDVYEEKLSPPFPQVTSFDTTRYFDEEFTAQMITITPPDQDSDS 457

QY 395 -VCVSSDYSIVNASVLEADDAFVGFSYA 421  
DB 458 MECVDS-----ERRPHFPQFSYS 475

RESULT 12  
A40831  
gag-akt polyprotein - AKT8 murine leukemia virus  
N;Contains: amino end of core protein p30; core protein p15; inner coat protein p12; kin  
C;Species: AKT8 murine leukemia virus  
C;Date: 12-Feb-1993 #sequence\_revision 12-May-1994 #text\_change 31-Dec-2004  
C;Accession: A40831; B40831  
R;Bellacosa, A.; Testa, J.R.; Staal, S.P.; Tsichlis, P.N.  
Science 254, 274-277, 1991  
A;Title: A retroviral oncogene, akt, encoding a serine-threonine kinase containing an SH  
A;Reference number: A40831; MUID:92022574; PMID:1833819  
A;Accession: A40831  
A;Molecule type: DNA  
A;Residues: 1-262 <BEL>  
A;Cross-references: UNIPARC:UPI00001725AF; GB:M80675  
A;Accession: B40831  
A;Molecule type: DNA

A;Residues: 262-763 <BE2>  
A;Cross-references: UNIPARC:UPI00001725B0; GB:M80675  
C;Genetics:  
A;Gene: gag-akt  
C;Keywords: ATP; core protein; glycoprotein; oncogene; phosphoprotein; phosphotransfera  
F;1-129/Product: core protein p15 #status predicted <CPI>  
F;130-214/Product: inner coat protein p12 #status predicted <CP2>  
F;284-763/Domain: kinase-related transforming protein akt #status predicted <AKT>  
F;287-389/Domain: pleckstrin repeat homology <PLK>  
F;431-691/Domain: protein kinase homology <KIN>  
F;439-447/Region: protein kinase ATP-binding motif  
F;25,337/Binding site: carboxylate (Asn) (covalent) #status predicted  
F;462/Active site: Lys #status predicted  
F;609/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 36.1%; Score 818.5; DB 1; Length 763;  
Best Local Similarity 40.8%; Pred. No. 9.1e-32;  
Matches 183; Conservative 63; Mismatches 145; Indels 57; Gaps 11;

QY 17 PDFIKORRAGLNEFIQNLVRYPELY--NHPDVRAFL-----QMDSPKHQSDPSEDED 66  
DB 325 PQDVQDRESPLNNF---SVAQCQLMKTERPRNTFIIRCLQWTTVTIERTFHVETPEEREE 381

QY 67 -----ERSSQKLHSTSQNLNLGPS-----GNPHAKPT--DFDFLKVIQK 103  
DB 382 WATAIQTVADGLKROEETMDFRSGSPSDNSGAEMEVSIAKPKHRVTWNEFEYLLKLGK 441

QY 104 GSFGKVLAKRKLDGKFYAVKVLQKKIVLNLRKEQKHMAERNVLLKNVXHPFLVGLHYSF 163  
DB 442 GTFGKVLVKEKATGRYYAMKILKEVIVAKDEVAHTLTE--NRVLQNSRHPFLTALKYSF 500

QY 164 QTTEKLYFVLDPVNGGELFFHLQRRSPPEHRRARYAABTASALGYLHSLIK-IVYRDLKP 222  
DB 501 QTHDRLCFVMEYANGGELFFHLRSRVSFSDRARFYGAIEVSALDYLSHSEKNVYVRDLKL 560

QY 223 ENILDSVGHVLTDFGLCKEGIAISDTTTFCTGTPYLAPEVIRKQPDNTVDMWCLGA 282  
DB 561 ENLMLDKOGHIKITDFGLCKEGIKDGNATMKTFCGTPYLAPEVLENDYGRAVDWMLGLV 620

QY 283 VLYEMLYGLPPFYCRDVAEMYDNILHKPLSLRPGVSLTAWSIIEELLEKDRQNL--GAKE 341  
DB 621 VMYEMMCGRLPFYFNQDHEKLFELILMEIRFPRTLGPPEAKSLSLGLLKKDPTQRLGGSGE 680

QY 342 DFLEIQNHPPFESLSWADLVQKKIPPPENPNVAGPDDIRNFDTAFTTEETVPYS----- 394  
DB 681 DAKIEWQHRFFANIVMQDVYEEKLSPPFPQVTSFDTTRYFDEEFTAQMITITPPDQDSDS 740

QY 395 -VCVSSDYSIVNASVLEADDAFVGFSYA 421  
DB 741 MECVDS-----ERRPHFPQFSYS 758

RESULT 13  
A93360  
protein kinase (EC 2.7.1.37) akt1 [validated] - human  
N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prot  
C;Species: Homo sapiens (man)  
C;Date: 20-Mar-1992 #sequence\_revision 12-May-1994 #text\_change 16-Aug-2004  
C;Accession: A93360; S36389; S18000; S20836  
R;Jones, P.F.; Jakubowicz, T.; Pitosi, F.J.; Maurer, F.; Hemmings, B.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 4171-4175, 1991  
A;Title: Molecular cloning and identification of a serine/threonine protein kinase of t  
A;Reference number: A93360; MUID:91239529; PMID:1851997  
A;Accession: A93360  
A;Molecule type: mRNA  
A;Residues: 1-480 <JON>  
A;Cross-references: UNIPROT:P31749; UNIPARC:UPI000002E75B; GB:M63167; NID:g190827; PID  
R;Coffer, P.J.; Woodgett, J.R.  
Eur. J. Biochem. 205, 1217, 1992  
A;Reference number: S24423; MUID:92249329; PMID:1533586  
A;Accession: S36389  
A;Status: nucleic acid sequence not shown; translation not shown



A;Molecule type: mRNA  
A;Residues: 63-172, 'A', 175-201, 'Q', 203-211, 'R', 213-245, 'A', 247-408, 'T', 410-475, 'P', 477, 'A';  
A;Cross-references: UNIPARC:UPI000016AEB1; EMBL:X61037; NID:G35480; PIDN:CAA43372.1; PID  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1991  
R;Coffer, P.J.; Woodgett, J.R.  
Eur. J. Biochem. 201, 475-481, 1991  
A;Title: Molecular cloning and characterisation of a novel putative protein-serine kinase  
A;Reference number: S17999; MUID:92037600; PMID:1718748  
A;Accession: S18000  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 63-70, 'TPSSAACGSLSSNAPSMMRLRLSGGVNRRHPDCGRRPQ', 'EAGGGGDLGVGLTORQLRGRDRGGV  
A;Cross-references: UNIPARC:UPI00001725AB; EMBL:X61037  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1991  
R;Coffer, P.  
submitted to the EMBL Data Library, July 1991  
A;Reference number: S20836  
A;Accession: S20836  
A;Molecule type: mRNA  
A;Residues: 63-70, 'TPSSAACGSLSSNAPSMMRLRLSGGVNRRHPDCGRRPQ', 'EAGGGGDLGVGLTORQLRGRDRGGV  
A;Cross-references: UNIPARC:UPI00001725AC; EMBL:X61037  
A;Note: this sequence has been revised in reference S24423  
R;Alessi, D.R.; Andjelkovic, M.; Caudwell, B.; Cron, P.; Morrice, N.; Cohen, P.; Hemming  
EMBO J. 15, 6541-6551, 1996  
A;Title: Mechanism of activation of protein kinase B by insulin and IGF-1.  
A;Reference number: A64192; MUID:97133284; PMID:8978681  
A;Contents: annotation; phosphorylation sites  
R;Roker, A.; Newton, A.C.  
J. Biol. Chem. 275, 8271-8274, 2000  
A;Title: Akt/protein kinase B is regulated by autophosphorylation at the hypothetical PD  
A;Reference number: A64193; MUID:20187529; PMID:10722653  
A;Contents: annotation; autophosphorylation site  
C;Comment: Akt1 is ubiquitous as an inactive multimeric complex. It binds phosphatidy-3-  
nt protein kinase 1 complex. Akt1 can then autophosphorylate and become fully active.  
C;Genetics:  
A;Gene: GDB:AKT1; RAC; PKB  
A;Cross-references: GDB:118989; OMIM:164730  
A;Map position: 14q32.32-14q32.32  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating various processes including insulin a  
e production  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; autophosphorylation; phosphoprotein; pleckstrin repeat homology; protein  
F;4-106/Domain: pleckstrin repeat homology <PLK>  
F;148-408/Domain: protein kinase homology <KIN>  
F;156-164/Region: protein kinase ATP-binding motif  
F;179/Active site: Lys #status Predicted  
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki  
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status experime  
Query Match 36.0%; Score 816.5; DB 1; Length 480;  
Best Local Similarity 41.0%; Pred. No. 7.3e-32;  
Matches 185; Conservative 63; Mismatches 146; Indels 57; Gaps 12;  
QY 17 PDFIKORRAGLNFQIQLVRYPELY--NHDPVRAFL-----QMDSPKHQSDPSEDED 66  
Db 42 PQDVQREAPLNNF---SVAQCQLMKTERPRNTFIICRLQVTIERTFHVTPERE 98  
QY 67 ERS-----OKLHSTSONILG-PSGNPH-----AKP-----TDFDLKVGK 103  
Db 99 WTTAIQTVAOGLKKQEEEMDFSGSPSDNSGAEVSLAKPHRVMTNEFFYLKLGK 158  
QY 104 GSGFKVLLAKRLDKGFYAVKVLQKKIVLNKRBQKHMAERNVLLKNVHPFLVGLHSYF 163  
Db 159 GTFGKVLVKEKATGRYYAMKILKEVIVAKDEVAHTLTE-NRVLQNSRHPFLTALKYSF 217  
QY 164 QTTEKLYFVLDFVNGGELFPHLORERSFPHEARFYAAETASALGYLHSK-IVYRDLKP 222  
Db 218 QTHRLCLFVMEYANGGELFPHLGRVFSRERFYCAETIVSALDYVHSEKNVYRDLK 277

QY 223 ENILLDSVGHVLTDFGLCKEGIAISDTTTCGTPEYLAPVIRKQPYDNTVDWMCIGA 282  
Db 278 ENLMKDKGHIKITDFGLCKEGIKDGMKTTCGTPEYLAPVLENDYDGRAVDWGLGV 337  
QY 283 VLYEMLYGLPPFYCRDVAEMYNILHKLPSLRPGVSLTAWMSILEELLEKDRQNL-CAKE 341  
Db 338 VYTEMCGRLFPFYNQDHEKLFELILMBEIRFPRTLGPESAKSLSLGLLKKDPKORLGGSE 397  
QY 342 DFLEIQNHPPFESLSWADLVQKKIPPPFNPNVAGPDDIRNFDTAFTTEVPYS----- 394  
Db 398 DAKEMQHRFFAGIVQHVYKELSPFPKQVTSQVTSQVTSQVTSQVTSQVTSQVTSQVTS 457  
QY 395 -VCVSSDYISVNASVLEADDAFVGFYSAPPS 424  
Db 458 MECVDS-----ERRPHFPQFSYASASS 478  
RESULT 14  
A53758  
protein kinase C (EC 2.7.1.1-) lambda - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Oct-2004  
C;Accession: A53758  
R;Akimoto, K.; Mizuno, K.; Osada, S.; Hirai, S.; Tanuma, S.; Suzuki, K.; Ohno, S.  
J. Biol. Chem. 269, 12677-12683, 1994  
A;Title: A new member of the third class in the protein kinase C family, PKClambda, exp  
A;Reference number: A53758; MUID:94230340; PMID:7513693  
A;Accession: A53758  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-586 <AKI>  
A;Cross-references: UNIPARC:UPI0000175566; GB:D28577; NID:G465397; PID:G465398  
C;Superfamily: protein kinase C, zeta/iota types; protein kinase C zinc-binding repeat  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase  
F;132-181/Domain: protein kinase C zinc-binding repeat homology <K21>  
F;242-512/Domain: protein kinase homology <KIN>  
F;250-258/Region: protein kinase ATP-binding motif  
Query Match 35.7%; Score 810; DB 2; Length 586;  
Best Local Similarity 41.3%; Pred. No. 1.8e-31;  
Matches 164; Conservative 75; Mismatches 124; Indels 34; Gaps 8;  
QY 43 HPD-VRAFLQMDSPKHQSDPSEDEDERSQKLHSTSONILGPSNPHAKPTDFDLKVI 101  
Db 199 HPDHTQTVIPYPPSSHESLDQVGEKEAMNTRSGKASSSLGQ-----DFDLURVI 250  
QY 102 KGSGFKVLLAKRLDKGFYAVKVLQKKIVLNKRBQKHMAERNVLLKNVHPFLVGLHY 161  
Db 251 GRGSYAKVLLVRLKKTDRIVAMKVVKKELVNDDDEDIDWQTEKHVFEQASNHFFVLGHS 310  
QY 162 SPOTTEKLYFVLDFVNGGELFPHLORERSFPHEARFYAAETASALGYLHSIKIVRDLK 221  
Db 311 CFQTESRFLFVIEYVNGGDLFMHMQRKLPEEHARFYSAETSLALNLYLHERGIYRDLK 370  
QY 222 PENILLDSVGHVLTDFGLCKEGIAISDTTTCGTPEYLAPVIRKQPYDNTVDWMCIG 281  
Db 371 LONVLDSGHIKLDYGMCKEGLRPGDITSTFCGPNYIAPILKEDYGFSDVMWALG 430  
QY 282 AVLLEYMLYGLPPFYCRDVAEMTDN-----ILHKPLSLRPGVSLTAWMSILEELL 329  
Db 431 VLMFEMWAGRSPP---DIVGSDNDPQNTEDYLFQVILEKQIRIPRSLSVKAASVLKSLF 487  
QY 330 EKDRQNLGA--KEDPLEIQNHPPFESLSWADLVQKKIPPPFNPNVAGPDDIRNFDTAFT 387  
Db 488 NKDPKERLGHCHPQTGTFADIQGHPPFFRNVDWDMEQKQVVPVPPFPKPNISGEGFLNFDQSFT 547  
QY 388 ESTVPYSVCVSSDYISVNASVLEADDA-FVGFYSAPP 423  
Db 548 NEPVQUT---PDDDDIVR-----KIDOSEPEGEYINP 577

RESULT 15

S62117  
protein kinase (EC 2.7.1.37) akt1 [similarity] - bovine  
N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prote  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 16-Aug-2004  
C;Accession: S62117; S24423; S17999; S15714; S36388  
R;Coffer, P.J.; Woodgett, J.R.  
submitted to the EMBL Data Library, December 1991  
A;Reference number: S62117  
A;Accession: S62117  
A;Molecule type: mRNA  
A;Residues: 1-480 <COW>  
A;Cross-references: UNIPROT:Q01314; UNIPARC:UPI000012E042; EMBL:X61036; NID:g630; PIDN:C  
A;Note: this is a revision to the sequence from reference S17999  
R;Coffer, P.J.; Woodgett, J.R.  
Eur. J. Biochem. 205, 1217, 1992  
A;Reference number: S24423; MUID:92249329; PMID:15333586  
A;Contents: erratum  
A;Accession: S24423  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 70-78,'N',80-145 <COW>  
A;Cross-references: UNIPARC:UPI0001725AD; EMBL:X61036  
A;Note: this is a revision to the sequence from reference S17999  
R;Coffer, P.J.; Woodgett, J.R.  
Eur. J. Biochem. 201, 475-481, 1991  
A;Title: Molecular cloning and characterisation of a novel putative protein-serine kinase  
A;Reference number: S17999; MUID:92037600; PMID:1718748  
A;Accession: S17999  
A;Molecule type: mRNA  
A;Residues: 1-70,'TPSSAACSGPRSSARSTWRPRSGVDHRHDPDGGRRAGCGDGLPVGLTRRELGGGAGVAGQ  
A;Cross-references: UNIPARC:UPI00001725AE; EMBL:X61036  
A;Note: this sequence has been revised in references S62117 and S24423  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating various processes  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene  
F;4-106/Domain: pleckstrin repeat homology <PLK>  
F;148-408/Domain: protein kinase homology <KIN>  
F;156-164/Region: protein kinase ATP-binding motif  
F;179/Active site: Lys #status predicted  
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki  
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 35.5%; Score 804.5; DB 1; Length 480;  
Best Local Similarity 39.9%; Pred. No. 2.7e-31;  
Matches 180; Conservative 66; Mismatches 142; Indels 63; Gaps 11;  
QY 17 PDFIKORRACLNIEFIQNLVRYPELY--NHPDVRAFL-----QMDSPKHQSDPSEDED 66  
DB 42 PQDLEQRESPLNPF---SVAQCQLMKTERPRNPNTFIIRCLQWTTVIERTFHVETPEERE 98  
QY 67 -----ERSSQKLHSTSQNINLGPS-----GNPHAKPT--DFDFLKVIGK 103  
DB 99 WTTAIQTVDGLKXQREETWDFRSGSPGSGAEEVSLAKPKHRTWNEFEYVKDLGK 158  
QY 104 GSFQKVLAKRKLDGKFYAVKVLQKKIVLNKKEQKIHMAERNVLLKNVHPFLVGLHYSF 163  
DB 159 GTFGKVLVKEKATAAYAMKILKEVIKVAKEVAHTLT-E-NRVLQNSRHPSLTALKYSF 217  
QY 164 QTTEKLYFVLDFVNGGELPFHLQORERSFPEHRARFYAAETASALGYLHSIK-IYVRDLKP 222  
DB 218 QTHRLCFVMEYANGGELPFHLRSERVFSDRARFYGAETVSALDYLHSEKEYVYRDLKL 277  
QY 223 ENILLDSVGHVLTDFGLCKEGIAISDTTTTCGTPEYLAPEVIRKOPYDNTVDWMLCGA 282  
DB 278 ENMLDKDGHKIKTDFGLCKEGIKDGNATMTKTCGTPEYLAPEVLENDYGRAVDWMLGV 337  
QY 283 VLYEMLYGLPPFYCRDVAEMYDNLHKPLSLRFGVSLTAWSLILEELLEKDRQNRL-CAKE 341  
DB 338 VYEMWCGRLFFYNQDHEKLFELLMBEIRFPRTLSPEAKSLLSGLLKKDKPKQRLGGGSE 397

QY 342 DFLEIQNHPPFESLSWADLVOKKIIPPFPNPVAGDDIIRNFDTAFTEETVPYSVCVSSDY 401  
DB 398 DAKIEMQHRFFASIVQDVYKSLGPPFKPQVTSETDTRFYDEEFTAQ----- 445  
QY 402 SIYNASVLEADDAFVG-----FSYA 421  
DB 446 -MITITPPDQDDSMEGVDSERRPFRPQFSYS 475

Search completed: January 27, 2006, 23:32:05  
Job time : 13.6811 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:08:15 ; Search time 69.8811 Seconds  
(without alignments)  
4331.236 Million cell updates/sec

Title: US-09-868-131A-4  
Perfect score: 2269  
Sequence: 1 MALKIPAKRIFGNFDPDFI.....EADDAFVGSFYAPSEDLFL 429

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2269	100.0	429	1	Q6FHV7 HUMAN
2	2269	100.0	496	1	SGK3 HUMAN
3	2269	100.0	496	2	Q5R7A7 PONPY
4	2264	99.8	496	2	Q5H905 HUMAN
5	2261	99.6	496	2	Q53EW6 HUMAN
6	2210	97.4	429	2	Q8VEK1 MOUSE
7	2210	97.4	496	1	SGK3 MOUSE
8	2140	94.3	490	2	Q5ZJQ4 CHICK
9	1783	78.6	518	2	Q4SFC2 TETNG
10	1501	66.2	526	2	Q5VY65 HUMAN
11	1482.5	65.3	421	2	Q5TCN4 HUMAN
12	1480	65.2	519	2	Q6NS95 MOUSE
13	1476	65.1	431	2	Q5TCN3 HUMAN
14	1476	65.1	431	2	Q68G05 RAT
15	1476	65.1	445	2	Q5TCN2 HUMAN
16	1474	65.0	432	2	Q6ULI9 CHICK
17	1473	64.9	431	2	Q4R633 MACFA
18	1472	64.9	431	1	SGK1 HUMAN
19	1468	64.7	431	1	SGK1 RABIT
20	1463	64.5	431	1	SGK1 MOUSE
21	1460	64.3	418	2	Q5BKX4 XENTR
22	1458.5	64.3	430	1	SGK1 RAT
23	1457	64.2	434	2	Q6GPN6 XENLA
24	1456	64.2	434	2	Q93524 XENLA
25	1453.5	64.1	433	2	Q7ZTW4 BRARE
26	1452	64.0	431	2	Q5Q0U5 FUNHE
27	1447	63.8	594	2	Q73927 SQUAC
28	1442	63.6	434	2	Q6GLY8 XENLA
29	1420.5	62.6	490	2	Q4RR91 TETNG
30	1414	62.3	433	2	Q73926 SQUAC
31	1328.5	58.6	427	1	SGK2_HUMAN

32	1328.5	58.6	427	2	Q5H8Y6 HUMAN	Q5H8Y6 homo sapien
33	1319.5	58.2	367	2	Q5RDZ9 PONPY	Q5rdz9 pongo pygma
34	1316.5	58.0	367	2	Q5TZR3 HUMAN	Q5tzr3 homo sapien
35	1313.5	57.9	393	2	Q52PK5 HUMAN	Q52pk5 homo sapien
36	1308	57.6	366	2	Q5H8Z1 HUMAN	Q5h8z1 homo sapien
37	1297.5	57.2	367	1	SGK2 MOUSE	Q9qzbs mus musculus
38	1292.5	57.0	350	2	Q4S7Y9 TETNG	Q4s7y9 tetraodon n
39	1241.5	54.7	1114	2	Q4SVX7 TETNG	Q4svx7 tetraodon n
40	1214	53.5	302	1	SGK2 RAT	Q8r4u9 rattus norv
41	1186.5	52.3	1550	2	Q4SY70 TETNG	Q4sy70 tetraodon n
42	1159	51.1	279	2	Q8R4V0 RAT	Q8r4v0 rattus norv
43	1110	48.9	285	2	Q5H8Y4 HUMAN	Q5h8y4 homo sapien
44	1039	45.8	316	2	Q4RI65 TETNG	Q4ri65 tetraodon n
45	1019.5	44.9	422	2	Q94365_CAEEL	Q94365 caenorhabdi

ALIGNMENTS

RESULT 1

Q6FHV7\_HUMAN

ID Q6FHV7\_HUMAN PRELIMINARY; PRT; 429 AA.

AC Q6FHV7;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE SGK1 protein.

GN Name=SGK1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,

RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,

RA Korn B., Zuo D., Hu Y., LaBaer J.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; CR536581; CAG38818.1; -; mRNA.

DR SMR; Q6FHV7; 1-58.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004574; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

DR GO; GO:0007242; P:intracellular signaling cascade; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR000961; Pkinase C.

DR InterPro; IPR000719; Prot\_kinase.

DR InterPro; IPR001683; PX.

DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.

DR InterPro; IPR002290; Ser\_thr\_pkinase.

DR InterPro; IPR001245; Tyr\_pkinase.

DR Pfam; PF00069; Pkinase; 1.

DR ProDom; PD000001; Prot\_kinase; 1.

DR SMART; SM00133; S\_TK\_X; 1.

DR SMART; SM00220; S\_TKC; 1.

DR SMART; SM00219; TyrKC; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.

DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.

DR PROSITE; PS0195; PX; 1.

SQ SEQUENCE 429 AA; 49004 MW; 2DDIF5ADD6C4234C CRC64;

Query Match 100.0%; Score 2269; DB 2; Length 429;

Best Local Similarity 100.0%; Pred. No. 9.9e-140;

Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALKIPAKRIFGNFDPDFIKQRRAGINEFIQNLVRYPELYNHPDVRAFLQMDSPKQSD 60

Db 1 MALKIPAKRIFGNFDPDFIKQRRAGINEFIQNLVRYPELYNHPDVRAFLQMDSPKQSD 60

Qy 61 PSEDEDSQKLHSTSQINILGPSGNPHAKPTDFDLKVIKGSFGKVLAKRKLQDKF 120

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Db 61 PSEDEDESSQKLHSTSNINLPGSGNPHAKPTDFDFLKVIGKSGFKVLLAKRKLGDGF 120
Qy 121 YAVKVLQKIVLNKKEQKHMAERNVLLKNVHPFLVGLHYSQTTEKLYFVLDFVNGGE 180
Db 121 YAVKVLQKIVLNKKEQKHMAERNVLLKNVHPFLVGLHYSQTTEKLYFVLDFVNGGE 180
Qy 181 LFFHLQERSFPPEHRAFYAAETASALGYLHSTIKIVYRDCLKPENILLDSVGHVVLTDGFL 240
Db 181 LFFHLQERSFPPEHRAFYAAETASALGYLHSTIKIVYRDCLKPENILLDSVGHVVLTDGFL 240
Qy 241 CKEGIAISDTTTFTCGTPPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVA 300
Db 241 CKEGIAISDTTTFTCGTPPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVA 300
Qy 301 EMDYDNLHKPLSLRPGVSLTAWSLBELLEKQNRILGAKEDFLEIQNHFFPESLSWADL 360
Db 301 EMDYDNLHKPLSLRPGVSLTAWSLBELLEKQNRILGAKEDFLEIQNHFFPESLSWADL 360
Qy 361 VQKKIPPPPNVAGPDDIRNFDTAFTTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 420
Db 361 VQKKIPPPPNVAGPDDIRNFDTAFTTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 420
Qy 421 APPSEDLFL 429
Db 421 APPSEDLFL 429

RESULT 2
SGK3 HUMAN
ID _SGK3 HUMAN STANDARD; PRT; 496 AA.
AC Q96BE1; Q9P1Q7; Q9UKG5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine-protein kinase Sgk3 (EC 2.7.1.37)
DE (Serum/glucocorticoid regulated kinase 3) (Serum/glucocorticoid
DE regulated kinase-like).
DE Names=SGK3; Synonyms=SGK3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE, PHOSPHORYLATION SITE THR-320, AND MUTAGENESIS OF
RP SER-486.
RX MEDLINE=20018032; PubMed=10548550; DOI=10.1042/0264-6021.3440189;
RX Kobayashi T., Deak M., Morrice N., Cohen P.;
RT "Characterization of the structure and regulation of two novel,
RT isoforms of serum- and glucocorticoid-induced protein kinase.";
RL Biochem. J. 344:189-197(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20054360; PubMed=10595774; DOI=10.1006/geno.1999.5969;
RX Dai F., Yu L., He H., Zhao Y., Yang J., Zhang X., Zhao S.;
RT "Cloning and mapping of a novel human Serum/Glucocorticoid regulated
RT kinase-like gene, SGK3, to chromosome 8q12.3-q13.1.";
RL Genomics 62:95-97(1999).
RN [3]
RP SEQUENCE REVISION.
RX Zhao Y.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Mammary gland;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
```

```
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vitalion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP FUNCTION.
RX MEDLINE=22284526; PubMed=12397388; DOI=10.1007/s00424-002-0873-2;
RX Gamber N., Fillon S., Feng Y., Friedrich B., Lang P.A., Henke G.,
RX Huber S.M., Kobayashi T., Cohen P., Lang F.;
RT "K(+) channel activation by all three isoforms of serum- and
RT glucocorticoid-dependent protein kinase SGK.";
RL Pfluegers Arch. 445:60-66(2002).
CC -!- FUNCTION: Involved in the activation of potassium channels.
CC Mediates cell IL-3-dependent survival signals (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localized in vesicle-like structures and in
CC the early endosome (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed in most tissues with highest levels
CC in pancreas, kidney liver, heart and brain and lower levels in
CC lung, placenta and skeletal muscle.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -!- SIMILARITY: Contains 1 PK (phox homology) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AF169035; AAF12758.1; ALT INIT; mRNA.
DR EMBL; AF085233; AAF27051.2; -; mRNA.
DR EMBL; BC015326; AAH15326.1; -; mRNA.
DR HSSP; P31751; 1GZK.
DR SMR; Q96BR1; 10-125.
DR Ensembl; ENSG00000104205; Homo sapiens.
DR HGNC; HGNC:10812; SGK3.
DR MIM; 607591; -.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR GO; GO:0006950; P:response to stress; TAS.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001683; PX.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; I.
DR Pfam; PF00433; Pkinase_C; 1.
DR Pfam; PF00787; PX; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00312; PX; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00195; PX; 1.
KW ATP-binding; kinase; Nucleotide-binding; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 12 124 PX.
FT DOMAIN 162 419 Protein kinase.
FT NP_BIND 168 176 ATP (By similarity).
FT MOTIF 195 205 Nuclear localization signal (By similarity).
```

FT ACT\_SITE 286 286 Proton acceptor (By similarity).  
 FT BINDING 191 191 ATP (By similarity).  
 FT MOD\_RES 320 320 Phosphothreonine (by PDPK1).  
 FT MUTAGEN 486 486 S->D: Increased activation.  
 FT CONFLICT 54 54 F -> V (in Ref. 2 and 3).  
 FT CONFLICT 127 127 D -> G (in Ref. 2 and 3).  
 FT CONFLICT 187 187 F -> V (in Ref. 2 and 3).  
 FT CONFLICT 294 294 L -> V (in Ref. 2 and 3).  
 FT CONFLICT 387 387 T -> R (in Ref. 2 and 3).  
 SQ SEQUENCE 496 AA; 57108 MW; 76A6CCEB69006CF1 CRC64;

Query Match 100.0%; Score 2269; DB 1; Length 496;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-139;  
 Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALKIPAKRIFGDNFDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKQSD 60  
 DB 68 MALKIPAKRIFGDNFDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKQSD 127  
 QY 61 PSEDEDRSSQKLHSTSQNLGSPGNPHAKPTDFDLKVIKSGSGFKVLLAKRKLQDKF 120  
 DB 128 PSEDEDRSSQKLHSTSQNLGSPGNPHAKPTDFDLKVIKSGSGFKVLLAKRKLQDKF 187  
 QY 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGE 180  
 DB 188 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGE 247  
 QY 181 LFPHLQERSFPFPHARFYAAETASALGYLHSIKIVYRDLKPNILLDSVGHVVLDTDFGL 240  
 DB 248 LFPHLQERSFPFPHARFYAAETASALGYLHSIKIVYRDLKPNILLDSVGHVVLDTDFGL 307  
 QY 241 CKEGIAISDTTTFCTGTPPEYLAPEVIRKQPDYNTVDMWCLGAVLYEMLYGLPPFYCRDVA 300  
 DB 308 CKEGIAISDTTTFCTGTPPEYLAPEVIRKQPDYNTVDMWCLGAVLYEMLYGLPPFYCRDVA 367  
 QY 301 EMYDNLHKPLSLRPGVSLTAWSLLELLEKDRQNLGAKEDFLEIQNHFFFSLSWADL 360  
 DB 368 EMYDNLHKPLSLRPGVSLTAWSLLELLEKDRQNLGAKEDFLEIQNHFFFSLSWADL 427  
 QY 361 VQKKIPPPNPNVAGPDDIRNFDFTAFTEETVPYSCVSSDYISVNASVLEADDAFVGFSY 420  
 DB 428 VQKKIPPPNPNVAGPDDIRNFDFTAFTEETVPYSCVSSDYISVNASVLEADDAFVGFSY 487  
 QY 421 APPSEDLFL 429  
 DB 488 APPSEDLFL 496

RESULT 3  
 QSR7A7\_PONPY  
 ID QSR7A7\_PONPY PRELIMINARY; PRT; 496 AA.  
 AC QSR7A7;  
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
 DE Hypothetical protein DKFZp469J0919.  
 GN Name=DKFZp469J0919;  
 OS Pongo pygmaeus (Orangutan).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;  
 OC Pongo.  
 OC NCBI\_TaxID=9600;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC The German cDNA Consortium;  
 RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,  
 RA Mewes H.W., Weil B., Amid C., Oeinger A., Fobo G., Han M., Wiemann S.;  
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.  
 DR ENBL; CR860211; CA92353.1; -, mRNA.  
 DR SNR; QSR7A7; 10-125.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 GO; GO:0007242; P:intracellular signaling cascade; IEA.  
 GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000961; Kinase C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR001693; PK.  
 DR InterPro; IPR008271; Ser\_thr\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF00069; Kinase; 1.  
 DR Pfam; PF00433; Kinase\_C; 1.  
 DR Pfam; PF00787; PK; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00312; PK; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR SMART; SM00219; Ty\_KC; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS00195; PK; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 496 AA; 57108 MW; 76A6CCEB69006CF1 CRC64;

Query Match 100.0%; Score 2269; DB 2; Length 496;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-139;  
 Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALKIPAKRIFGDNFDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKQSD 60  
 DB 68 MALKIPAKRIFGDNFDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKQSD 127  
 QY 61 PSEDEDRSSQKLHSTSQNLGSPGNPHAKPTDFDLKVIKSGSGFKVLLAKRKLQDKF 120  
 DB 128 PSEDEDRSSQKLHSTSQNLGSPGNPHAKPTDFDLKVIKSGSGFKVLLAKRKLQDKF 187  
 QY 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGE 180  
 DB 188 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGE 247  
 QY 181 LFPHLQERSFPFPHARFYAAETASALGYLHSIKIVYRDLKPNILLDSVGHVVLDTDFGL 240  
 DB 248 LFPHLQERSFPFPHARFYAAETASALGYLHSIKIVYRDLKPNILLDSVGHVVLDTDFGL 307  
 QY 241 CKEGIAISDTTTFCTGTPPEYLAPEVIRKQPDYNTVDMWCLGAVLYEMLYGLPPFYCRDVA 300  
 DB 308 CKEGIAISDTTTFCTGTPPEYLAPEVIRKQPDYNTVDMWCLGAVLYEMLYGLPPFYCRDVA 367  
 QY 301 EMYDNLHKPLSLRPGVSLTAWSLLELLEKDRQNLGAKEDFLEIQNHFFFSLSWADL 360  
 DB 368 EMYDNLHKPLSLRPGVSLTAWSLLELLEKDRQNLGAKEDFLEIQNHFFFSLSWADL 427  
 QY 361 VQKKIPPPNPNVAGPDDIRNFDFTAFTEETVPYSCVSSDYISVNASVLEADDAFVGFSY 420  
 DB 428 VQKKIPPPNPNVAGPDDIRNFDFTAFTEETVPYSCVSSDYISVNASVLEADDAFVGFSY 487  
 QY 421 APPSEDLFL 429  
 DB 488 APPSEDLFL 496

RESULT 4  
 QSH9Q5\_HUMAN  
 ID QSH9Q5\_HUMAN PRELIMINARY; PRT; 496 AA.  
 AC QSH9Q5;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DE Hypothetical protein DKFZp781N0293.  
 GN Name=DKFZp781N0293;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;



Db 188 YAVKVLQKIVLNKEQKHMAERNVLLKNVHPPELVGLHYSTFQTEKLYFVLDVNGGE 247  
Qy 181 LFFHLQERSPEPHRARFYAAEIASALGYLHSIKIVYRDLPENILLLDSVGHVVLTDGFL 240  
Db 248 LFFHLQERSPEPHRARFYAAEIASALGYLHSIKIVYRDLPENILLLDSVGHVVLTDGFL 307  
Qy 241 CKEGIAISDTTTCGTPPEYLAPEVIRKQPDYNTVDMWCLGAVLYEMLYGLPPFCRDVA 300  
Db 308 CKEGIAISDTTTCGTPPEYLAPEVIRKQPDYNTVDMWCLGAVLYEMLYGLPPFCRDVA 367  
Qy 301 EMDYNIHLKPLSLRPGVSLTAWSLLELEKDRQNLGAKEDFLEIQNHPPFESLSWADL 360  
Db 368 EMDYNIHLKPLSLRPGVSLTAWSLLELEKDRQNLGAKEDFLEIQNHPPFESLSWADL 427  
Qy 361 VQKKIPPPFNPNVAGPDDIRNFDTAFTETVPYSVCVSSDYISVNASVLEADDAFVGFSY 420  
Db 428 VQKKIPPPFNPNVAGPDDIRNFDTAFTETVPYSVCVSSDYISVNASVLEADDAFVGFSY 487  
Qy 421 APPSEDLFL 429  
Db 488 APPSEDLFL 496

## RESULT 6

Q8VEK1 MOUSE PRELIMINARY; PRT; 429 AA.  
AC Q8VEK1;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Sgk3 protein.  
GN Name=Sgk3;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[1]  
[2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
RX MEDLINE=2238257; PubMed=12477933; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Faney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP NUCLEOTIDE SEQUENCE  
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
DR EMBL: BC018363; AALH8363.1; -; mRNA.  
DR HSP; P31751; INKY.  
DR SWR; Q8VEK1; 1-58.  
DR MGI; MGI:2182369; Sgk3.  
GO; GO:0016023; C:cytoplasmic membrane-bound vesicle; IDA.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.  
DR GO; GO:0006916; P:anti-apoptosis; IDA.  
DR InterPro; IPR000961; Pkinase\_C.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR001683; PK.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR Pfam; PF00069; Pkinase; 1.  
DR Pfam; PF00433; Pkinase\_C; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TKC; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS00111; PROTEIN KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE; PS00195; PK; 1.  
DR ATP-binding; Kinase; Nucleotide-binding;  
KW Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 429 AA; 49077 MW; A9C6B7A0C34031F3 CRC64;

Query Match 97.4%; Score 2210; DB 2; Length 429;  
Best Local Similarity 97.0%; Pred. No. 6.9e-136;  
Matches 416; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MALKIPAKRIFGDNFDFIKQRRAGLNFEIQLVRYPELYNHPDVRAFLQMDSPKQSD 60  
Db 1 MALKIPAKRIFGDNFDFIKQRRAGLNFEIQLVRYPELYNHPDVRAFLQMDSPKQSD 60  
Qy 61 PSEDEDSRQKLHSTQNLGPGSNPHAKPTDFDLKVIKSGSGFKVLLAKRKLQKGF 120  
Db 61 PSEDEDSRQKLHSTQNLGPGSNPHAKPTDFDLKVIKSGSGFKVLLAKRKLQKGF 120  
Qy 121 YAVKVLQKIVLNKEQKHMAERNVLLKNVHPPELVGLHYSTFQTEKLYFVLDVNGGE 180  
Db 121 YAVKVLQKIVLNKEQKHMAERNVLLKNVHPPELVGLHYSTFQTEKLYFVLDVNGGE 180  
Qy 181 LFFHLQERSPEPHRARFYAAEIASALGYLHSIKIVYRDLPENILLLDSVGHVVLTDGFL 240  
Db 181 LFFHLQERSPEPHRARFYAAEIASALGYLHSIKIVYRDLPENILLLDSVGHVVLTDGFL 240  
Qy 241 CKEGIAISDTTTCGTPPEYLAPEVIRKQPDYNTVDMWCLGAVLYEMLYGLPPFCRDVA 300  
Db 241 CKEGIAISDTTTCGTPPEYLAPEVIRKQPDYNTVDMWCLGAVLYEMLYGLPPFCRDVA 300  
Qy 301 EMDYNIHLKPLSLRPGVSLTAWSLLELEKDRQNLGAKEDFLEIQNHPPFESLSWADL 360  
Db 301 EMDYNIHLKPLSLRPGVSLTAWSLLELEKDRQNLGAKEDFLEIQNHPPFESLSWADL 360  
Qy 361 VQKKIPPPFNPNVAGPDDIRNFDTAFTETVPYSVCVSSDYISVNASVLEADDAFVGFSY 420  
Db 361 VQKKIPPPFNPNVAGPDDIRNFDTAFTETVPYSVCVSSDYISVNASVLEADDAFVGFSY 420  
Qy 421 APPSEDLFL 429  
Db 421 APPSEDLFL 429

## RESULT 7

SGK3\_MOUSE  
ID SGK3\_MOUSE STANDARD; PRT; 496 AA.  
AC Q8VEK3;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Serine/threonine-protein kinase Sgk3 (EC 2.7.1.37)  
DE (Serum/glucocorticoid regulated kinase 3) (Serum/glucocorticoid  
DE regulated kinase-like) (Cytokine independent survival kinase).  
GN Name=Sgk3; Synonym=Cisk, Sgk3;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;

RN NUCLEOTIDE SEQUENCE (ISOFORM 1), AND MUTAGENESIS OF LYS-191.  
 RP MEDLINE=20504817; PubMed=11036/S0960-9822(00)00733-8;  
 RX Liu D., Yang X., Songyang Z.;  
 RA "Identification of CISK, a new member of the SGK kinase family that  
 RT promotes IL-3-dependent survival.";  
 RL Curr. Biol. 10:1233-1236(2000).  
 RN  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).  
 RC STRAIN=C57BL/6J; TISSUE=Forelimb, Ovary, and Uterus;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.D.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sadelain A., Schneider C., Sempile C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh K., Kagawa I.,  
 RA Miyazaki A., Sakai K., Saeki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RL 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN  
 RP CHARACTERIZATION, AND MUTAGENESIS OF ARG-90.  
 RX MEDLINE=21405768; PubMed=11514587; DOI=10.1083/jcb.200105089;  
 RA Xu J., Liu D., Gill G., Songyang Z.;  
 RT "Regulation of cytokine-independent survival kinase (CISK) by the Phox  
 RT homology domain and phosphoinositides.";  
 RL J. Cell Biol. 154:699-705(2001).  
 CC -I- FUNCTION: Involved in the activation of potassium channels (By  
 CC similarity). Mediates cell IL-3-dependent survival signals. Can  
 CC inhibit pro-apoptotic FOXO3a in vitro.  
 CC -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -I- SUBCELLULAR LOCATION: Localized in vesicle-like structures and in  
 CC the early endosome.  
 CC -I- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q9ERE3-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q9ERE3-2; Sequence=VSP\_004934, VSP\_004935;  
 CC Note=No experimental confirmation available;  
 CC -I- TISSUE SPECIFICITY: Widely expressed, predominantly in the heart,  
 CC spleen and 7-day embryo.  
 CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 CC -I- SIMILARITY: Contains 1 PX (phox homology) domain.  
 CC  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 CC EMBL; AF312007; AAC34115.1; -; mRNA.  
 CC EMBL; AK028722; BAC26083.1; -; mRNA.

DR EMBL; AK030314; BAC26895.1; -; mRNA.  
 DR EMBL; AK031133; BAC27269.1; -; mRNA.  
 DR EMBL; AK031328; BAC27349.1; -; mRNA.  
 DR PDB; 1XTE; X-ray; A=7-160.  
 DR PDB; 1XTN; X-ray; A/B=7-126.  
 DR Ensembl; ENSMUSG0000025915; Mus musculus.  
 DR MGI; MGI:2182368; Sgk3.  
 DR GO; GO:0016023; C:cytoplasmic membrane-bound vesicle; IDA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.  
 DR GO; GO:0006916; P:anti-apoptosis; IDA.  
 DR InterPro; IPR000961; Pkinase C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR001693; PX.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase\_C; 1.  
 DR Pfam; PF00787; PX; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00312; PX; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00220; S\_TK; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS00195; PX; 1.  
 DR 3D-structure; Alternative splicing; ATP-binding; Kinase;  
 KW Nucleotide-binding; Phosphorylation; Serine/threonine-protein kinase;  
 KW Transferase.  
 FT DOMAIN 12 124 PX.  
 FT DOMAIN 162 419 Protein kinase.  
 FT NP\_BIND 168 176 ATP (By similarity).  
 FT MOTIF 195 205 Nuclear localization signal (By similarity).  
 FT ACT\_SITE 286 286 Proton acceptor (By similarity).  
 FT BINDING 191 191 ATP (By similarity).  
 FT MOD\_RES 320 320 Phosphothreonine (by PDPK1) (By similarity).  
 FT VARSP\_LIC 327 333 YLAPEVI -> VRNMSDH (in isoform 2).  
 FT VARSP\_LIC 334 496 /FTId=VSP\_004934.  
 FT VARSP\_LIC 334 496 Missing (in isoform 2).  
 FT MUTAGEN 90 90 R->A: Diminishes binding to phosphoinositides.  
 FT MUTAGEN 191 191 K->A: No activity.  
 FT CONFLICT 114 114 R -> G (in Ref. 2; BAC27349).  
 FT CONFLICT 204 204 Q -> P (in Ref. 2; BAC27349).  
 SQ SEQUENCE 496 AA; 57145 MW; 4B7D2804A5948BAD CRC64;  
 Query Match 97.4%; Score 2210; DB 1; Length 496;  
 Best Local Similarity 97.0%; Pred. No. 8.2e-136;  
 Matches 416; Conservative 7; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 MALKTPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELVNHPDVRALQMDSPKHQSD 60  
 DB 68 MALKTPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELVNHPDVRALQMDSPKHQSD 127  
 QY 61 PSEDEDESSQKLHSTSQNLGSPGNPHAKPTDFDLKVIKGSFGKVLAKRKLGDGF 120  
 DB 128 PSEDEDESRSTKPHSTSRNINLPGTGNPHAKPTDFDLKVIKGSFGKVLAKRKLGDGF 187  
 QY 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSPQTTEKLYFVLDVFNGGE 180  
 DB 188 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSPQTTEKLYFVLDVFNGGE 247  
 QY 181 LFFHQLRERSFFPHEHARFYAAIASALGYLHSIKIVYRDLKPNILLDSVGHVLTDFGL 240  
 DB 248 LFFHQLRERSFFPHEHARFYAAIASALGYLHSIKIVYRDLKPNILLDSVGHVLTDFGL 307  
 QY 241 CKEGIAISDTTTFCTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVA 300  
 DB 308 CKEGIAISDTTTFCTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVA 367

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QY 301 EMDNIIHKPLSLRPGVSLTAWSTLEELLEKDRQNLGAKEDFLEIQNHPPFESLSWADL 360
Db 368 EMDNIIHKPLSLRPGVSLTAWSTLEELLEKDRQNLGAKEDFLEIQNHPPFESLSWADL 427
QY 361 VQKKIPPPNPVAGPDDIRNFDTAFTEETVPYSCVSSDYSIYNASVLEADDAFVGFSY 420
Db 428 VQKKIPPPNPVAGPDDIRNFDTAFTEETVPYSCVSSDYSIYNASVLEADDAFVGFSY 487
QY 421 APPSEDLFL 429
Db 488 APPSEDLFL 496

RESULT 8
Q5ZJQ4_CHICK
ID Q5ZJQ4_CHICK PRELIMINARY; PRT; 490 AA.
AC Q5ZJQ4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=RCJMB04.1698;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
RA Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursa lymphocytes to facilitate
RT gene function analysis";
RL Genome Biol. 6:R6-R6(2005).
DR EMBL; AJ720380; CAG32039.1; -; mRNA.
DR SMR; Q5ZJQ4; 4-119.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0007422; P:intracellular signaling cascade; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001683; PX_kinase.
DR InterPro; IPR008271; Ser_thr_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR Pfam; PF00787; PX; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00312; PX; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TYK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00195; PX; 1.
KW Hypothetical protein.
SQ SEQUENCE 490 AA; 56260 MW; 756D6F95B3EB3P5 CRC64;

Query Match 94.3%; Score 2140; DB 2; Length 490;
Best Local Similarity 93.74; Pred. No. 3e-131;
Matches 401; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALKIPAKRIFGNFDDFDFKORRAGINEFIQNLVRYPELYNHPDVRAFLOMDSPKHSD 60
Db 62 MNLKIPAKRIFGNFDDFDFKORRAGINEFIQNLVRYPELYNHPDVRAFLOMDSPKHSD 121
QY 61 PSEDEDESSQKLHSTSQNLINLPGSNPHAKPTDFDFLKVIGKSGFKVLLAKRKLKGK 120

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Db 122 PSEDEDESSQKLHSTSQNLINLPGSNPHAKPTDFDFLKVIGKSGFKVLLAKRKLKGK 181
QY 121 YAKVLOKKLVLRKQKHIMAEARNVLLKNVHPFLYGLHYSFOTTEKLYFVLDPVNGGE 180
Db 182 YAKVLOKKLVLRKQKHIMAEARNVLLKNVHPFLYGLHYSFOTTEKLYFVLDPVNGGE 241
QY 181 LFFHLQERSFPPEHRAFYAAEIASALGYLHLSIKIVYRDLPKPNILDSVGHVVLTFDGL 240
Db 242 LFFHLQERSFPPEHRAFYAAEIASALGYLHLSINIVYRDLPKPNILDSVGHVVLTFDGL 301
QY 241 CKEGIALSDTTTTCGTPPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPPYCRDVA 300
Db 302 CKEGIALSDTTTTCGTPPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPPYCRDVA 361
QY 301 EMDNIIHKPLSLRPGVSLTAWSTLEELLEKDRQNLGAKEDFLEIQNHPPFESLSWADL 360
Db 362 EMDNIIHKPLSLRPGVSLTAWSTLEELLEKDRQNLGAKEDFLEIQNHPPFESLSWADL 421
QY 361 VQKKIPPPNPVAGPDDIRNFDTAFTEETVPYSCVSSDYSIYNASVLEADDAFVGFSY 420
Db 422 VQKKIPPPNPVAGPDDIRNFDTAFTEETVPYSCVSSDYSIYNASVLEADDAFVGFSY 481
QY 421 APPSEDLFL 428
Db 482 APPSEDLFL 489

RESULT 9
Q4SFC2_TETNG
ID Q4SFC2_TETNG PRELIMINARY; PRT; 518 AA.
AC Q4SFC2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 6 SCAF14605, whole genome shotgun sequence.
GN ORFNames=GSTENG00019161001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bounneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Farra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAEE01014605; CAG00660.1; -; Genomic DNA.
SQ SEQUENCE 518 AA; 59656 MW; 4CFC4E51FF8BA3E5 CRC64;

Query Match 78.6%; Score 1783; DB 2; Length 518;
Best Local Similarity 77.8%; Pred. No. 5.8e-108;
Matches 332; Conservative 45; Mismatches 46; Indels 4; Gaps 1;

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QY 3 LKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELVNHPDVRAFLQWDSFKHQSDPS 62  
Db 96 LKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELVNHPDVRAFLQWDSFKHQSDPS 155  
QY 63 EDEDERSSQKLHSTSONINLGPSGNPHAKPTDFDLKVLGKSGFGKVLAKRLDKGFYA 122  
Db 156 EDEDERKN---NSTSGNINLGPSANPQAKPTDFDLKVLGKSGFGKVLAKRLDKGFYA 211  
QY 123 VYLQKQKIVLNKREKQKHMAERNVLLKNVHPFLVLGLHYHSFQTTEKLYFVLDFVNGGELF 182  
Db 212 IKVLQKQKIVLNKREKQKHMAERNVLLKNVHPFLVLGLHYHSFQSTDKLYFVLDFVNGGELF 271  
QY 183 FHLQERSFPEHRARFYAAIASALGYLHSIKIVYRDLKPNILLDSGVHVTDFGLCK 242  
Db 272 FHLQKERTPEPRAKIFYAEMASALGYLHSINIVYRDLKPNILLDSGVHVTDFGLCK 331  
QY 243 EGIAISDTTFTTCGTPPEYLAPEVRKOPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEM 302  
Db 332 EGISQSDTSTTCGTPPEYLAPEVRKOPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEM 391  
QY 303 YDNILHKPLSLRPGVSLTAWSIILELLEKDRQNLGAKEDFLBIONHPFFESLSWADLVQ 362  
Db 392 YDNILHKPLAMRAGASSTAWSLQGLLEKDGTHRLGSRNDFDIKVNHPFSSINWDDLQ 451  
QY 363 KKIPTPPFPNPVAGDDIRNFTDFTBETVPYSCVSDSYIVNASVLEADDAFVGFSYAP 422  
Db 452 KKIPTPPFPNPVAGDDIRNFTDFTBETVPYSCVSDSYIVNASVLEADDAFVGFSYAP 511  
QY 423 PSEDLFL 429  
Db 512 PSEDSFL 518

RESULT 10  
Q5YV65 HUMAN  
ID Q5YV65 HUMAN PRELIMINARY; PRT; 526 AA.  
AC Q5YV65;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE OTTHUMP0000017246  
GN Name=SGK; ORFNames=RP1-188K17.1-001;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Hall R.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
[2]  
RP NUCLEOTIDE SEQUENCE.  
RA Tracey A.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
[3]  
RN NUCLEOTIDE SEQUENCE.  
RA Milne S.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
DR ENBL; AL355881; CA172579.1; -; Genomic DNA.  
DR ENBL; AL35839; CA119721.1; -; Genomic DNA.  
DR ENBL; Z84486; CA121678.1; -; Genomic DNA.  
DR ENBL; AL35839; CA172579.1; JOINED; Genomic DNA.  
DR ENBL; Z84486; CAH72579.1; JOINED; Genomic DNA.  
DR ENBL; Z84486; CA119721.1; JOINED; Genomic DNA.  
DR ENBL; Z84486; CA119721.1; JOINED; Genomic DNA.  
DR ENBL; AL35839; CA121678.1; JOINED; Genomic DNA.  
DR ENBL; AL35839; CA121678.1; JOINED; Genomic DNA.  
DR Ensembl; ENSG00000118515; Homo sapiens.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

DR GO; GO:0004688; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000961; Pkinase C.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; Pkinase; 1.  
DR Pfam; PF00433; Pkinase C; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TK; 1.  
DR SMART; SM00219; TyKc; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS0011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW Kinase.  
SQ SEQUENCE 526 AA; 59904 MW; 8CE1E9DFB949D5A5 CRC64;  
Query Match 66.2%; Score 1501; DB 2; Length 526;  
Best Local Similarity 66.8%; Pred. No. 1.4e-89;  
Matches 286; Conservative 52; Mismatches 76; Indels 14; Gaps 3;  
QY 6 PAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELVNHPDVRAFLQWDSFKHQSDPS 61  
Db 109 PDKRTFTWNTDDAFMKQRRLGNDLFQKIANNYSACKHPVQSIKISQPEPELMNAP 168  
QY 62 SEDEDERSSQKLHSTSONINLGPSGNPHAKPTDFDLKVLGKSGFGKVLAKRLDKGFY 121  
Db 169 SPPP-----SPSQINLGPSGNPHAKPSDFHLKVLGKSGFGKVLAKRLDKGFY 219  
QY 122 AVKVLQKQKIVLNKREKQKHMAERNVLLKNVHPFLVLGLHYHSFQTTEKLYFVLDFVNGGEL 181  
Db 220 AVKVLQKQKIVLNKREKQKHMAERNVLLKNVHPFLVLGLHYHSFQTTEKLYFVLDFVNGGEL 279  
QY 182 FHLQERSFPEHRARFYAAIASALGYLHSIKIVYRDLKPNILLDSGVHVTDFGLC 241  
Db 280 FHLQERSFPEHRARFYAAIASALGYLHSIKIVYRDLKPNILLDSGVHVTDFGLC 339  
QY 242 KEGIAISDTTFTTCGTPPEYLAPEVRKOPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAE 301  
Db 340 KENIEHNSTTSTFCGTPPEYLAPEVRKOPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAE 399  
QY 302 MYDNILHKPLSLRPGVSLTAWSIILELLEKDRQNLGAKEDFLBIONHPFFESLSWADLV 361  
Db 400 MYDNILHKPLSLRPGVSLTAWSIILELLEKDRQNLGAKEDFLBIONHPFFESLSWADLV 459  
QY 362 QKKIPPPFPNPVAGDDIRNFTDFTBETVPYSCVSDSYIVNASVLEADDAFVGFSYA 421  
Db 460 NKKIPPPFPNPVAGDDIRNFTDFTBETVPYSCVSDSYIVNASVLEADDAFVGFSYA 519  
QY 422 PSEDLFL 429  
Db 520 PPT-DSFL 526  
RESULT 11  
Q5TCN4 HUMAN  
ID Q5TCN4 HUMAN PRELIMINARY; PRT; 421 AA.  
AC Q5TCN4;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE OTTHUMP0000017249  
GN Name=SGK; ORFNames=RP1-188K17.1-011;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Tracey A.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.



EMBL; AL135839; CA119718.1; -, Genomic\_DNA.  
GO; GO:0005524; F:ATP binding; IEA.  
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
GO; GO:0006468; P:protein-tyrosine kinase activity; IEA.  
InterPro; IPR000961; Pkinase\_C.  
InterPro; IPR000719; Prot\_kinase.  
InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
InterPro; IPR002290; Ser\_thr\_pkinase.  
InterPro; IPR001245; Tyr\_pkinase.  
Pfam; PF00069; Pkinase; 1.  
Pfam; PF00433; Pkinase; 1.  
ProDom; PD000001; Prot\_kinase; 1.  
SMART; SM00133; S\_TK\_X; 1.  
SMART; SM00220; S\_TK\_X; 1.  
SMART; SM00219; TyrKc; 1.  
PROSITE; PS0107; PROTEIN KINASE ATP; 1.  
PROSITE; PS0011; PROTEIN KINASE DOM; 1.  
PROSITE; PS0108; PROTEIN KINASE ST; 1.  
SEQUENCE 421 AA; 47910 MW; 6BDCD1FA7D9AFD0E CRC64;  
Query Match 65.3%; Score 1482.5; DB 2; Length 421;  
Best Local Similarity 66.0%; Pred. No. 1.8e-88;  
Matches 285; Conservative 53; Mismatches 73; Indels 21; Gaps 5;  
QY 6 PAKRIFGDNFDDP----FIKORRAGLNEFIQNLVYPPELVNHPDVRAPFLQMDSPKH--- 57  
DB 3 PSKRFF---ISPPSSTAFMKQRRMGLNDFIQKIANNVYACVHPVQSIKISQPELPM 59  
QY 58 QSDPSEDESSQKLHSTQNTINLGPSSNPHAKPTDFLKVIGKSGFGKVLAKRKL 117  
DB 60 NAMPSPPP-----SPSQINLGPSSNPHAKPSDFHLKVIGKSGFGKVLARHAE 110  
QY 118 GKFAVAVLVOKIVLNRKEQKHIWAERNVLLKNVGHFPLVGLHVSFOTTEKLYFVLDPVN 177  
DB 111 EVFAVAVLVOKAILKKKEKHINSERNVLLKNVGHFPLVGLHVSFOTADKLYFVLDPVN 170  
QY 178 GGELFFHLQERSPEPRARFYAAEIASALGYLHSIKIVYRDLKPNILLDSVGHVVLTD 237  
DB 171 GGELFYHLQERCFLEPRARFYAAEIASALGYLHSINIVYRDLKPNILLDSQGHVVLTD 230  
QY 238 FGLCKEGIALSTTTTCGTPPEYLAPEVIRKQPDVNTVWCLGAVLYEMLYGLPPPYCR 297  
DB 231 FGLCKENIEHSTSTFCGTPPEYLAPEVIRKQPDVNTVWCLGAVLYEMLYGLPPPYCR 290  
QY 298 DVAEVYDNIHLKPLSLPAGVSLTAWSTLEELLEKDRQNRGLGAKEDFLEIQNHPPFESLSW 357  
DB 291 NTAEMYDNIHLKPLSLPAGVSLTAWSTLEELLEKDRQNRGLGAKEDFLEIQNHPPFESLSW 350  
QY 358 ADLVQKIPPPFPNPNVAGPDIDRFDTAFTEETVPVSCVSSDYIVNAGVLEADDAFVG 417  
DB 351 DDLINKKITPPFPNPNVSGPNDLRHDFDPEFTPEEPVPSNIGKSPDSVLVTASVKEAAEAF 410  
QY 418 FSVAPSEDPL 429  
DB 411 FSVAPPT-DSFL 421

RESULT 12  
Q6NS85\_MOUSE  
ID Q6NS85\_MOUSE PRELIMINARY; PRT; 519 AA.  
AC Q6NS85;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Sgk protein.  
GN Sgk protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]

RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Phosphorylates a large number of substrates in the  
cytoplasm and the nucleus (By similarity).  
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (inactive holoenzyme and  
monomeric catalytic subunit). Translocates into the nucleus  
(monomeric catalytic subunit) (By similarity).  
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
EMBL; BC070401; AAH70401.1; -, mRNA.  
HSSP; P05132; 1ATP.  
DR Ensembl; ENSMUSG00000019970; Mus musculus.  
DR MGI; MGI:1340062; Sgk  
GO; GO:0004672; P:protein kinase activity; IEA.  
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
GO; GO:0006974; P:response to DNA damage stimulus; IEA.  
DR InterPro; IPR000961; Pkinase\_C.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; Pkinase; 1.  
DR Pfam; PF00433; Pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TK\_X; 1.  
DR SMART; SM00219; TyrKc; 1.  
DR PROSITE; PS0107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS0108; PROTEIN KINASE ST; 1.  
KW ATP-binding; Kinase; Nucleotide-binding;  
SX Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 519 AA; 58984 MW; BB79975BA911DEC3 CRC64;  
Query Match 65.2%; Score 1480; DB 2; Length 519;  
Best Local Similarity 66.6%; Pred. No. 3.3e-88;  
Matches 285; Conservative 49; Mismatches 80; Indels 14; Gaps 3;  
QY 6 PAKRIFGDNFDDPFIKORRAGLNEFIQNLVYPPELVNHPDVRAPFLQMDSPKH---QSDP 61  
DB 102 PDPRTFTWTDAAAFMKQRRMGLNDFIQKIANNVYACVHPVQSIKISQPELPMANP 161  
QY 62 SEDEDESSQKLHSTQNTINLGPSSNPHAKPTDFLKVIGKSGFGKVLAKRKLQK 121  
DB 162 SPPP-----SPSQINLGPSSNPHAKPSDFHLKVIGKSGFGKVLARHAEV 212  
QY 122 AVKVLQKIVLNRKEQKHIWAERNVLLKNVGHFPLVGLHVSFOTTEKLYFVLDPVNGEL 181

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Db 213 AVKVLQKALKKKKEKHGINSERNVLLKNVGHFLVGLHFSQTADKLYFVLVDYINGGEL 272
Qy 182 FFHLQERSPEHRAFYAAEIASALGYLHSIKIVYRDLKPNILLDSVGHVVLTDPLGLC 241
Db 273 FYHLQERCFLEPRARFYAAEIASALGYLHSINIVYRDLKPNILLDSQGHIVLTDPLGLC 332
Qy 242 KEGIALSDTTTTCCGTPPEYLAPVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAE 301
Db 333 KENIEHNGTTSTFCGTPPEYLAPVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAE 392
Qy 302 MYDNILHKPLSLRPGVSLTAWSLTELELLEKDRQNLGAKEDFLEIQNHPPFESLSWADLV 361
Db 393 MYDNILNKPLQKLPNTNSARHLLGGLLKQRTKRLGAKDDFNEIKSHVFFSLINWDDLI 452
Qy 362 QKKIPFPNPNVAGPDIDRNFDTAFTTEVPYSCVSSDYSIYNASVLEADDAFVGFSYA 421
Db 453 NKKITPPFNPNVSGPSDLRHFDPFTEEPVPSIGRSPDSILVTASVKEAAEAFLGFSYA 512
Qy 422 PPSDELFL 429
Db 513 PP-VDSFL 519
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## RESULT 13

```
Q5TCN3_HUMAN
ID Q5TCN3_HUMAN PRELIMINARY; PRT; 431 AA.
AC Q5TCN3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE OTHUMP00000017247.
GN Name=SGK; ORFNames=RP1-188K17.1-009;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tracey A.;
RA Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; AL135839; CAT19719.1; -; Genomic_DNA.
DR GO; GO:0005524; F-ATP binding; IEA.
DR GO; GO:0004574; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR InterPro; IPR01245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase.1.
DR Pfam; PF00433; Pkinase C.1.
DR SMART; SM00133; S_TK_X.1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
SQ SEQUENCE 431 AA; 48942 MW; F3697C63AB1F499D CRC64;
```

```
Query Match 65.1%; Score 1476; DB 2; Length 431;
Best Local Similarity 67.5%; Pred. No. 4.8e-88;
Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;
Qy 19 FIKQRAGLNEFTQNLVRYPELVNHPDVRFAFLQWDSPKH-----QSDPSDEDESSQKLH 74
Db 27 FMKQRRLGNLDFIQKIANNSSYACKHPDEVOSILKIQFQPELMNANPSPPP----- 77
Qy 75 STSQINILGSPGNPHAKPTDFDLKVIKGSGFGKVLAKRKLKDGKYAVKVLQKQKIVLNR 134
Db 78 SPSSQINLGSPSNPHAKPSDFHLKVIKGSGFGKVLARHKAEEVYAVKVLQKQKAILKK 137
```

```
Qy 135 KEQKHMAERNVLLKNVGHFLVGLHYSQTTEKLYFVLVDYNGGELFFHLQERSFPPEH 194
Db 138 KEEKHMSERNVLLKNVGHFLVGLHFSQTADKLYFVLVDYNGGELFFHLQERCFLEP 197
Qy 195 RARFYAAEIASALGYLHSIKIVYRDLKPNILLDSVGHVVLTDPLGLCKEGIAISDTTTTF 254
Db 198 RARFYAAEIASALGYLHSINIVYRDLKPNILLDSQGHIVLTDPLGLCKENIEHNTSTTF 257
Qy 255 CQTPEYLAPVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMYDNILHKPLSLR 314
Db 258 CQTPEYLAPVIRKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYDNILNKPLQLK 317
Qy 315 PGVSLTAWSLTELELLEKDRQNLGAKEDFLEIQNHPPFESLSWADLVQKKIPFPNPNVA 374
Db 318 PNITNSARHLLGGLLKQRTKRLGAKDDFNEIKSHVFFSLINWDDLIINKKITPPFPNVS 377
Qy 375 GPDDIRNFDTAFTTEVPYSCVSSDYSIYNASVLEADDAFVGFSYAPPSDELFL 429
Db 378 GPNDLRHFDPEFTEEPVPSIGRSPDSVLVTASVKEAAEAFLGFSYAPPT-DSFL 431

RESULT 14
Q68G05_RAT
ID Q68G05_RAT PRELIMINARY; PRT; 431 AA.
AC Q68G05;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Serum/glucocorticoid regulated kinase.
GN Name=SGK;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC078843; AAH78843.1; -; mRNA.
DR Ensembl; ENSRNOG0000011815; Rattus norvegicus.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
```

```
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00219; Ty_KC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 431 AA; 49024 MW; 35261E7AC839CB3P CRC64;

Query Match 65.1%; Score 1476; DB 2; Length 431;
Best Local Similarity 67.7%; Pred. No. 4.8e-86;
Matches 281; Conservative 50; Mismatches 70; Indels 14; Gaps 3;

QY 19 FIKORRAGLNEFIQNLVRYPELVNHPDVRAPFLQWDSPKH---QSDPSEDEDESSQKLH 74
DB 27 FMKQRRGLNDFIQKLANNVYACKHPEVQSYLKISQPEPELMNANFSPPP----- 77

QY 75 STSQINILGPSGNPHAKPTDFDLKLVIGKSGFGKVLAKRKLKGKFYAVKVLQKKIYVLR 134
DB 78 SPSQOINLGPSSNPHAKPSDFHFLKVIKSGSGFKVLLARHKAEEAFYAVKVLQKKAILKK 137

QY 135 KEQKHMAERNVLLKNVQHPFLVGLHYSTQTTTEKLYFVLDVNGGELFFHLOERSPEH 194
DB 138 KEKHIMSERNVLLKNVQHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLOERCFLP 197

QY 195 RARFYAAEIASALGYLHSIKIVYRDLPENILLDSVGHVLTDFGLCKEGIAISDTTTF 254
DB 198 RARFYAAEIASALGYLHSINIVYRDLPENILLDSQGHIVLTDFGLCKENIEHNTSTF 257

QY 255 CGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMYDNILHKPLSLR 314
DB 258 CGTPEYLAPEVLHKQPYDRTVDWCLGAVLYEMLYGLPPFYSRNTAEMYDNILKPLQLK 317

QY 315 PGVSLTAWSLLEELLEKRONRIGAKEDFLEIQNHPPFESLSWADLVQKKIPPPFNVA 374
DB 318 PNITNSARHLLEGLLQKORTKRLGAKDDFMEIKSHIFFSLINDDLLINKKITPPFPNVS 377

QY 375 GPDDIRNFDTAFTTEETVPYSCVSSDYSIYNASVLEADDAFVGFSPAPPSEDLFL 429
DB 378 GPSDLRHDFDEFTTEEPVPSSIGRSPDSILVTASVKEAAEAFVGFSPAPPM-DSFL 431
```

## RESULT 15

```
Q5TCN2_HUMAN
ID Q5TCN2_HUMAN PRELIMINARY; PRT; 445 AA.
AC Q5TCN2;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE OTTHUMP0000017248.
GN Name=SGK; ORFNames=RP1-188K17.1-010;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tracey A.;
RL Submitted
DR EMBL; ALI35839; CAI19720.1; -; Genomic DNA.
DR Ensembl; ENSG00000118515; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase_C.
```

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DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00219; Ty_KC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
SQ SEQUENCE 445 AA; 50623 MW; DC7076E1F43BCBAB CRC64;

Query Match 65.1%; Score 1476; DB 2; Length 445;
Best Local Similarity 67.5%; Pred. No. 5e-88;
Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;

QY 19 FIKORRAGLNEFIQNLVRYPELVNHPDVRAPFLQWDSPKH---QSDPSEDEDESSQKLH 74
DB 41 FMKQRRGLNDFIQKLANNVYACKHPEVQSYLKISQPEPELMNANFSPPP----- 91

QY 75 STSQINILGPSGNPHAKPTDFDLKLVIGKSGFGKVLAKRKLKGKFYAVKVLQKKIYVLR 134
DB 92 SPSQOINLGPSSNPHAKPSDFHFLKVIKSGSGFKVLLARHKAEEAFYAVKVLQKKAILKK 151

QY 135 KEQKHMAERNVLLKNVQHPFLVGLHYSTQTTTEKLYFVLDVNGGELFFHLOERSPEH 194
DB 152 KEKHIMSERNVLLKNVQHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLOERCFLP 211

QY 195 RARFYAAEIASALGYLHSIKIVYRDLPENILLDSVGHVLTDFGLCKEGIAISDTTTF 254
DB 212 RARFYAAEIASALGYLHSINIVYRDLPENILLDSQGHIVLTDFGLCKENIEHNTSTF 271

QY 255 CGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMYDNILHKPLSLR 314
DB 272 CGTPEYLAPEVLHKQPYDRTVDWCLGAVLYEMLYGLPPFYSRNTAEMYDNILKPLQLK 331

QY 315 PGVSLTAWSLLEELLEKRONRIGAKEDFLEIQNHPPFESLSWADLVQKKIPPPFNVA 374
DB 332 PNITNSARHLLEGLLQKORTKRLGAKDDFMEIKSHIFFSLINDDLLINKKITPPFPNVS 391

QY 375 GPDDIRNFDTAFTTEETVPYSCVSSDYSIYNASVLEADDAFVGFSPAPPSEDLFL 429
DB 392 GPDLRHDFDEFTTEEPVPSSIGRSPDSILVTASVKEAAEAFVGFSPAPPT-DSFL 445
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Search completed: January 27, 2006, 23:31:07

Job time : 70.8811 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:06:05 ; Search time 76.0006 Seconds  
(without alignments)  
2468.595 Million cell updates/sec

Title: US-09-868-131A-8

Perfect score: 2311

Sequence: 1 MQGLLTSGRRKPSGGRCRGR.....ASSAFLGFSYAPDDDDILDC 427

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2311	100.0	427	3	AAY95276 Human ser
2	2311	100.0	427	8	ADQ88284 Human 549
3	2124.5	91.9	398	6	ADA05780 Human NOV
4	2094.5	90.6	398	8	ADN62944 Human NOV
5	2005	86.8	382	4	AAM25594 Human pro
6	2005	86.8	396	9	ADY37607 Lung canc
7	1954	84.6	367	3	AAY95275 Human ser
8	1954	84.6	367	4	AAU28087 Novel hum
9	1954	84.6	367	5	AAE22765 Human ser
10	1954	84.6	367	7	ADD45799 Human Pro
11	1954	84.6	367	8	ADI29317 Human MAR
12	1954	84.6	367	8	ADJ45521 LXR-ligan
13	1952	84.5	367	4	AAB65708 Novel pro
14	1848	80.0	367	3	AAY95277 Mouse ser
15	1848	80.0	367	7	ADD45797 Rat prote
16	1691	73.2	319	4	AAB99838 AGC prote
17	1691	73.2	319	8	ADJ38886 SGK2 amin
18	1677	72.6	335	8	ADP29822 Human sec
19	1665	72.0	330	8	ADN61463 Human Kpp
20	1435.5	62.1	788	7	ADD93289 p53-SGK(6
21	1420	61.4	431	3	AAB24116 Rat serum
22	1420	61.4	431	3	AAY93530 A rat ser
23	1419	61.4	407	7	ADC69794 Human ser
24	1419	61.4	431	2	AAW90139 Human sgk

25	1419	61.4	431	6	ADA10889	Ada10889 Human cdn
26	1419	61.4	431	7	ADG31708	Adg31708 Human pro
27	1419	61.4	431	7	ADK50982	Adk50982 Human NOV
28	1419	61.4	431	7	ADK50984	Adk50984 Human NOV
29	1419	61.4	431	8	ADO55118	Ado55118 Protein #
30	1419	61.4	431	9	ADY14632	Ady14632 PRO polyp
31	1419	61.4	431	9	ADY19878	Ady19878 PRO polyp
32	1419	61.4	431	9	AEA04529	Aea04529 Human pro
33	1419	61.4	442	7	ADG31706	Adg31706 Human pro
34	1419	61.4	445	7	ADC69792	Adc69792 Human pro
35	1419	61.4	526	6	ADA54293	Ada54293 Human pro
36	1419	61.4	526	7	ADG31710	Adg31710 Human pro
37	1416	61.3	431	8	ADO60030	Ado60030 CRH signa
38	1416	61.3	431	8	ADO44573	Ado44573 Serum/glu
39	1415	61.2	430	2	ADN95921	Adn95921 Human BEC
40	1415	61.2	431	2	AAW77217	Aaw77217 Human cel
41	1415	61.2	431	3	AAY95279	Aay95279 Human ser
42	1415	61.2	431	3	AAB24115	Aab24115 Human ser
43	1415	61.2	431	4	AAB65613	Aab65613 Novel pro
44	1415	61.2	431	7	ADD14174	Add14174 Human src
45	1415	61.2	431	7	ADE31655	Ade31655 Human 290

## ALIGNMENTS

RESULT 1  
AAY95276  
ID AAY95276 standard; protein; 427 AA.  
AC AAY95276;  
XX  
DT 12-SFP-2000 (first entry)  
XX  
DE Human serum and glucocorticoid-induced protein kinase 2-beta.  
XX  
KW Serum and glucocorticoid-induced protein kinase 2; SGK2-beta; human;  
KW phosphorylation; cancer; diabetes; ischaemia; therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 339  
FT /note= "O-phosphorylated"  
FT Modified-site 394  
FT /note= "O-phosphorylated"  
XX  
PN WO200035946-A1.  
XX  
PD 22-JUN-2000.  
XX  
PF 14-DEC-1999; 99WO-GB004232.  
XX  
PR 14-DEC-1998; 98US-0112217P.  
PR 19-AUG-1999; 99GB-00019676.  
XX  
(UYDU-) UNIV DUNDEE.  
XX  
PI Cohen P, Kobayashi T, Deak M;  
XX  
DR WPI; 2000-442364/38.  
XX  
DR N-PSDB; AAA27857.  
XX  
PT Modulation of serum and glucocorticoid-induced protein kinase (SGK) by  
PT phosphorylation with 3-phosphoinositide-dependent protein kinase-1 (PDK1)  
PT or dephosphorylation, useful for treatment of cancer, diabetes and  
XX ischemic diseases.  
XX  
PS Disclosure; Page 6-7; 127pp; English.  
XX  
CC The present sequence is that of human serum and glucocorticoid-induced  
CC protein kinase (SGK) isoform 2-beta. SGK (see AAY95279) was initially  
CC identified as a glucocorticoid and osmotic stress-responsive gene. Novel

CC isoforms, SGK2 and SGK3, were isolated from EST database searches, and 2  
CC splice variants of SGK2, i.e. SGK2-beta and -alpha (see AY95275), which  
CC contains 60 fewer N-terminal residues, were identified. SGK2-beta is  
CC expressed in liver and kidney. It is activated by phosphorylation in a  
CC similar manner to SGK. The invention provides methods of activating SGK  
CC activity by phosphorylation using 3-phosphoinositide-dependent protein  
CC kinase-1 (PK1), and of reducing the activity of SGK by  
CC dephosphorylation. The invention also provides a method of identifying a  
CC compound that modulates the activity of SGK. Such compounds are useful  
CC for treating patients requiring modulation of SGK, such as patients with  
CC cancer, diabetes or ischaemic disease  
XX  
SQ Sequence 427 AA;

Query Match 100.0%; Score 2311; DB 3; Length 427;  
Best Local Similarity 100.0%; Pred. NO. 1.6e-202;  
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQGLLTSGRKPSGGGRCCTGRGGWRCQCLKPMWGGADPPTTSLCLLPVPPPLPDHCYR 60  
Db 1 MQGLLTSGRKPSGGGRCCTGRGGWRCQCLKPMWGGADPPTTSLCLLPVPPPLPDHCYR 60  
Qy 61 MNSSPAGTSPQPSRANGNINLGPSPNPAQPTDFDLKVIKGNYGKVLAKRKSDFGAF 120  
Db 61 MNSSPAGTSPQPSRANGNINLGPSPNPAQPTDFDLKVIKGNYGKVLAKRKSDFGAF 120  
Qy 121 YAVKVLQKSIKKKEQSHIMAERSVLLKNVRHPLVGLRYSQTPEKLYFVLDYNGGE 180  
Db 121 YAVKVLQKSIKKKEQSHIMAERSVLLKNVRHPLVGLRYSQTPEKLYFVLDYNGGE 180  
Qy 181 LFFHLQRRERFLEPRARFYAAEASVAGYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 240  
Db 181 LFFHLQRRERFLEPRARFYAAEASVAGYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 240

Qy 241 CKEGVEPEDTTSFCGTPEYLAPEVLRKEPYDRAVDWMCGLGAVLYEMLHGLPPFYSDVS 300  
Db 241 CKEGVEPEDTTSFCGTPEYLAPEVLRKEPYDRAVDWMCGLGAVLYEMLHGLPPFYSDVS 300  
Qy 301 QMVENILHQPLOIPGGRTVAACDLQLLHKDQRLGSKADFLKINHVFFSPINWDDL 360  
Db 301 QMVENILHQPLOIPGGRTVAACDLQLLHKDQRLGSKADFLKINHVFFSPINWDDL 360  
Qy 361 YHXRLTTPPNPNVTGPADLKHDFEPTQEAUSKISGCTPDTVASSGASSAFILGFSVAPE 420  
Db 361 YHXRLTTPPNPNVTGPADLKHDFEPTQEAUSKISGCTPDTVASSGASSAFILGFSVAPE 420  
Qy 421 DDDILDC 427  
Db 421 DDDILDC 427

RESULT 2  
ADQ88284  
ID ADQ88284 standard; protein; 427 AA.

XX ADQ88284;

AC ADQ88284;

XX 21-OCT-2004 (first entry)

DE Human 54946 protein, a Ser/Thr protein kinase SGK2.

XX human; cardiovascular disorder; thrombotic disorder;  
KW differential expression; gene therapy; aberrant vascularisation;  
KW atherosclerosis; thrombosis; coronary artery disease; hyperlipidaemia;  
KW dyslipidaemia; high blood pressure; heart failure; cardiac;  
KW thrombolytic; anticoagulant; antilipaeamic; hypotensive; cardiac;  
KW Ser/Thr protein kinase; SGK2; EC 2.7.1.37; enzyme.  
XX  
OS Homo sapiens.  
XX  
PN WO2004063340-A2.  
XX  
PD 29-JUL-2004.

XX 13-JAN-2004; 2004WO-US000393.  
PF  
XX 13-JAN-2003; 2003US-0439683P.  
PR 05-FEB-2003; 2003US-0445216P.  
PR 18-FEB-2003; 2003US-0448036P.  
PR 12-MAR-2003; 2003US-0454189P.  
PR 25-MAR-2003; 2003US-0457541P.  
PR 29-APR-2003; 2003US-0466411P.  
PR 08-MAY-2003; 2003US-0469041P.  
PR 10-JUN-2003; 2003US-0477414P.  
PR 13-JUN-2003; 2003US-0478560P.  
PR 24-JUL-2003; 2003US-0489772P.  
PR 28-JUL-2003; 2003US-0490660P.  
PR 03-SEP-2003; 2003US-0499838P.  
PR 22-SEP-2003; 2003US-0504786P.  
PR 24-SEP-2003; 2003US-0505570P.  
PR 17-OCT-2003; 2003US-0512418P.  
PR 27-OCT-2003; 2003US-0514660P.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Stagliano NE, Healy A, Acton SL, Galvin KM, Donoghue MA;  
PI Rogrigue-Way A, Tomlinson JE;  
DR WPI; 2004-553729/53.  
DR N-PSDB; ADQ88283.  
XX  
PT Identifying a compound for treating a cardiovascular or thrombotic  
PT disorder by combining a compound to be tested with e.g., a 9380, 9462,  
PT 8701 or 2419 polypeptide or with a host cell expressing the polypeptide  
PT and detecting the binding.  
XX  
PS Claim 1; SEQ ID NO 126; 512bp; English.  
XX  
CC This invention relates to a novel compound that is capable of treating a  
CC cardiovascular or thrombotic disorder. Specifically, it refers to the  
CC identification of nucleic acid molecules, and the encoded proteins  
CC thereof, which are differentially expressed in cardiovascular disease  
CC states relative to their normal expression in non-diseased tissue. The  
CC present invention describes test compounds (i.e. small molecules,  
CC peptides or antibodies) that can bind to and modulate the activity of  
CC these differentially expressed membrane-bound polypeptides, where binding  
CC is detected by a competition binding assay, immunoassay or yeast two-  
CC hybrid assay. Accordingly, pharmaceutical compositions can be developed  
CC and used via gene therapy to treat aberrant vascularisation,  
CC atherosclerosis, thrombosis, coronary artery disease, hyperlipidaemia,  
CC dyslipidaemia, high blood pressure or heart failure. As such, they  
CC exhibit cardiac, thrombolytic, anticoagulant, antilipaeamic, hypotensive  
CC and cardiac activities. This polypeptide sequence is a human protein  
CC that is differentially expressed in a patient with a cardiovascular  
CC disorder, given in an exemplification of the invention.  
XX  
SQ Sequence 427 AA;

Query Match 100.0%; Score 2311; DB 8; Length 427;  
Best Local Similarity 100.0%; Pred. NO. 1.6e-202;  
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MQGLLTSGRKPSGGGRCCTGRGGWRCQCLKPMWGGADPPTTSLCLLPVPPPLPDHCYR 60  
Db 1 MQGLLTSGRKPSGGGRCCTGRGGWRCQCLKPMWGGADPPTTSLCLLPVPPPLPDHCYR 60  
Qy 61 MNSSPAGTSPQPSRANGNINLGPSPNPAQPTDFDLKVIKGNYGKVLAKRKSDFGAF 120  
Db 61 MNSSPAGTSPQPSRANGNINLGPSPNPAQPTDFDLKVIKGNYGKVLAKRKSDFGAF 120  
Qy 121 YAVKVLQKSIKKKEQSHIMAERSVLLKNVRHPLVGLRYSQTPEKLYFVLDYNGGE 180  
Db 121 YAVKVLQKSIKKKEQSHIMAERSVLLKNVRHPLVGLRYSQTPEKLYFVLDYNGGE 180  
Qy 181 LFFHLQRRERFLEPRARFYAAEASVAGYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 240

Db 181 LFFHLQRRERFLEPRAFYAAEASATGYLHSLNIIYRDLKPEINILLDCQGHVVLTDFGL 240  
Qy 241 CKGEVEPEDTTSTFCGTPPEYLAPEVLKPEYDRAVDWVCLGAVLYEMLHGLPPFYSDVS 300  
Db 241 CKGEVEPEDTTSTFCGTPPEYLAPEVLKPEYDRAVDWVCLGAVLYEMLHGLPPFYSDVS 300  
Qy 301 QMYENILHQLIPIGGRVTAACDQLQLLHKDQORLGSKADFLFIKNHVFVFFSPINWDDL 360  
Db 301 QMYENILHQLIPIGGRVTAACDQLQLLHKDQORLGSKADFLFIKNHVFVFFSPINWDDL 360  
Qy 361 YHKELTPPENVTGPADLKHFDPEFTQEAIVSKSIGCTPTDVASSSGASSAFLGFSVAPE 420  
Db 361 YHKELTPPENVTGPADLKHFDPEFTQEAIVSKSIGCTPTDVASSSGASSAFLGFSVAPE 420  
Qy 421 DDDILDC 427  
Db 421 DDDILDC 427

RESULT 3

ID ADA05780 standard; protein; 398 AA.  
AC ADA05780;

06-NOV-2003 (first entry)

Human NOV33a protein SEQ ID NO:140.

KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;  
KW immunomodulator; cytosolic; nootropic; neuroprotective;  
KW antiparkinsonian; antilipemic; gene therapy; human disease;  
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;  
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;  
KW immune disorder; haematopoietic disorder; dyslipidaemia.

OS Homo sapiens.

PN WO2003029424-A2.

XX 10-APR-2003.

PD 02-OCT-2002; 2002WO-US031373.

XX 02-OCT-2001; 2001US-0326483P.

PR 05-OCT-2001; 2001US-0327435P.

PR 05-OCT-2001; 2001US-0327449P.

PR 09-OCT-2001; 2001US-0327917P.

PR 09-OCT-2001; 2001US-0328029P.

PR 09-OCT-2001; 2001US-0328044P.

PR 09-OCT-2001; 2001US-0328056P.

PR 12-OCT-2001; 2001US-0328849P.

PR 15-OCT-2001; 2001US-0329414P.

PR 17-OCT-2001; 2001US-0330142P.

PR 18-OCT-2001; 2001US-0330309P.

PR 22-OCT-2001; 2001US-0341058P.

PR 24-OCT-2001; 2001US-0339266P.

PR 29-OCT-2001; 2001US-0343629P.

PR 01-NOV-2001; 2001US-0349575P.

PR 17-APR-2002; 2002US-0346357P.

PR 19-APR-2002; 2002US-0373815P.

PR 19-APR-2002; 2002US-0373817P.

PR 01-OCT-2002; 2002US-00262511.

XX (CURA-) CURAGEN CORP.

XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;

PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;

PI Ort T, Gorman L, Zehrusen BD, Anderson DW, Zhong M, Catterton E;

PI Ji W, Miller CB, Rastelli L, Stone DJ, Pena CE, Shenoy SG;

PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;

PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

XX WPI; 2003-381626/36.

DR N-PSDB; ADA05779.

XX New NOVX polypeptides and nucleic acids, useful for diagnosing,

PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,

PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or

PT pharmacogenomics.

XX Claim 1; Page 219; 586pp; English.

XX The present invention describes NOVX proteins, where X can be 1 to 55

CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide

CC described above and a carrier; (2) a kit comprising, in one or more

CC containers, the composition described above; (3) an isolated nucleic acid

CC molecule which encodes a NOVX protein of the invention; (4) a vector

CC comprising the nucleic acid molecule described above; (5) a cell

CC comprising the above vector; (6) an antibody that immunospecifically

CC binds to the polypeptide described above; (7) methods for determining the

CC presence or amount of the above polypeptide or nucleic acid molecule in a

CC sample; (8) methods for determining the presence of or predisposition to

CC a disease associated with altered levels of expression of the above

CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a

CC method of identifying an agent that binds to the polypeptide described

CC above; (10) a method for identifying a potential therapeutic agent for

CC use in treating a pathology that is related to an aberrant expression or

CC aberrant physiological interactions of the polypeptide; (11) a method of

CC screening for a modulator of activity or of latency or predisposition to

CC a pathology associated with the polypeptide; (12) a method for modulating

CC or preventing a pathology associated with the above polypeptide in a

CC mammal; and (14) a method for producing the above polypeptide. NOVX

CC sequences have antidiabetic, anorectic, antibacterial, virucide,

CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian

CC and antilipemic activities, and can be used in gene therapy. The

CC polypeptide is useful in manufacturing a medicament for treating a

CC syndrome associated with a human disease. The polypeptide or the nucleic

CC acid molecule may be used to diagnose, treat or prevent metabolic

CC disorders such as diabetes or obesity, infections, cachexia, cancer,

CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's

CC disease, immune disorders, haematopoietic disorders and various

CC dyslipidaemias. The nucleic acids can also be used as hybridisation

CC probes, in chromosome mapping, tissue typing, preventive medicine and

CC pharmacogenomics. The present sequence represents a human NOVX from the

XX present invention.

XX Sequence 398 AA;

XX Query Match 91.9%; Score 2124.5; DB 6; Length 398;

XX Best Local Similarity 93.2%; Pred. No. 1.8e-185;

XX Matches 398; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

Qy 1 MQGLLTSGRKPSGGGRCCTGRGWGQWCLKPNWGGADPPTTSCLLLPPELPDHCYR 60

Db 1 MQGLLTSGRKPSGGGRCCTGRGWGQWCLKPNWGGADPPTTSCLLLPPELPDHCYR 60

Qy 61 MNSSPAGTSPQPSRANGINILGPSANPNAQPTDFDLKVIKGNYGKVLAKRKSDGAF 120

Db 61 MNSSPAGTSPQPSRANGINILGPSANPNAQPTDFDLKVIKGNYGKVLAKRKSDGAF 120

Qy 121 YAVKVLQKKSILKKKESQSHIMAERSVLLKNVRHFFLVGLRYSFQTPEKLYFVLDYNGGE 180

Db 121 YAVKVLQKKSILKKKESQSHIMAERSVLLKNVRHFFLVGLRYSFQTPEKLYFVLDYNGGE 180





CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious  
CC disease, anorexia, cancer, cancer-associated cachexia, immunodegenerative  
CC disorders, Alzheimer's Disease, Parkinson's Disease, immune disorders,  
CC haematopoietic disorders, and the various dyslipidaemias, metabolic  
CC disturbances associated with obesity, the metabolic syndrome X and  
CC wasting disorders associated with chronic diseases and various cancers.  
CC They may also be used as antibacterial agents. The present sequence  
CC represents the amino acid sequence of a human NOVX protein.  
XX  
SQ Sequence 398 AA;

Query Match 90.6%; Score 2094.5; DB 8; Length 398;  
Best Local Similarity 92.3%; Pred. No. 9.8e-183;  
Matches 394; Conservative 1; Mismatches 3; Indels 29; Gaps 1;

QY 1 MOGLTSGRPGSGGRCGTGRGWGQCLKPMWGDADPTTSLCLLPVPPPELPHCYR 60  
DB 1 MOGLTSGRPGSGGRCGTGRGWGQCLKPMWGDADPTTSLCLLPVPPPELPHCYR 60  
QY 61 MNSSPAGTSPQPSRANGNINLGPSANPNAPQTDFFLKVIGKNGYGVLLAKKSDGAF 120  
DB 61 MNSSPAGTSPQPSRANGNINLGPSANPNAPQTDFFLKVIGKNGYGVLLAKKSDGAF 120  
QY 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFOTPEKLYFVLDYNGGE 180  
DB 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFOTPEKLYFVLDYNGGE 180  
QY 181 LFPHLOQRERFLPRAPRYAAEVASATGYLHSLNIIYRDLKPNILDDCQHVLTDFGL 240  
DB 181 LFPHLOQRERFLPRAPRYAAEVASATGYLHSLNIIYRDLKPNILDDCQHVLTDFGL 240  
QY 241 CKEGVEPEDTTSTFCGTPPEYLAPEVLRKEPVDRAVDMWCLGAVLYEMLHGLPPYSQDVS 300  
DB 231 -----YLAPEVLRKEPVDRAVDMWCLGAVLYEMLHGLPPYSQDVS 271  
QY 301 QMVENILHQLPIPGGRTVAACDLQLLHKDQRLGSKADFLKKNHVFVFPINWDDL 360  
DB 272 QMVENILHQLPIPGGRTVAACDLQLLHKDQRLGSKADFLKKNHVFVFPINWDDL 331  
QY 361 YHKLRLPPNPNTGADLKHDFEFTQEAUVSKSIGCTPDTVASSGASSAFIGFSVAPE 420  
DB 332 YHKLRLPPNPNTGADLKHDFEFTQEAUVSKSIGCTPDTVASSGASSAFIGFSVAPE 391  
QY 421 DDILDC 427  
DB 392 DDILDC 398

## RESULT 5

AAM25594

ID AAM25594 standard; protein; 382 AA.

XX AC AAM25594;

XX 16-OCT-2001 (first entry)

DT Human protein sequence SEQ ID NO:1109.

DE

XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;

KW anti-inflammatory; antirheumatic; antiarthritic; immunosuppressive;

KW antibacterial; endocrine; cardiac; central nervous system; virucide;

KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;

KW antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;

KW dermatological; aniallergic; antiaesthetic; antidiabetic; cyostatic;

KW neuroprotective; antidepressant; neurotropic; antiparkinsonian; infection;

KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;

KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;

KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;

KW genetic disease; haematopoietic disorder; platelet disorder; asthma;

KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;

KW allergic rhinitis; diabetes; multiple sclerosis; depression;

KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;

KW neurological disorder.

XX

OS Homo sapiens.

XX WO200153455-A2.

XX 26-JUL-2001.

XX 22-DEC-2000; 2000MO-US035017.

XX 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-00488725.

XX 25-APR-2000; 2000US-00552317.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-457603/49.

XX N-PSDB; AAH99535.

XX Isolated human polynucleotides encoding polypeptides, useful for the

XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection.

XX Claim 20; Page 227; 1217pp; English.

XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to

XX AAM25963. The proteins can have activities based on the tissues and cells

XX they are expressed in, such as: antiinflammatory; antirheumatic;

XX central nervous system; virucide; anti-HIV; fungicide; antimutagen;

XX cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;

XX antiulcer; osteopathic; dermatological; antiallergic; antiaesthetic;

XX antidiabetic; cyostatic; neuroprotective; antidepressant; neurotropic;

XX antiparkinsonian; and immunostimulant. The proteins and polynucleotides

XX encoding them can be used in gene therapy, antisense therapy and vaccine

XX production. The proteins and polynucleotides are useful for screening for

XX agonists or antagonists of a protein and for the treatment and diagnosis

XX of disorders associated with the activity of a protein e.g. inflammation,

XX rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,

XX neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal

XX infections, autoimmunity, genetic diseases, haematopoietic disorders,

XX anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,

XX osteoporosis, severe combined immunodeficiency, eczema, allergic

XX rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,

XX Alzheimer's disease, Parkinson's disease, neurodegenerative and

XX neurological disorders

XX SQ Sequence 382 AA;

Query Match 86.8%; Score 2005; DB 4; Length 382;

Best Local Similarity 100.0%; Pred. No. 1.5e-174; Indels 0; Gaps 0;

Matches 375; Conservative 0; Mismatches 0;

QY 53 ELPDHCYRMNSPAGTSPQPSRANGNINLGPSANPNAPQTDFFLKVIGKNGYGVLLA 112

DB 8 ELPDHCYRMNSPAGTSPQPSRANGNINLGPSANPNAPQTDFFLKVIGKNGYGVLLA 67

QY 113 KRKSDGAFYAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFOTPEKLYFV 172

DB 68 KRKSDGAFYAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFOTPEKLYFV 127

QY 173 LDVYNGGELFFHLOQRERRFLPRAPRYAAEVASATGYLHSLNIIYRDLKPNILDDCQH 232

DB 128 LDVYNGGELFFHLOQRERRFLPRAPRYAAEVASATGYLHSLNIIYRDLKPNILDDCQH 187

QY 233 VVLTDFGLCKEGVEPEDTTSTFCGTPPEYLAPEVLRKEPVDRAVDMWCLGAVLYEMLHGLP 292

DB 188 VVLTDFGLCKEGVEPEDTTSTFCGTPPEYLAPEVLRKEPVDRAVDMWCLGAVLYEMLHGLP 247

QY 293 PFYSQDVSQMYENILHQLPIPGGRTVAACDLQLLHKDQRLGSKADFLKKNHVFV 352

DB 248 PFYSQDVSQMYENILHQLPIPGGRTVAACDLQLLHKDQRLGSKADFLKKNHVFV 307



CC methods of activating SGK activity by phosphorylation using 3-phosphoinositide-dependent protein kinase-1 (PDK1), and of reducing the activity of SGK by dephosphorylation. The invention also provides a method of identifying a compound that modulates the activity of SGK. Such compounds are useful for treating patients requiring modulation of SGK, such as patients with cancer, diabetes or ischaemic disease

XX Seq Sequence 367, AA;

Query Match 84.6%; Score 1954; DB 3; Length 367;  
Best Local Similarity 100.0%; Pred. No. 6.5e-170;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 MNSSPAGTSPQPSRANGNINLPSANPNAQPTDFDLKVIKGNKGVLLAKRKSQDGF 120  
Db 1 MNSSPAGTSPQPSRANGNINLPSANPNAQPTDFDLKVIKGNKGVLLAKRKSQDGF 60  
Qy 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYNGGE 180  
Db 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYNGGE 120  
Qy 181 LFFHLQRRERFLEPRARFYAAEVAASAIYGLHSLNIIYRDLKPNILLDCQGHVLTDFGL 240  
Db 121 LFFHLQRRERFLEPRARFYAAEVAASAIYGLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180  
Qy 241 CKEGVEPEDTTSTFCGTPPEYLAPVLRKEPYDRAVDWVWCLGAVLYEMLHGLPPFYSQDVS 300  
Db 181 CKEGVEPEDTTSTFCGTPPEYLAPVLRKEPYDRAVDWVWCLGAVLYEMLHGLPPFYSQDVS 240  
Qy 301 QMVENILHQLPQTGGRTVAACDLQLLHKDQORLGSKADFLIEIKNHYFFSPINWDDL 360  
Db 241 QMVENILHQLPQTGGRTVAACDLQLLHKDQORLGSKADFLIEIKNHYFFSPINWDDL 300  
Qy 361 YHKRLTPFPNPNVTGPADLKHDFEFTQEAIVSKSIGCTPDTVASSGSAFGLGFSVAPE 420  
Db 301 YHKRLTPFPNPNVTGPADLKHDFEFTQEAIVSKSIGCTPDTVASSGSAFGLGFSVAPE 360  
Qy 421 DDDILDC 427  
Db 361 DDDILDC 367

RESULT 8  
AAU28087  
ID AAU28087 standard; protein; 367 AA.  
XX AAU28087;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Novel human secretory protein, Seq ID No 256.  
XX

KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;  
KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;  
KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;  
KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;  
KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;  
KW gut protection; lung; liver fibrosis; immune deficiency; infection;  
KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;  
KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;  
XX fertility; analgesic; pain; antigen.  
OS Homo sapiens.  
XX  
PN WO200166689-A2.  
XX  
PD 13-SEP-2001.  
XX  
XX 05-MAR-2001; 2001WO-US0004942.  
XX  
XX 07-MAR-2000; 2000US-00519705.  
PR 19-MAY-2000; 2000US-00574454.  
PR 17-JUN-2000; 2000US-00596193.

PR 14-JUL-2000; 2000US-00616847.  
PR 19-SEP-2000; 2000US-00665363.  
PR 20-OCT-2000; 2000US-00693267.  
XX  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;  
PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;  
XX  
XX WPI; 2001-589934/66.  
DR N-PSDB; AAS44987.  
XX

Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders.

Example 4; SEQ ID NO 256; 107pp; English.

XX The invention relates to novel isolated human secreted polypeptides (I) and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopoiesis, stem cell survival, bone growth and remodeling. (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis. In addition, (I) is involved in chemotactic or chemokinetic activity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (I) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, SCID, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (I) affects biorhythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAU28020-AAU28395 represent novel human secreted protein amino acid sequences of the invention

XX Seq Sequence 367 AA;

Query Match 84.6%; Score 1954; DB 4; Length 367;  
Best Local Similarity 100.0%; Pred. No. 6.5e-170;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 MNSSPAGTSPQPSRANGNINLPSANPNAQPTDFDLKVIKGNKGVLLAKRKSQDGF 120  
Db 1 MNSSPAGTSPQPSRANGNINLPSANPNAQPTDFDLKVIKGNKGVLLAKRKSQDGF 60  
Qy 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYNGGE 180  
Db 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYNGGE 120  
Qy 181 LFFHLQRRERFLEPRARFYAAEVAASAIYGLHSLNIIYRDLKPNILLDCQGHVLTDFGL 240  
Db 121 LFFHLQRRERFLEPRARFYAAEVAASAIYGLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180  
Qy 241 CKEGVEPEDTTSTFCGTPPEYLAPVLRKEPYDRAVDWVWCLGAVLYEMLHGLPPFYSQDVS 300  
Db 181 CKEGVEPEDTTSTFCGTPPEYLAPVLRKEPYDRAVDWVWCLGAVLYEMLHGLPPFYSQDVS 240

QY 301 QMYENILHQLOIPGGRTVAACDLQSLHLKQORQLGSKADFLKINKNHVFFSPINWDDL 360  
DB 241 QMYENILHQLOIPGGRTVAACDLQSLHLKQORQLGSKADFLKINKNHVFFSPINWDDL 300  
QY 361 YHKRLTPPPNPNTGPDADLKHPDFTQEAHSVKSIGCTPDTVASSGASSAFLGFSYAPE 420  
DB 301 YHKRLTPPPNPNTGPDADLKHPDFTQEAHSVKSIGCTPDTVASSGASSAFLGFSYAPE 360  
QY 421 DDDILDC 427  
DB 361 DDDILDC 367  
RESULT 9  
AAE22765  
ID AAE22765 standard; protein; 367 AA.  
XX  
AC AAE22765;  
XX  
DT 09-AUG-2002 (first entry)  
XX  
DE Human serum and glucocorticoid-induced protein kinase, SGK2-alpha.  
XX  
KW Human; cytostatic; antisense gene therapy; screening; protein kinase;  
KW cancer; liver; colon; tumour; inflammation; arthritic synovium; enzyme;  
KW serum and glucocorticoid-induced protein kinase; SGK2-alpha.  
XX  
OS Homo sapiens.  
XX  
PN WO200224947-A2.  
XX  
PD 28-MAR-2002.  
XX  
PF 20-SEP-2001; 2001WO-IB002237.  
XX  
PR 20-SEP-2000; 2000US-0233999P.  
PR 02-OCT-2000; 2000US-0237419P.  
PR 02-OCT-2000; 2000US-0237423P.  
PR 04-OCT-2000; 2000US-0238588P.  
PR 10-MAY-2001; 2001US-0290555P.  
XX  
PA (KINE-) KINETEK PHARM INC.  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
XX  
XX  
XX Yoganathan T; Delaney AD;  
XX  
XX WPI: 2002-394145/42.  
DR N-PSDB; AAD36141.  
XX  
XX  
PT Diagnosing cancer, comprises determining the upregulation of expression  
PT of a nucleic acid sequence encoding a protein kinase or upregulation of  
PT expression of the protein kinase, in the cancer.  
XX  
XX  
PS Claim 1; Page 66-67; 87pp; English.  
XX  
CC The invention relates to a method for screening biologically active agent  
CC that modulates cancer associated protein kinase function. The invention  
CC also relates to a method for diagnosing cancer comprising determining the  
CC upregulation of expression of a nucleic acid sequence encoding a protein  
CC kinase. The method is useful for diagnosing cancer. A protein kinase is  
CC useful for screening biological agents that modulate cancer associated  
CC protein kinase function. Downregulating the activity of protein kinase is  
CC useful for inhibiting the growth of a cancer cell, e.g. liver or colon  
CC cancer. A nucleic acid encoding protein kinase is useful to screen biopsy  
CC derived tumours and inflammatory samples such as arthritic synovium, for  
CC amplified DNA in the cell or increased expression of corresponding mRNA  
CC or protein and is also useful to detect differences in expression levels  
CC such as molecular weight, amino acid and nucleotide sequences between the  
CC two cells. The present sequence is human serum and glucocorticoid-induced  
CC protein kinase, SGK2-alpha  
XX  
XX Sequence 367 AA;

Query Match 84.6%; Score 1954; DB 5; Length 367;  
Best Local Similarity 100.0%; Pred. No. 6.5e-170;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 61 MNSSPAGTSPSPSRANGNINIGPSANPNAQPTDFDLKVIKGNYGKVLAKRKSDGAF 120  
DB 1 MNSSPAGTSPSPSRANGNINIGPSANPNAQPTDFDLKVIKGNYGKVLAKRKSDGAF 60  
QY 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYNGGE 180  
DB 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYNGGE 120  
QY 181 LFFHLQRRRFLPRARFYAAEVASAIYGLHLSINIYRDLPENILLLDCQGHVLTDFGL 240  
DB 121 LFFHLQRRRFLPRARFYAAEVASAIYGLHLSINIYRDLPENILLLDCQGHVLTDFGL 180  
QY 241 CKEGVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLPPFYSQDVS 300  
DB 181 CKEGVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLPPFYSQDVS 240  
QY 301 QMYENILHQLOIPGGRTVAACDLQSLHLKQORQLGSKADFLKINKNHVFFSPINWDDL 360  
DB 241 QMYENILHQLOIPGGRTVAACDLQSLHLKQORQLGSKADFLKINKNHVFFSPINWDDL 300  
QY 361 YHKRLTPPPNPNTGPDADLKHPDFTQEAHSVKSIGCTPDTVASSGASSAFLGFSYAPE 420  
DB 301 YHKRLTPPPNPNTGPDADLKHPDFTQEAHSVKSIGCTPDTVASSGASSAFLGFSYAPE 360  
QY 421 DDDILDC 427  
DB 361 DDDILDC 367  
RESULT 10  
ADD45799  
ID ADD45799 standard; protein; 367 AA.  
XX  
AC ADD45799;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human Protein XP\_009494, SEQ ID NO 11468.  
XX  
KW Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
OS Homo sapiens.  
XX  
PN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX  
XX WPI: 2003-268312/26.  
DR GENEANK; XP\_009494.  
XX  
XX New composition comprising two or more isolated polypeptides, useful for  
XX preparing a medicament for treating pain in an animal.  
PS Claim 1; Page; 1017pp; English.  
XX

CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 367 AA;

Query Match 84.6%; Score 1954; DB 7; Length 367;  
Best Local Similarity 100.0%; Pred. No. 6.5e-170;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 MNSSPAGTSPQPSRANGNINLGSANPNAQPTDFDLKVGKNGYKVLAKRKSQDGF 120  
DB 1 MNSSPAGTSPQPSRANGNINLGSANPNAQPTDFDLKVGKNGYKVLAKRKSQDGF 60  
QY 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLVDYNGGE 180  
DB 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLVDYNGGE 120  
QY 181 LFFHLQRRERFLPRARFYAAEVAASAIYGLHSLNIIYRDLKPNILLDCQGHVLTDFGL 240  
DB 121 LFFHLQRRERFLPRARFYAAEVAASAIYGLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180  
QY 241 CKEGVEPEDTSTFCGTPEYLAPEVRKEPYDRAVDWMCGLGAVLYEMLHGLPPFYSDVDS 300  
DB 181 CKEGVEPEDTSTFCGTPEYLAPEVRKEPYDRAVDWMCGLGAVLYEMLHGLPPFYSDVDS 240  
QY 301 QMYENILHQLQIPGGRTVAACDLQSLHLKQORQLGSKADFLKKNHVFSPINWDDL 360  
DB 241 QMYENILHQLQIPGGRTVAACDLQSLHLKQORQLGSKADFLKKNHVFSPINWDDL 300  
QY 361 YHKRLTPPPNPVNTGADLKHFDPPTQEAVSKSIGCTPTDVASSSGASSAFGLGFSYAPE 420  
DB 301 YHKRLTPPPNPVNTGADLKHFDPPTQEAVSKSIGCTPTDVASSSGASSAFGLGFSYAPE 360  
QY 421 DDILDC 427  
DB 361 DDILDC 367

RESULT 11

ID ADI29317  
AC ADI29317 standard; protein; 367 AA.  
XX ADI29317;  
XX ADI29317;  
DT 22-APR-2004 (first entry)  
XX Human MARK3-associated protein #87.  
XX

KW Human; antisense gene therapy; MARK3;  
KW MAP/microtubule affinity-regulating kinase 3; cancer;  
KW Alzheimer's disease; neurodegenerative disorder;  
KW hyperproliferative disorder; cytostatic.

OS Homo sapiens.

XX US2003232771-A1.

XX 18-DEC-2003.

XX 17-JUN-2002; 2002US-00174319.

XX 17-JUN-2002; 2002US-00174319.

PA (ISIS-) ISIS PHARM INC.

PI Ward DT, Freier SM, Dobie KW;

XX WPI; 2004-052188/05.

DR N-PSDB; ADI29435.

XX New antisense compound targeted to a nucleic acid molecule encoding  
PT microtubule-affinity-regulating kinases (MARK3), useful for modulating  
PT expression of MARK3 or for treating cancer or Alzheimer's disease.

XX Disclosure; SEQ ID NO 237; 233pp; English.

XX The invention relates to a compound comprising a sequence comprising 8-80  
CC base pairs (bp) targeted to a nucleic acid encoding MARK3  
CC (MAP/microtubule affinity-regulating kinase 3), that specifically  
CC hybridizes with the nucleic acid encoding MARK3 and inhibits expression  
CC of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a  
CC composition comprising the compound and a carrier or diluent, inhibiting or  
CC the expression of MARK3 in cells or tissues, treating an animal having or  
CC suspected of having a disease or condition associated with MARK3 and  
CC screening for an antisense compound. The antisense oligonucleotide is  
CC useful for preparing a composition for treating hyperproliferative  
CC disorder, particularly cancer and neurodegenerative diseases e.g.  
CC Alzheimer's disease. The present sequence is a MARK3 associated protein  
CC included in the figures but not mentioned anywhere else in the  
CC specification.

XX SQ Sequence 367 AA;

Query Match 84.6%; Score 1954; DB 8; Length 367;  
Best Local Similarity 100.0%; Pred. No. 6.5e-170;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 MNSSPAGTSPQPSRANGNINLGSANPNAQPTDFDLKVGKNGYKVLAKRKSQDGF 120  
DB 1 MNSSPAGTSPQPSRANGNINLGSANPNAQPTDFDLKVGKNGYKVLAKRKSQDGF 60  
QY 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLVDYNGGE 180  
DB 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLVDYNGGE 120  
QY 181 LFFHLQRRERFLPRARFYAAEVAASAIYGLHSLNIIYRDLKPNILLDCQGHVLTDFGL 240  
DB 121 LFFHLQRRERFLPRARFYAAEVAASAIYGLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180  
QY 241 CKEGVEPEDTSTFCGTPEYLAPEVRKEPYDRAVDWMCGLGAVLYEMLHGLPPFYSDVDS 300  
DB 181 CKEGVEPEDTSTFCGTPEYLAPEVRKEPYDRAVDWMCGLGAVLYEMLHGLPPFYSDVDS 240  
QY 301 QMYENILHQLQIPGGRTVAACDLQSLHLKQORQLGSKADFLKKNHVFSPINWDDL 360  
DB 241 QMYENILHQLQIPGGRTVAACDLQSLHLKQORQLGSKADFLKKNHVFSPINWDDL 300  
QY 361 YHKRLTPPPNPVNTGADLKHFDPPTQEAVSKSIGCTPTDVASSSGASSAFGLGFSYAPE 420  
DB 301 YHKRLTPPPNPVNTGADLKHFDPPTQEAVSKSIGCTPTDVASSSGASSAFGLGFSYAPE 360

QY 421 DDILDC 427  
 Db 361 DDILDC 367

RESULT 12  
 ADJ45521  
 ID ADJ45521 standard; protein; 367 AA.  
 AC  
 AC ADJ45521;  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE LXR-ligand induced transcript seq id 52.  
 XX  
 KW LXR; liver X receptor; cholesterol; gallstone; atherosclerosis;  
 KW lipid storage disease; obesity; diabetes; hypercholesterolaemia;  
 KW LXR-ligand induced 1; LXRL1; human; LXR-ligand induced transcript;  
 KW LXR regulated gene.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004023276-A1.  
 XX  
 PD 05-FEB-2004.  
 XX  
 PF 02-MAY-2003; 2003US-00429160.  
 XX  
 PR 03-MAY-2002; 2002US-0377714P.  
 XX  
 PA (WARD/) WARD T R.  
 PA (MAOM/) MAO M.  
 PA (LINS/) LINSLEY P S.  
 PA (LUND/) LUND E.  
 XX  
 PI Ward TR, Mao M, Linsley PS, Lund E;  
 XX  
 DR WPI; 2004-224687/21.  
 DR N-PSDB; ADJ45520.  
 XX  
 PT New purified Liver X receptor (LXR) nucleic acids, useful for diagnosing  
 PT a disease involving LXR activity, such as cholesterol gallstones,  
 PT atherosclerosis, lipid storage diseases, obesity, diabetes, or  
 PT hypercholesterolemia.  
 XX  
 PS Example 1; SEQ ID NO 52; 141pp; English.  
 XX  
 CC The invention describes a purified nucleic acid comprising a fully  
 CC defined sequence of 1586 bp (SEQ ID NO: 1) as given in the specification,  
 CC or its complement. The methods and compositions are useful for diagnosing  
 CC a disease or disorder involving LXR (liver X receptor) activity in a  
 CC sample by detecting an increase or decrease in the transcript level  
 CC relative to the amount present in an analogous sample from a subject not  
 CC having the disease or disorder or not subjected to therapy, wherein the  
 CC disease or disorder is cholesterol gallstones, atherosclerosis, lipid  
 CC storage diseases, obesity, diabetes, or hypercholesterolemia. They are  
 CC also used to identify a compound that changes LXR activity, wherein the  
 CC compound changes the estimated level of LXR activity in a sample from the  
 CC subject contacted with the compound relative to the estimated level of  
 CC LXR activity in an analogous sample from the subject not contacted with  
 CC the compound. This is the amino acid sequence of an LXR regulated  
 CC protein.

QY 61 MNSSPAGTPSPQPSRANGNINLGPSPNPAQPTDFDLKVGKNGYKVLAKRKSDFGAF 120  
 Db 1 MNSSPAGTPSPQPSRANGNINLGPSPNPAQPTDFDLKVGKNGYKVLAKRKSDFGAF 60

Query Match 84.6%; Score 1954; DB 8; Length 367;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-170;  
 Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 YAVKVLQKSIILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLQVYNGGE 180  
 Db 61 YAVKVLQKSIILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLQVYNGGE 120

QY 181 LFFHLQRRRRFLEPRARFYAAEVASAIQYLHLSNIITYRDLKPENIILLDCQGHVVLTDFFGL 240  
 Db 121 LFFHLQRRRRFLEPRARFYAAEVASAIQYLHLSNIITYRDLKPENIILLDCQGHVVLTDFFGL 180

QY 241 CKEGVEPEDTTSTFCGTPEYLAPVLRKEPYDRAVDWMCIGAVLYEMLHGLPPFYQDVVS 300  
 Db 181 CKEGVEPEDTTSTFCGTPEYLAPVLRKEPYDRAVDWMCIGAVLYEMLHGLPPFYQDVVS 240

QY 301 OMVENILHQPLOIPGGRVTAAACDLQSLHKKORQLGSKADPFLKTNHFFSPINWDDL 360  
 Db 241 OMVENILHQPLOIPGGRVTAAACDLQSLHKKORQLGSKADPFLKTNHFFSPINWDDL 300

QY 361 YHKRLTTPPNPNVTGPAADLKHPDPEFTQEAIVSKSIGCTPDTVASSSGASSAFGLGFSYAPE 420  
 Db 301 YHKRLTTPPNPNVTGPAADLKHPDPEFTQEAIVSKSIGCTPDTVASSSGASSAFGLGFSYAPE 360

QY 421 DDILDC 427  
 Db 361 DDILDC 367

RESULT 13  
 AAB65708  
 ID AAB65708 standard; protein; 367 AA.  
 XX  
 AC AAB65708;  
 XX  
 DT 27-MAR-2001 (first entry)  
 XX  
 DE Novel protein kinase, SEQ ID NO: 237.  
 XX  
 KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;  
 KW immunosuppressive; cardiac; renal; antiinflammatory; antiasthmatic;  
 KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;  
 KW immune disorder; cardiovascular disease; neurodegenerative disease;  
 KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;  
 KW inflammatory pelvic disease; multiple sclerosis; psoriasis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200073469-A2.  
 XX  
 PD 07-DEC-2000.  
 XX  
 PF 26-MAY-2000; 2000WO-US014842.  
 XX  
 PR 28-MAY-1999; 99US-0136503P.  
 XX  
 PA (SUGB-) SUGEN INC.  
 XX  
 PI Plowman GD, Martinez R, Whyte D, Sudersanam S;  
 XX  
 DR WPI; 2001-032161/04.  
 DR N-PSDB; AAF44737.  
 XX  
 PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and  
 PT treating immune-related diseases and disorders, cardiovascular disease,  
 PT neurodegenerative diseases and/or cancers.  
 XX  
 PS Claim 10; Fig 1; 310pp; English.  
 XX  
 CC The present sequence is a novel protein kinase. The novel protein kinases  
 CC and the nucleic acids that encode them may be used in the treatment and  
 CC diagnosis of diseases associated with inappropriate kinase expression  
 CC such as immune-related diseases and disorders, cardiovascular disease,  
 CC neurodegenerative diseases and/or cancers. The nucleic acids and  
 CC complementary sequences may also be used as DNA probes in diagnostic  
 CC assays. The kinase polypeptides may be used as antigens in the production  
 CC of antibodies of kinase expression and activity. Anti-kinase antibodies

CC and kinase antagonists may also be used to down regulate kinase  
CC expression and activity. Diseases related to kinase expression and  
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune  
CC disorders, complications of organ transplantation, myocardial infarction,  
CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-  
CC stress related disorders, chronic inflammatory bowel disease, chronic  
CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,  
CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive  
CC disorders

XX Sequence 367 AA;

Query Match 84.5%; Score 1952; DB 4; Length 367;  
Best Local Similarity 99.7%; Pred. No. 9.9e-170;  
Matches 366; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 61 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVGKNGYGVLLAKKSDGAF 120  
DB 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVGKNGYGVLLAKKSDGAF 60  
QY 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFOTPEKLYFVLDYVNGGE 180  
DB 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFOTPEKLYFVLDYVNGGE 120  
QY 181 LFFHLQRRERFLEPRARFYAAEVAASAIYGLHSLNIIYRDLKPENILLDCQGHVVLTDGFL 240  
DB 121 LFFHLQRRERFLEPRARFYAAEVAASAIYGLHSLNIIYRDLKPENILLDCQGHVVLTDGFL 180  
QY 241 CKGEVPEDETTSTFCGTPEYLAPEVLKKEPYDRAVDMWCLGAVLYEMLHGLPPPYSDQVS 300  
DB 181 CKGEVPEDETTSTFCGTPEYLAPEVLKKEPYDRAVDMWCLGAVLYEMLHGLPPPYSDQVS 240  
QY 301 QMYENILHQPLOIPGGRVTAAACDLQSLHKKQRLGSKADFELEIKNHVFFSPINWDDL 360  
DB 241 QMYENILHQPLOIPGGRVTAAACDLQSLHKKQRLGSKADFELEIKNHVFFSPINWDDL 300  
QY 361 YHKELTPFPNPNVTGPADLKHDFDPEFTQEAUVSKSIGCTPTDVTASSSGASSAFLGFSYAPE 420  
DB 301 YHKELTPFPNPNVTGPADLKHDFDPEFTQEAUVSKSIGCTPTDVTASSSGASSAFLGFSYAPE 360  
QY 421 DDDILDC 427  
DB 361 DDDILDC 367

RESULT 14

AA95277  
ID AA95277 standard; protein; 367 AA.

XX AA95277;

XX 12-SEP-2000 (first entry)

XX Mouse serum and glucocorticoid-induced protein kinase 2.

XX Serum and glucocorticoid-induced protein kinase 2; SGK2; mouse;  
XX phosphorylation; cancer; diabetes; ischaemia; therapy.

XX Mus musculus.

XX WO200035946-A1.

XX 22-JUN-2000.

XX 14-DEC-1999; 99WO-GB004232.

XX 14-DEC-1998; 98US-0112217P.

XX 19-AUG-1999; 99GB-00019676.

XX (UYDU-) UNIV DUNDEE.

XX Cohen P, Kobayashi T, Deak M;

XX

DR WPI; 2000-442364/38.

XX Modulation of serum and glucocorticoid-induced protein kinase (SGK) by  
PT phosphorylation with 3-phosphoinositide-dependent protein kinase-1 (PDK1)  
PT or dephosphorylation, useful for treatment of cancer, diabetes and  
PT ischaemic diseases.

XX Disclosure; Page 7; 127pp; English.

XX The present sequence is that of mouse serum and glucocorticoid-induced  
CC protein kinase (SGK) isoform 2, a protein activated by phosphorylation.  
CC The invention provides methods of activating SGK (see also AAY95275-79)  
CC by phosphorylation using 3-phosphoinositide-dependent protein kinase-1  
CC (PDK1), and of reducing the activity of SGK by dephosphorylation. The  
CC invention also provides a method of identifying a compound that modulates  
CC the activity of SGK. Such compounds are useful for treating patients  
CC requiring modulation of SGK, such as patients with cancer, diabetes or  
CC ischaemic disease

XX Sequence 367 AA;

Query Match 80.0%; Score 1848; DB 3; Length 367;  
Best Local Similarity 94.3%; Pred. No. 3.3e-160;  
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 61 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVGKNGYGVLLAKKSDGAF 120  
DB 1 MASSPVGVPSQPSRANGNINLGPSANPNAQPTDFDLKVGKNGYGVLLAKKSDGAF 60  
QY 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFOTPEKLYFVLDYVNGGE 180  
DB 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFOTPEKLYFVLDYVNGGE 120  
QY 181 LFFHLQRRERFLEPRARFYAAEVAASAIYGLHSLNIIYRDLKPENILLDCQGHVVLTDGFL 240  
DB 121 LFFHLQRRERFLEPRARFYAAEVAASAIYGLHSLNIIYRDLKPENILLDCQGHVVLTDGFL 180  
QY 241 CKGEVPEDETTSTFCGTPEYLAPEVLKKEPYDRAVDMWCLGAVLYEMLHGLPPPYSDQVS 300  
DB 181 CKGEVPEDETTSTFCGTPEYLAPEVLKKEPYDRAVDMWCLGAVLYEMLHGLPPFNTDVA 240  
QY 301 QMYENILHQPLOIPGGRVTAAACDLQSLHKKQRLGSKADFELEIKNHVFFSPINWDDL 360  
DB 241 QMYENILHQPLOIPGGRVTAAACDLQSLHKKQRLGSKADFELEIKNHVFFSPINWDDL 300  
QY 361 YHKELTPFPNPNVTGPADLKHDFDPEFTQEAUVSKSIGCTPTDVTASSSGASSAFLGFSYAPE 420  
DB 301 YHKELTPFPNPNVTGPADLKHDFDPEFTQEAUVSKSIGCTPTDVTASSSGASSAFLGFSYAQD 360  
QY 421 DDDILD 426  
DB 361 DDDILD 366

RESULT 15

ADD45797  
ID ADD45797 standard; protein; 367 AA.

XX ADD45797;

XX 29-JAN-2004 (first entry)

XX Rat Protein AAF12756, SEQ ID NO 11466.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX



PF 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
XX (GEO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
XX Woolf C, D'urso D, Befort K, Costigan M;  
XX WPI; 2003-268312/26.  
DR GENBANK; AAF12756.  
XX  
XX New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
PT  
XX  
XX Claim 1; Page; 1017pp; English.  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. Gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 367 AA;

Query Match 80.0%; Score 1848; DB 7; Length 367;  
Best Local Similarity 94.3%; Pred. No. 3.3e-160;  
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 61 MNSSPACTPSPQPSRANGNINLGSANPNAPQTDDEFLKVIGKNGYKVLAKRKS DGAP 120  
DB 1 MASSPGVSPQPSRANGNINLGSANPNARPTDFELKVIGKNGYKVLAKRKS DGAP 60  
QY 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYVNGGE 180  
DB 61 YAVKVLQKKSILKNKEQHIMAERNVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYVNGGE 120  
QY 181 LFFHLQRRERFLPRARFYAAEVASAIQYUHSNIIYRDLKPNILLDCQGHVVLTD FGL 240  
DB 121 LFFHLQRRERFLPRARFYTAEVASAIQYUHSNIIYRDLKPNILLDCQGHVVLTD FGL 180  
QY 241 CKEGVEPDTTSTFCGTPPEYLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPPFYSDVVS 300  
DB 181 CKECVPEETSTSTFCGTPPEYLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPPFFNTDVA 240  
QY 301 QMYENILHQLQIPGGRTVAACDLQSLHKKQQRGLSKADFEIKNHVFFSPINWDDL 360  
DB 241 QMYENILHQLQIPGGRTVAACDLQGLLHKKQQRGLSKEDFLDIKNHMFSPINWDDL 300

QY 361 YHKRLTPPENPNVTGPADLKHFDPERTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 420  
DB 301 YHKRLTPPENPNVVEGPA DLKHFDPERTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAO D 360  
QY 421 DDDILD 426  
DB 361 DDDILD 366

Search completed: January 27, 2006, 23:26:44  
Job time : 79.0006 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:21:11 ; Search time 20.1415 Seconds  
(without alignments)  
1752.724 Million cell updates/sec

Title: US-09-868-131A-8

Perfect score: 2311

Sequence: 1 MQGLLTSGRKPSGGRCRTGR.....ASSAFLGFSYAPEDDDILDC 427

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pap.\*
- 2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pap.\*
- 3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pap.\*
- 4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pap.\*
- 5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pap.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1419	61.4	407	2	US-10-067-977-4
2	1419	61.4	445	2	US-10-067-977-2
3	1415	61.2	431	2	US-09-031-295-2
4	1415	61.2	431	2	US-10-000-039-2
5	1411.5	61.1	430	1	US-08-712-709-9
6	1411.5	61.1	430	2	US-09-111-444-9
7	1411.5	61.1	430	2	US-09-541-228-9
8	1411	61.1	431	1	US-08-712-709-5
9	1411	61.1	431	2	US-09-111-444-5
10	1411	61.1	431	2	US-09-541-228-5
11	891	38.6	479	2	US-09-771-161A-246
12	891	38.6	479	2	US-09-771-161A-247
13	891	38.6	479	2	US-09-771-161A-248
14	883.5	38.2	465	2	US-09-526-043-2
15	882.5	38.2	454	2	US-09-526-043-17
16	878.5	38.0	480	2	US-09-590-740-6
17	876	37.9	480	2	US-09-526-043-13
18	876	37.9	481	2	US-09-538-092-1054
19	874.5	37.8	480	2	US-09-091-058-2
20	874.5	37.8	480	2	US-09-590-740-2
21	874.5	37.8	480	2	US-09-538-092-1053
22	874.5	37.8	480	2	US-09-526-043-14
23	874.5	37.8	480	2	US-09-771-161A-223
24	874.5	37.8	726	2	US-09-417-197-71
25	874.5	37.8	727	2	US-09-417-197-139
26	856	37.0	417	2	US-09-590-740-4
27	849.5	36.8	480	2	US-09-205-658-157

28	844.5	36.5	470	2	US-09-248-796A-18482	Sequence 18482, A
29	801	34.7	637	2	US-09-817-310-2	Sequence 2, Appli
30	801	34.7	637	2	US-10-355-724A-2	Sequence 2, Appli
31	799.5	34.6	587	1	US-08-313-274-2	Sequence 2, Appli
32	799.5	34.6	655	2	US-09-949-016-11676	Sequence 11676, A
33	788.5	34.1	482	2	US-09-430-564-2	Sequence 2, Appli
34	788.5	34.1	495	2	US-09-430-564-3	Sequence 3, Appli
35	788.5	34.1	495	2	US-09-762-258-2	Sequence 2, Appli
36	788	34.1	546	2	US-09-205-658-155	Sequence 155, App
37	783.5	33.9	541	2	US-09-205-658-154	Sequence 154, App
38	782.5	33.9	502	2	US-09-538-092-996	Sequence 996, App
39	782.5	33.9	525	1	US-08-749-902-7	Sequence 7, Appli
40	782.5	33.9	525	1	US-08-749-902-8	Sequence 8, Appli
41	782.5	33.9	525	2	US-09-430-564-16	Sequence 16, Appli
42	782.5	33.9	525	2	US-09-762-258-4	Sequence 4, Appli
43	770	33.3	737	2	US-09-772-647-4	Sequence 4, Appli
44	770	33.3	737	2	US-10-328-931-4	Sequence 4, Appli
45	769	33.3	568	2	US-09-949-016-7970	Sequence 7970, Ap

ALIGNMENTS

RESULT 1

US-10-067-977-4

; Sequence 4, Application US/10067977

; Patent No. 6830911

; GENERAL INFORMATION:

; APPLICANT: YAN, Chunhua and KE, Zhaoxi

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; FILE REFERENCE: CL001313

; CURRENT APPLICATION NUMBER: US/10/067,977

; CURRENT FILING DATE: 2002-02-08

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 407

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-067-977-4

Query Match	61.4%	Score 1419	DB 2	Length 407;
Best Local Similarity	68.3%	Pred. No. 5.3e-125;		
Matches 267;	Conservative 56;	Mismatches 54;	Indels 14;	Gaps 4;
Qy	38	PPTFTLSCLLPVPPPELPHCYRMSSPAGTPSPQPSRANGNTINLGPSANPNAPQPTDFD	97	
Db	28	PEVQSILKISQPEPEL-----MNANP--SPPPSPSQ---QINLGSSNPHAKPSDFHF	76	
Qy	98	LKVIKGNVGVLLAKRKSDGAFYAVKVLQKKSILKKKESHIMAEKSVLLKNVRHPLV	157	
Db	77	LKVIKGNVGVLLAKRKSDGAFYAVKVLQKKSILKKKESHIMAEKSVLLKNVRHPLV	136	
Qy	158	GLRYSQTPTEKLFYLDVYNGGELPFHLQREERFLPRPRFYAEVASAIGYLHSLNIY	217	
Db	137	GLHFSQTDKLVFDVLDYNGGELFHLQREERFLPRPRFYAEVASAIGYLHSLNIY	196	
Qy	218	RLDKPENILLDCQGHVVLTDVGLCKEGVPEPTTSTFCGTPPEYLAPEVLKPEYDRAVDW	277	
Db	197	RLDKPENILLDSQGHVLTDFGLCKENIEHNSSTTFCGTPPEYLAPEVLKPEYDRTVDW	256	
Qy	278	WCLGAVLYEMHLGHPFFYQDVSMYENILHQLQIPGGRVTAACDLQLSLHKDQKRL	337	
Db	257	WCLGAVLYEMLYGLPPFFYSRNTAEYDNLINKLQLKPNITNSARHLLEGLLQDKTKRL	316	
Qy	338	GSKADFLKTNHVFSPINWDDLYHKRLTPPNPNVTGPADLKHFDPEFTQEA VSKSIGC	397	
Db	317	GAKDPEWIKSHVFFFLINWDDLLINKKITPPFPNPNVSGPNDLRHFDPEFTPEEPVPSIGK	376	
Qy	398	TPDVTV---ASSGASSAFLGFSYAPEDDDIL 425		

```
Db 377 SPDSVLVTASVKEAAEAFGLGFSYAPPTDSFL 407

RESULT 2
US-10-067-977-2
; Sequence 2, Application US/10067977
; Patent No. 6830911
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua and KE, Zhaoxi
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001313
; CURRENT APPLICATION NUMBER: US/10/067,977
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-977-2

Query Match 61.4%; Score 1419; DB 2; Length 445;
Best Local Similarity 68.3%; Pred. No. 6.1e-125;
Matches 267; Conservative 56; Mismatches 54; Indels 14; Gaps 4;

QY 38 PPTPTLSCLLLVPPELPDHCYMNSSPAGTSPQPSRANGNINLGPSPNNAQPTDFDF 97
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 66 PEVQSILKISQOEPEL-----MNAHP--SPPPSPSQ---QINLGFSSNPHAKPSDFHF 114
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 98 LKVIKGNKGVKLLAKRKSDGAFYAVKVLQKKSILKKKEQSHIMAEVSLLKNVRHPELV 157
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 115 LKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKKEKHIMSERVLLKNVKHPFLV 174
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 158 GLRYSQTPEKLYFVLDYVNGGELFFHLQRRERFLEPRARFYAAEVAASAIYGLHSLNIY 217
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 175 GLHFSQTADKLYFVLDYINGGELFYHLQRCFLPRARFYAAETASALYGLHSLNIY 234
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 218 RDLKPENILDCQGHVLTDFGLCKEGVEPEDTSTFCGTPEYLAPEVLKPEYDRAVDW 277
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 RDLKPENILDSQGHVLTDFGLCKENIEHNS--TSTFCGTPEYLAPEVLHKQPYDRTVDW 294
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 278 WCLGAVLYEMLHGLPPFYSDVSMYENILHQPLOIPGGRTVAACDLQSLHKKQORQL 337
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 295 WCLGAVLYEMLYGLPPFYSRNTAEYDNIILNKPLQKPNITNSARHLLGLLQKDRTKRL 354
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 338 GSKADFLKINHVFFSPINWDDLYHKRLTPFPNPNVTGPADLKHFPDPEFTQEAVSIGC 397
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 355 GAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNPNVSGPNDLHRHFDPEETEEFPVNSIGK 414
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 398 TPDTV---ASSSGASSAFGLGSYAPEDDDIL 425
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 415 SPDSVLVTASVKEAAEAFGLGFSYAPPTDSFL 445

RESULT 3
US-09-031-295-2
; Sequence 2, Application US/09031295
; Patent No. 6326181
; GENERAL INFORMATION:
; APPLICANT: LANG, Florian
; APPLICANT: WALDEGGER, Tubingen
; TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
```



Db	411	KEAAEAFLGFSYAPPMDSFL	430
<p>GENERAL INFORMATION:</p> <p>APPLICANT: Au-Young, Janice</p> <p>APPLICANT: Guegler, Karl J.</p> <p>APPLICANT: Hawkins, Phillip R.</p> <p>TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES</p> <p>NUMBER OF SEQUENCES: 9</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: Incyte Pharmaceuticals, Inc.</p> <p>STREET: 3174 Porter Drive</p> <p>CITY: Palo Alto</p> <p>STATE: CA</p> <p>COUNTRY: U.S.</p> <p>ZIP: 94304</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Diskette</p> <p>COMPUTER: IBM Compatible</p> <p>OPERATING SYSTEM: DOS</p> <p>SOFTWARE: FastSeq Version 1.5</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/09/111.444</p> <p>FILING DATE:</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: 08/712,709</p> <p>FILING DATE:</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Billings, Lucy J</p> <p>REGISTRATION NUMBER: 36,749</p> <p>REFERENCE/DOCKET NUMBER: PF-0118 US</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 415-855-0555</p> <p>TELEFAX: 415-845-4166</p> <p>INFORMATION FOR SEQ ID NO: 9:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 430 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: single</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: peptide</p> <p>IMMEDIATE SOURCE:</p> <p>LIBRARY: GenBank</p> <p>CLONE: 294637</p> <p>US-09-111-444-9</p>			
Qy	49	PVPPELPDHCYRMNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNYGK	108
Db	63	PQPELP-----MNANP--SPPPSPSQ--QINLGPSNPHAKPSDFHFLKVIKGSFGK	111
Qy	109	VLLAKRKSDGAFYAVKVLQKKSILKKKQSHIMAERSVLLKNVHPFLVGLRYSFQTPK	168
Db	112	VLLARHKAEEAFYAVKVLQKKAAILKKKEKHIMSERNVLLKNVHPFLVGLHFSFQADK	171
Qy	169	LYFVLVDYNGGELFPHLQRRERFLPRARFYAAEVAASAIGYLHSLNIIYRDLKPENILLD	228
Db	172	LYFVLVDYNGGELFPHLQRRERFLPRARFYAAEIASALGYLHSLNIIYRDLKPENILLD	231
Qy	229	CQGHVVLTDFGLCKEGVPEDTTSTFCGTPEYLAPEVLKRPYDRAVDWNCGLGAVLYEML	288
Db	232	SGQHIVLTDFGLCKENIEHNGTTSTFCGTPEYLAPEVLHQPYDRTVDWNCGLGAVLYEML	291
Qy	289	HGLPPFYSDVSQMYENILHQPQIPGGRTVAACDLQSLHKKOORQLGSKADFLKIN	348
Db	292	YGLPPFYSRNTAEYDNIINLKPLQK-NITNSARHLLGLLQKORTKRLGAKDDFMBIKS	350
Qy	349	HYFFPSINWDDLYHKELTPPNPNVTGADLKHPDPEFTQEAIVSKISCTPDTV---ASS	405
Db	351	HIFFLSINWDDLIINKKITPPFNPNVSGPSDLRHFDPEFTFVPVSSIGRSPDSLVTASV	410
Qy	406	SGASSAFLGFSYAPEDDDIL	425
<p>Query Match 61.1%; Score 1411.5; DB 2; Length 430;</p> <p>Best Local Similarity 69.7%; Pred. No. 2.9e-124;</p> <p>Matches 265; Conservative 56; Mismatches 44; Indels 15; Gaps 5;</p>			
Qy	49	PVPPELPDHCYRMNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNYGK	108
Db	63	PQPELP-----MNANP--SPPPSPSQ--QINLGPSNPHAKPSDFHFLKVIKGSFGK	111
Qy	109	VLLAKRKSDGAFYAVKVLQKKSILKKKQSHIMAERSVLLKNVHPFLVGLRYSFQTPK	168
Db	112	VLLARHKAEEAFYAVKVLQKKAAILKKKEKHIMSERNVLLKNVHPFLVGLHFSFQADK	171
Qy	169	LYFVLVDYNGGELFPHLQRRERFLPRARFYAAEVAASAIGYLHSLNIIYRDLKPENILLD	228
Db	172	LYFVLVDYNGGELFPHLQRRERFLPRARFYAAEIASALGYLHSLNIIYRDLKPENILLD	231
Qy	229	CQGHVVLTDFGLCKEGVPEDTTSTFCGTPEYLAPEVLKRPYDRAVDWNCGLGAVLYEML	288
Db	232	SGQHIVLTDFGLCKENIEHNGTTSTFCGTPEYLAPEVLHQPYDRTVDWNCGLGAVLYEML	291
Qy	289	HGLPPFYSDVSQMYENILHQPQIPGGRTVAACDLQSLHKKOORQLGSKADFLKIN	348
Db	292	YGLPPFYSRNTAEYDNIINLKPLQK-NITNSARHLLGLLQKORTKRLGAKDDFMBIKS	350
Qy	349	HYFFPSINWDDLYHKELTPPNPNVTGADLKHPDPEFTQEAIVSKISCTPDTV---ASS	405
Db	351	HIFFLSINWDDLIINKKITPPFNPNVSGPSDLRHFDPEFTFVPVSSIGRSPDSLVTASV	410
Qy	406	SGASSAFLGFSYAPEDDDIL	425

QY 349 HVFFSPINDDLVHKLTPFPNVTGPADLKHDFEFTQEA VSKSIGCTPDTV---ASS 405  
Db 351 HIFFSLINDDLINKKITPFPNVTGPNVSGPSDLRHFDFEFTPEEPVPSIGRSPDSILVTASV 410  
QY 406 SGASSAFGFSYAPEDDDIL 425  
Db 411 KEAAEAFGFSYAPPMDSFL 430  
RESULT 8  
US-08-712-709-5  
; Sequence 5, Application US/08712709  
; Patent No. 5863780  
; GENERAL INFORMATION:  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Hawkins, Phillip R.  
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/712,709  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0118 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 431 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE: Consensus  
US-08-712-709-5  
Query Match 61.1%; Score 1411; DB 1; Length 431;  
Best Local Similarity 68.0%; Pred. No. 3.3e-124;  
Matches 266; Conservative 56; Mismatches 55; Indels 14; Gaps 4;  
QY 38 PPTPTLSCULLPVPPPLPDHPCYRNMSSPAGTSPQSPSRANGINLGPSANPNAPQTFDFP 97  
Db 52 PEVQSIKISQPEPEL-----MNA NP--SPPPSPQ---QINLGPSNPHAKPSDFHF 100  
QY 98 LKVIKGNKGVLLAKRSDGAFYAVKVLQKKSILKKEQSHMAERSVLLKNVRHPLV 157  
Db 101 LKVIKGSFGKVLARHAEVYAVKVLQKKAAILKKKEKHIMSERVLLKNVRHPLV 160  
QY 158 GLYSFQTPKLYFVLDYVNGGELFFHLQRRRFLPRARFYAAEYASVAGVLSLNIY 217  
Db 161 GLHFSQTADLYFVLDYNGGELFYHLQRRCFLEPRARSYAAETASALGVLSLNIY 220  
QY 218 RDLKPNILLDCGHVLLTDFGLCKEGVEPDTTSTFCGTPPEYLAPEVLKRPYRADVM 277  
Db 221 RDLKPNILLDSQGHVLLTDFGLCKENIEHNSTTSTFCGTPPEYLAPEVLHQPYDRTVDW 280

QY 278 WCLGAVLYEMLHGLPPFYSDVSMYENILHOPLOIPGGRTVAACDLQSLHKKDQORL 337  
Db 281 WCLGAVLYEMLYGLPPFYSRNTAEWYDNLNKPLOLKPNTITSARHLLEGLLQKDRKRL 340  
QY 338 GSKADPLEIKNHVFFSPINWDDLYHKLTPFPNVTGPADLKHDFEFTQEA VSKSIGC 397  
Db 341 GAKDDFMEIKSHVFFSLINWDDLINKKITPFPNVTGPNVSGPNDLRHFDPEFTPEEPVNSIGK 400  
QY 398 TPDTV---ASSSGASSAFGFSYAPEDDDIL 425  
Db 401 SPDSVLVTASVKEAAEAFGFSYAPPTDSFL 431  
RESULT 9  
US-09-111-444-5  
; Sequence 5, Application US/09111444  
; Patent No. 6045792  
; GENERAL INFORMATION:  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Hawkins, Phillip R.  
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/111,444  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/712,709  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0118 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 431 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE: Consensus  
US-09-111-444-5  
Query Match 61.1%; Score 1411; DB 2; Length 431;  
Best Local Similarity 68.0%; Pred. No. 3.3e-124;  
Matches 266; Conservative 56; Mismatches 55; Indels 14; Gaps 4;  
QY 38 PPTPTLSCULLPVPPPLPDHPCYRNMSSPAGTSPQSPSRANGINLGPSANPNAPQTFDFP 97  
Db 52 PEVQSIKISQPEPEL-----MNA NP--SPPPSPQ---QINLGPSNPHAKPSDFHF 100  
QY 98 LKVIKGNKGVLLAKRSDGAFYAVKVLQKKSILKKEQSHMAERSVLLKNVRHPLV 157  
Db 101 LKVIKGSFGKVLARHAEVYAVKVLQKKAAILKKKEKHIMSERVLLKNVRHPLV 160

QY 158 GLRYSQTPKLYFVLDYVNGGELFPHLOBERFLEPRARFYAAEVASAIYGLHSLNIY 217  
DB 161 GLHFSQTDKLYFVLDYINGGELFYHLQRCFCLEPRARSYAAETASALYGLHSLNIY 220  
QY 218 RDLKPNILLDCQGHVVLTDGFLCKEGVEPEDTSTFCGTPEYLAPEVLKKEPYDRAVDW 277  
DB 221 RDLKPNILLDSQGHIVLTDGFLCKENIEHNTSTSTFCGTPEYLAPEVLKKEPYDRTVDW 280  
QY 278 WCLGAVLYEMLHGLPPFYSDVSQMYENILHQPLOGGRTVAACDLLOSLLHKDQORQL 337  
DB 281 WCLGAVLYEMLYGLPPFYSRNTAEMYDNILNKPLQLKPNITNSARHLLGGLQKDRTKRL 340  
QY 338 GSKADFLKIKNVHVFSPINWDDLKRLTPPNPNVTGRADLKHFPDPEFTQEAUSKISGC 397  
DB 341 GAKDDFMEIKSHVFFSLINWDDLKINKITPPFPNPNVSGNDLRFHDPPEFTPEEPVNSIGK 400  
QY 398 TPDTV---ASSSGASSAFLGFSYAPEDDDIL 425  
DB 401 SPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 431

## RESULT 10

US-09-541-228-5  
; Sequence 5, Application US/09541228  
; Patent No. 6232077  
; GENERAL INFORMATION:  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Hawkins, Phillip R.  
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA: US/09/541,228  
FILING DATE:  
PRIORITY APPLICATION DATA:  
FILING DATE:  
APPLICATION NUMBER: 08/712,709  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0118 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 431 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE: Consensus

## US-09-541-228-5

Query Match 61.1%; Score 1411; DB 2; Length 431;  
Best Local Similarity 68.0%; Pred. No. 3.3e-124;  
Matches 266; Conservative 56; Mismatches 55; Indels 14; Gaps 4;  
QY 38 PPTFTLSCLLLPVPELPDPHCYRMNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDF 97

DB 52 PEVQSILKISQOEPEL-----MNAHP--SPPPSPQ---QINLGSSNPHAKPSDFHF 100  
QY 98 LKVIKGNKYGVLLAKRKSDGAFYAVKVLQKKSILKKEQSHIMAERSVLLKNVRHPFLV 157  
DB 101 LKVIKGSFGVLLARHKAEEVFYAVKVLQKAILKKKEKHIMSERVLLKNVHPFLV 160  
QY 158 GLRYSQTPKLYFVLDYVNGGELFPHLOBERFLEPRARFYAAEVASAIYGLHSLNIY 217  
DB 161 GLHFSQTDKLYFVLDYINGGELFYHLQRCFCLEPRARSYAAETASALYGLHSLNIY 220  
QY 218 RDLKPNILLDCQGHVVLTDGFLCKEGVEPEDTSTFCGTPEYLAPEVLKKEPYDRAVDW 277  
DB 221 RDLKPNILLDSQGHIVLTDGFLCKENIEHNTSTSTFCGTPEYLAPEVLKKEPYDRTVDW 280  
QY 278 WCLGAVLYEMLHGLPPFYSDVSQMYENILHQPLOGGRTVAACDLLOSLLHKDQORQL 337  
DB 281 WCLGAVLYEMLYGLPPFYSRNTAEMYDNILNKPLQLKPNITNSARHLLGGLQKDRTKRL 340  
QY 338 GSKADFLKIKNVHVFSPINWDDLKRLTPPNPNVTGRADLKHFPDPEFTQEAUSKISGC 397  
DB 341 GAKDDFMEIKSHVFFSLINWDDLKINKITPPFPNPNVSGNDLRFHDPPEFTPEEPVNSIGK 400  
QY 398 TPDTV---ASSSGASSAFLGFSYAPEDDDIL 425  
DB 401 SPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 431

## RESULT 11

US-09-771-161A-246  
; Sequence 246, Application US/09771161A  
; Patent No. 6936450  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 246  
; LENGTH: 479  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-771-161A-246

Query Match 38.6%; Score 891; DB 2; Length 479;  
Best Local Similarity 48.5%; Pred. No. 3.4e-75;  
Matches 182; Conservative 55; Mismatches 100; Indels 38; Gaps 8;  
QY 60 RMNSSPAGTSPQPSRAN--GNINLGPSANPNAQPT--DFDFLKVIKGNKYGVLLAKRK 115  
DB 116 RMNCSPT-----SQIDNIGEEEMDASTTHHKRKTMDNDFYLLKLGKGTFGKVLVREK 168  
QY 116 SDGAFYAVKVLQKKSILKKEQSHIMAERSVLLKNVRHPFLVGLRYSFOTPEKLYFVLDY 175  
DB 169 ASGKYAMKILKEVIAKDEVAHTLTSRVLKNTKTRHPFLVSLKYSFOTKRLCFVMEY 227  
QY 176 VNGGELFPHLOBERFLEPRARFYAAEVASAIYGLHSLNIYRDLKPNILLDCQGHVVL 235  
DB 228 VNGGELFPHLSRERVSEDRTRYGAEIVSALDYLSHGKIVYEDLKENLMDKDGHIKI 287  
QY 236 TDFGLCKEGVEPEDTSTFCGTPEYLAPEVLKKEPYDRAVDWVWCLGAVLYEMLHGLPPFY 295  
DB 288 TDFGLCKEGITDAATMKTFCGTPEYLAPEVLENDYGRAVDWVWGLGVWVYEMMCGRLPFY 347  
QY 296 SDVSQMYENILHQPLOGGRTVAACDLLOSLLHKDQORQL--GSKADFLKIKNVHVFSP 354

Db 348 NQDEKLFELIMEDIKPPRTLSDDAKSLLSGLLIKDPNKRKLGCGPDPAKEIMRHSFFSG 407  
QY 355 INWDDLYHKRLTPPENNVNTPGADLKHFDPFTQEAIVSKSGCTPDTVASSSGASSAFLG 414  
Db 408 VNMQDVYDKKLVPPFKQVTSSETDTRYFDEEFT-----AQITITTP----- 448

QY 415 FSYAPE--DDILDC 427  
Db 449 ----PEKYDEGDMDC 459

## RESULT 12

US-09-771-161A-247

; Sequence 247, Application US/09771161A

; Patent No. 6936450

; GENERAL INFORMATION:

; APPLICANT: LEVINE, et al.

; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES

; FILE REFERENCE: 802620-2005.1

; CURRENT APPLICATION NUMBER: US/09/771.161A

; CURRENT FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: 09/724,676

; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: 136776

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: 135619

; PRIOR FILING DATE: 2000-04-12

; NUMBER OF SEQ ID NOS: 273

; SOFTWARE: Patentin version 3.0

; SEQ ID NO 247

; LENGTH: 479

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-771-161A-247

Query Match 38.6%; Score 891; DB 2; Length 479;  
Best Local Similarity 48.5%; Pred. No. 3.4e-75;  
Matches 182; Conservative 55; Mismatches 100; Indels 38; Gaps 8;

QY 60 RMNSSPAGTSPQPSRAN--GNINLGPSANPNAQPT--DFDFLKVKVIGKNGYKVLAKRK 115  
Db 116 RMNCSTP-----SQIDNIGEEEMDASTTHHKKRTMNDPDKLKGKTFGKVLVREK 168  
QY 116 SDGAFYAVKVLQKKSILKKKEQSHIMAEVSVLLKNVHHPFLVGLRYSFQTPKLYFVLDY 175  
Db 169 ASKYYAMKILKKEVIIAKDEVAHTLTE-SRVLKNTKHPFLTSLKYSFQTKDRLCFWVEY 227  
QY 176 VNGGELFFHLQRRERFLEPRARYAFAVSAIGYLHSLNIYYRDLKPENILLDCQGHVVL 235  
Db 228 VNGGELFFHLRSRVSFSDRTFRYGAEIVSALDYLSHGIYVRDLKLENLMKDGHGIKI 287  
QY 236 TDFGLCKEGVEPDDTSTFCGTPPEYLAPEVLRKEPYDRAVDMWCLGAVLYEMHLGLPPFY 295  
Db 288 TDFGLCKEGITDAATKTKTCGTPPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFY 347  
QY 296 SQDVSMYENILHQPILQIPGGRVVAACDLQLSLHDKDQORL--GSKADFLIEIKNVHFFSP 354  
Db 348 NQDEKLFELIMEDIKPPRTLSDDAKSLLSGLLIKDPNKRKLGCGPDPAKEIMRHSFFSG 407

QY 355 INWDDLYHKRLTPPENNVNTPGADLKHFDPFTQEAIVSKSGCTPDTVASSSGASSAFLG 414  
Db 408 VNMQDVYDKKLVPPFKQVTSSETDTRYFDEEFT-----AQITITTP----- 448

QY 415 FSYAPE--DDILDC 427  
Db 449 ----PEKYDEGDMDC 459

RESULT 13  
US-09-771-161A-248  
; Sequence 248, Application US/09771161A  
; Patent No. 6936450

; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771.161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 248  
; LENGTH: 479  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-771-161A-248

Query Match 38.6%; Score 891; DB 2; Length 479;

Best Local Similarity 48.5%; Pred. No. 3.4e-75;

Matches 182; Conservative 55; Mismatches 100; Indels 38; Gaps 8;

QY 60 RMNSSPAGTSPQPSRAN--GNINLGPSANPNAQPT--DFDFLKVKVIGKNGYKVLAKRK 115  
Db 116 RMNCSTP-----SQIDNIGEEEMDASTTHHKKRTMNDPDKLKGKTFGKVLVREK 168  
QY 116 SDGAFYAVKVLQKKSILKKKEQSHIMAEVSVLLKNVHHPFLVGLRYSFQTPKLYFVLDY 175  
Db 169 ASKYYAMKILKKEVIIAKDEVAHTLTE-SRVLKNTKHPFLTSLKYSFQTKDRLCFWVEY 227  
QY 176 VNGGELFFHLQRRERFLEPRARYAFAVSAIGYLHSLNIYYRDLKPENILLDCQGHVVL 235  
Db 228 VNGGELFFHLRSRVSFSDRTFRYGAEIVSALDYLSHGIYVRDLKLENLMKDGHGIKI 287  
QY 236 TDFGLCKEGVEPDDTSTFCGTPPEYLAPEVLRKEPYDRAVDMWCLGAVLYEMHLGLPPFY 295  
Db 288 TDFGLCKEGITDAATKTKTCGTPPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFY 347  
QY 296 SQDVSMYENILHQPILQIPGGRVVAACDLQLSLHDKDQORL--GSKADFLIEIKNVHFFSP 354  
Db 348 NQDEKLFELIMEDIKPPRTLSDDAKSLLSGLLIKDPNKRKLGCGPDPAKEIMRHSFFSG 407

QY 355 INWDDLYHKRLTPPENNVNTPGADLKHFDPFTQEAIVSKSGCTPDTVASSSGASSAFLG 414  
Db 408 VNMQDVYDKKLVPPFKQVTSSETDTRYFDEEFT-----AQITITTP----- 448

QY 415 FSYAPE--DDILDC 427

Db 449 ----PEKYDEGDMDC 459

RESULT 14  
US-09-526-043-2  
; Sequence 2, Application US/09526043  
; Patent No. 6881555  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Kun  
; APPLICANT: Pagnoni, Marco  
; APPLICANT: Clark, Kenneth  
; APPLICANT: Ivashchenko, Yuri  
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF  
; FILE REFERENCE: A3278A-US  
; CURRENT APPLICATION NUMBER: US/09/526,043  
; CURRENT FILING DATE: 2000-03-14  
; EARLIER APPLICATION NUMBER: 60/125,108  
; EARLIER FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 465  
; TYPE: PRT

Query Match 38.6%; Score 891; DB 2; Length 479;  
Best Local Similarity 48.5%; Pred. No. 3.4e-75;  
Matches 182; Conservative 55; Mismatches 100; Indels 38; Gaps 8;

QY 60 RMNSSPAGTSPQPSRAN--GNINLGPSANPNAQPT--DFDFLKVKVIGKNGYKVLAKRK 115  
Db 116 RMNCSTP-----SQIDNIGEEEMDASTTHHKKRTMNDPDKLKGKTFGKVLVREK 168  
QY 116 SDGAFYAVKVLQKKSILKKKEQSHIMAEVSVLLKNVHHPFLVGLRYSFQTPKLYFVLDY 175  
Db 169 ASKYYAMKILKKEVIIAKDEVAHTLTE-SRVLKNTKHPFLTSLKYSFQTKDRLCFWVEY 227  
QY 176 VNGGELFFHLQRRERFLEPRARYAFAVSAIGYLHSLNIYYRDLKPENILLDCQGHVVL 235  
Db 228 VNGGELFFHLRSRVSFSDRTFRYGAEIVSALDYLSHGIYVRDLKLENLMKDGHGIKI 287  
QY 236 TDFGLCKEGVEPDDTSTFCGTPPEYLAPEVLRKEPYDRAVDMWCLGAVLYEMHLGLPPFY 295  
Db 288 TDFGLCKEGITDAATKTKTCGTPPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFY 347  
QY 296 SQDVSMYENILHQPILQIPGGRVVAACDLQLSLHDKDQORL--GSKADFLIEIKNVHFFSP 354  
Db 348 NQDEKLFELIMEDIKPPRTLSDDAKSLLSGLLIKDPNKRKLGCGPDPAKEIMRHSFFSG 407

QY 355 INWDDLYHKRLTPPENNVNTPGADLKHFDPFTQEAIVSKSGCTPDTVASSSGASSAFLG 414  
Db 408 VNMQDVYDKKLVPPFKQVTSSETDTRYFDEEFT-----AQITITTP----- 448

QY 415 FSYAPE--DDILDC 427  
Db 449 ----PEKYDEGDMDC 459

RESULT 14  
US-09-526-043-2  
; Sequence 2, Application US/09526043  
; Patent No. 6881555  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Kun  
; APPLICANT: Pagnoni, Marco  
; APPLICANT: Clark, Kenneth  
; APPLICANT: Ivashchenko, Yuri  
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF  
; FILE REFERENCE: A3278A-US  
; CURRENT APPLICATION NUMBER: US/09/526,043  
; CURRENT FILING DATE: 2000-03-14  
; EARLIER APPLICATION NUMBER: 60/125,108  
; EARLIER FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 465  
; TYPE: PRT

Query Match 38.6%; Score 891; DB 2; Length 479;  
Best Local Similarity 48.5%; Pred. No. 3.4e-75;  
Matches 182; Conservative 55; Mismatches 100; Indels 38; Gaps 8;

QY 60 RMNSSPAGTSPQPSRAN--GNINLGPSANPNAQPT--DFDFLKVKVIGKNGYKVLAKRK 115  
Db 116 RMNCSTP-----SQIDNIGEEEMDASTTHHKKRTMNDPDKLKGKTFGKVLVREK 168  
QY 116 SDGAFYAVKVLQKKSILKKKEQSHIMAEVSVLLKNVHHPFLVGLRYSFQTPKLYFVLDY 175  
Db 169 ASKYYAMKILKKEVIIAKDEVAHTLTE-SRVLKNTKHPFLTSLKYSFQTKDRLCFWVEY 227  
QY 176 VNGGELFFHLQRRERFLEPRARYAFAVSAIGYLHSLNIYYRDLKPENILLDCQGHVVL 235  
Db 228 VNGGELFFHLRSRVSFSDRTFRYGAEIVSALDYLSHGIYVRDLKLENLMKDGHGIKI 287  
QY 236 TDFGLCKEGVEPDDTSTFCGTPPEYLAPEVLRKEPYDRAVDMWCLGAVLYEMHLGLPPFY 295  
Db 288 TDFGLCKEGITDAATKTKTCGTPPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFY 347  
QY 296 SQDVSMYENILHQPILQIPGGRVVAACDLQLSLHDKDQORL--GSKADFLIEIKNVHFFSP 354  
Db 348 NQDEKLFELIMEDIKPPRTLSDDAKSLLSGLLIKDPNKRKLGCGPDPAKEIMRHSFFSG 407

QY 355 INWDDLYHKRLTPPENNVNTPGADLKHFDPFTQEAIVSKSGCTPDTVASSSGASSAFLG 414  
Db 408 VNMQDVYDKKLVPPFKQVTSSETDTRYFDEEFT-----AQITITTP----- 448

QY 415 FSYAPE--DDILDC 427  
Db 449 ----PEKYDEGDMDC 459

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; ORGANISM: Homo sapiens
US-09-526-043-2

Query Match      38.2%; Score 883.5; DB 2; Length 465;
Best Local Similarity 51.2%; Pred. No. 1.7e-74;
Matches 173; Conservative 53; Mismatches 99; Indels 13; Gaps 5;

QY 60 RMNSSPAGTSPQPSRAN--GNNLGFSPANPNAOPT--DFDFLKVTGKNGYKVLAKRK 115
Db 116 RMNCSPT-----SQIDNIGSEMDASTTHHKRTKMNDPFDYKLLGKGTGKGVILVREK 168
QY 116 SDGAFYAVKVLQKSKILKKKEQSHIMAERSVLLKNVRHPELVGLRYSFQTPPEKLYFVLDY 175
Db 169 ASGKYVAMKLLKEVIAKDEVAHTLITE-SRVUKNTRHPPLTSLKYSFQTKDRLCFMVEY 227
QY 176 VNGGELFFHLQRRRRFLEPRARYAAEVAASAIGYLHSLNIIYRDLPENILLDCQGHVVL 235
Db 228 VNGGELFFHLRSRERFSEDRTRFYGAIEVSALDYLSHGKIVYRDYLDKLENLMLDKDGHKI 287
QY 236 TDFGLCKEGVEPEDTTSTFCGTPEYLAPVLRKEPYDRAVDWMCGLGAVLYEMLHGLPPFY 295
Db 288 TDFGLCKEGITDAATWKTFCGTPEYLAPVLENDYGRAVDWMCGLGVVYMMCMGRLPFY 347
QY 296 SQDVSOQMYENILHQPILQIPGGRITVAACDLQLSLHLKQDQORL--GSKADFLKIKNHVFFSP 354
Db 348 NQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLIKDPNKRLLGGGPDPAKEIMRHSFFSG 407
QY 355 INWDDLYHKRLTTPFPNPNTGADLKHDPFPTQEAVS 392
Db 408 VNWQDVYDKLVPPFKPQVTSETDTRYFDEEFTAQIT 445
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Search completed: January 27, 2006, 23:33:32  
Job time : 21.1415 secs

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RESULT 15
US-09-526-043-17
; Sequence 17, Application US/09526043
; Patent No. 6881555
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/09/526,043
; CURRENT FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: 60/125,108
; EARLIER FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-09-526-043-17

Query Match      38.2%; Score 882.5; DB 2; Length 454;
Best Local Similarity 51.2%; Pred. No. 2e-74;
Matches 173; Conservative 53; Mismatches 99; Indels 13; Gaps 5;

QY 60 RMNSSPAGTSPQPSRAN--GNNLGFSPANPNAOPT--DFDFLKVTGKNGYKVLAKRK 115
Db 116 RMNCSPT-----SQIDNIGSEMDASTTHHKRTKMNDPFDYKLLGKGTGKGVILVREK 168
QY 116 SDGAFYAVKVLQKSKILKKKEQSHIMAERSVLLKNVRHPELVGLRYSFQTPPEKLYFVLDY 175
Db 169 ASGKYVAMKLLKEVIAKDEVAHTLITE-SRVUKNTRHPPLTSLKYSFQTKDRLCFMVEY 227
QY 176 VNGGELFFHLQRRRRFLEPRARYAAEVAASAIGYLHSLNIIYRDLPENILLDCQGHVVL 235
Db 228 VNGGELFFHLRSRERFSEDRTRFYGAIEVSALDYLSHGKIVYRDYLDKLENLMLDKDGHKI 287
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:31:20 ; Search time 74.9264 Seconds  
(without alignments)  
2381.178 Million cell updates/sec

Title: US-09-868-131A-8

Perfect score: 2311

Sequence: 1 MQGLLTSGRKPSGGRTGR.....ASSAFLGSYAPDDDDILDC 427

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_Main:\*

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2: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep:\*

3: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep:\*

4: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep:\*

5: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep:\*

6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2311	100.0	427	5	US-10-753-267-126
2	2124.5	91.9	398	4	US-10-262-511-140
3	2005	86.8	382	4	US-10-296-115-1109
4	2005	86.8	396	5	US-10-926-543-83
5	1954	84.6	367	3	US-09-971-118-2
6	1954	84.6	367	4	US-10-291-172-256
7	1954	84.6	367	4	US-10-429-160-52
8	1954	84.6	367	4	US-10-221-278-256
9	1954	84.6	367	4	US-10-380-235-6
10	1421.5	61.5	388	4	US-10-131-410-104
11	1419	61.4	407	4	US-10-067-977-4
12	1419	61.4	407	4	US-10-827-272-4
13	1419	61.4	431	3	US-09-981-353-7
14	1419	61.4	431	4	US-10-403-161-2
15	1419	61.4	431	4	US-10-403-161-4
16	1419	61.4	445	4	US-10-067-977-2
17	1419	61.4	445	4	US-10-827-272-2
18	1419	61.4	526	4	US-10-094-749-1861
19	1415	61.2	431	4	US-10-000-039-2
20	1415	61.2	431	4	US-10-353-690-12
21	1415	61.2	431	5	US-10-756-149-5279
22	1415	61.2	431	6	US-11-044-570-2
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24	1411	61.1	431	3	US-09-810-808-5
25	1392	60.2	594	5	US-10-732-923-10768
26	1390.5	60.2	433	5	US-10-732-923-10767
27	1342.5	58.1	340	4	US-10-217-574-17

28	1342.5	58.1	340	4	US-10-217-555-17	Sequence 17, Appl
29	1328.5	57.5	429	4	US-10-295-027-116	Sequence 116, App
30	1328.5	57.5	496	3	US-09-764-875-746	Sequence 746, App
31	1328.5	57.5	496	3	US-09-764-875-900	Sequence 900, App
32	1328.5	57.5	496	5	US-10-737-450-4	Sequence 4, Appli
33	1326.5	57.4	496	3	US-09-784-249-2	Sequence 2, Appli
34	1317.5	57.0	496	4	US-10-755-889-42	Sequence 42, Appl
35	1164.5	50.4	308	4	US-10-664-421-85	Sequence 85, Appl
36	1164.5	50.4	308	5	US-10-941-635-85	Sequence 85, Appl
37	983	42.5	422	4	US-10-369-493-7027	Sequence 7027, Ap
38	891	38.6	479	3	US-09-771-161A-246	Sequence 246, App
39	891	38.6	479	3	US-09-771-161A-247	Sequence 247, App
40	891	38.6	479	3	US-09-771-161A-248	Sequence 248, App
41	891	38.6	479	4	US-10-394-322A-3	Sequence 3, Appli
42	891	38.6	479	4	US-10-217-574-33	Sequence 33, Appl
43	891	38.6	479	4	US-10-217-555-33	Sequence 33, Appl
44	891	38.6	479	5	US-10-753-267-108	Sequence 108, App
45	888.5	38.4	276	3	US-09-764-868-669	Sequence 669, App

## ALIGNMENTS

## RESULT 1

US-10-753-267-126  
; Sequence 126, Application US/10753267  
; Publication No. US20050037946A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Stagliano, Nancy E.  
; APPLICANT: Healy, Aileen  
; APPLICANT: Acton, Susan L.  
; APPLICANT: Galvin, Katherine M.  
; APPLICANT: Donoghue, Mary A.  
; APPLICANT: Rodriguez-Way, Amelie  
; APPLICANT: Tomlinson, James E.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,  
; TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,  
; TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701,  
; TITLE OF INVENTION: 3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 33770,  
; TITLE OF INVENTION: 9380, 2569654, 33556, 53656, 44143, 32612, 10671, 261,  
; TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955,  
; TITLE OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 36005, 554, 16408,  
; TITLE OF INVENTION: 42028, 112091, 13886, 13942, 1673, 54946 OR 2419  
; FILE REFERENCE: MPI03-003PIRNMNM  
; CURRENT APPLICATION NUMBER: US/10/753,267  
; PRIOR FILING DATE: 2004-01-08  
; PRIOR APPLICATION NUMBER: US 60/439,683  
; PRIOR FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: US 60/445,216  
; PRIOR FILING DATE: 2003-02-05  
; PRIOR APPLICATION NUMBER: US 60/448,036  
; PRIOR FILING DATE: 2003-02-18  
; PRIOR APPLICATION NUMBER: US 60/454,189  
; PRIOR FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 60/457,541  
; PRIOR FILING DATE: 2003-03-25  
; PRIOR APPLICATION NUMBER: US 60/466,411  
; PRIOR FILING DATE: 2003-04-29  
; PRIOR APPLICATION NUMBER: US 60/469,041  
; PRIOR FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: US 60/477,414  
; PRIOR FILING DATE: 2003-06-10  
; PRIOR APPLICATION NUMBER: US 60/478,560  
; PRIOR FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: US 60/489,772  
; PRIOR FILING DATE: 2003-07-24  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 126  
; LENGTH: 427

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-753-267-126

Query Match      100.0%; Score 2311; DB 5; Length 427;
Best Local Similarity 100.0%; Pred. No. 1e-158;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQGLLTSGRKPSSGGRCCTGRGWRGQWCLKPMWGGADPPTPTLSCLLLPVPPPELPHCYR 60
Db 1 MQGLLTSGRKPSSGGRCCTGRGWRGQWCLKPMWGGADPPTPTLSCLLLPVPPPELPHCYR 60

QY 61 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSDDGAF 120
Db 61 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSDDGAF 120

QY 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYNGGE 180
Db 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYNGGE 180

QY 181 LFFHLQRRERFLPRARFYAAEVAISAIGYLHSLNIYRDLKPNILLDCQGHVLTDFGL 240
Db 181 LFFHLQRRERFLPRARFYAAEVAISAIGYLHSLNIYRDLKPNILLDCQGHVLTDFGL 240

QY 241 CKEGVPEPDTTSTFCGTPEYLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPPFYSDVVS 300
Db 241 CKEGVPEPDTTSTFCGTPEYLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPPFYSDVVS 300

QY 301 QMYENILHQPLOIPGGRTVAACDLQLSLHKKQORQLGSKADFLKKNHVFFSPINWDDL 360
Db 301 QMYENILHQPLOIPGGRTVAACDLQLSLHKKQORQLGSKADFLKKNHVFFSPINWDDL 360

QY 361 YHKRLTPPNVNTGPDALKHFDPEFTQEAIVSKSIGCTPDTVASSGASSAFILGFSYAPE 420
Db 361 YHKRLTPPNVNTGPDALKHFDPEFTQEAIVSKSIGCTPDTVASSGASSAFILGFSYAPE 420

QY 421 DDDILDC 427
Db 421 DDDILDC 427

RESULT 2
US-10-262-511-140
; Sequence 140, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Ellerman, Karen
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.

; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 140
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-140

Query Match      91.9%; Score 2124.5; DB 4; Length 398;
Best Local Similarity 93.2%; Pred. No. 2.8e-145;
Matches 398; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

QY 1 MQGLLTSGRKPSSGGRCCTGRGWRGQWCLKPMWGGADPPTPTLSCLLLPVPPPELPHCYR 60
Db 1 MQGLLTSGRKPSSGGRCCTGRGWRGQWCLKPMWGGADPPTPTLSCLLLPVPPPELPHCYR 60

QY 61 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSDDGAF 120
Db 61 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSDDGAF 120

QY 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYNGGE 180
Db 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYNGGE 180

QY 181 LFFHLQRRERFLPRARFYAAEVAISAIGYLHSLNIYRDLKPNILLDCQGHVLTDFGL 240
Db 181 LFFHLQRRERFLPRARFYAAEVAISAIGYLHSLNIYRDLKPNILLDCQGHVLTDFGL 240

QY 241 CKEGVPEPDTTSTFCGTPEYLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPPFYSDVVS 300
Db 241 CKEGVPEPDTTSTFCGTPEYLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPPFYSDVVS 300

QY 301 QMYENILHQPLOIPGGRTVAACDLQLSLHKKQORQLGSKADFLKKNHVFFSPINWDDL 360
Db 301 QMYENILHQPLOIPGGRTVAACDLQLSLHKKQORQLGSKADFLKKNHVFFSPINWDDL 360

QY 361 YHKRLTPPNVNTGPDALKHFDPEFTQEAIVSKSIGCTPDTVASSGASSAFILGFSYAPE 420
Db 361 YHKRLTPPNVNTGPDALKHFDPEFTQEAIVSKSIGCTPDTVASSGASSAFILGFSYAPE 420

QY 421 DDDILDC 427
Db 392 DDDILDC 398

RESULT 3
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US-10-296-115-1109  
; Sequence 1109, Application US/10296115  
; Publication No. US20040053248A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq Inc  
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 784PCT  
; CURRENT APPLICATION NUMBER: US/10/296.115  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: US09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: US09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 1478  
; SEQ ID NO 1109  
; LENGTH: 382  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-296-115-1109  
Query Match 86.8%; Score 2005; DB 4; Length 382;  
Best Local Similarity 100.0%; Pred. No. 1.2e-136;  
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 53 ELPDHCYRMNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLA 112  
Db 8 ELPDHCYRMNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLA 67  
Qy 113 KRKSDGAFYAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPPFLVGLRYSFQTPKLYFV 172  
Db 68 KRKSDGAFYAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPPFLVGLRYSFQTPKLYFV 127  
Qy 173 LDYVNGGELFFHLQRRERFLEPRARFYAAEVAASVLAIGYLSLNIYRDLKPENILLDCQGH 232  
Db 128 LDYVNGGELFFHLQRRERFLEPRARFYAAEVAASVLAIGYLSLNIYRDLKPENILLDCQGH 187  
Qy 233 VLTDFGLCKEGVEPEDTTSTFCGTPYLAPEVLRKEPYDRAVDWVWCLGAVLYEMLHGLP 292  
Db 188 VLTDFGLCKEGVEPEDTTSTFCGTPYLAPEVLRKEPYDRAVDWVWCLGAVLYEMLHGLP 247  
Qy 293 PFYSQDVSMYENILHQPLOIPGRTVAACDLLOSLLHKDQORQLGSKADFLKIKNVHVF 352  
Db 248 PFYSQDVSMYENILHQPLOIPGRTVAACDLLOSLLHKDQORQLGSKADFLKIKNVHVF 307  
Qy 353 SPINWDDLHKRLTPFPNPNVTGPADLKHPDPEFTQEAUSKSICTPDTVASSSGASSAF 412  
Db 308 SPINWDDLHKRLTPFPNPNVTGPADLKHPDPEFTQEAUSKSICTPDTVASSSGASSAF 367  
Qy 413 LGFSYAPEDDDIILDC 427  
Db 368 LGFSYAPEDDDIILDC 382  
RESULT 4  
US-10-296-543-83  
; Sequence 83, Application US/10926543  
; Publication No. US20050048589A1  
; GENERAL INFORMATION:  
; APPLICANT: Jendoubi, Moncef  
; TITLE OF INVENTION: LUNG CANCER SPECIFIC GENE PRODUCTS: THEIR CODING SEQUENCE, THEIR  
; TITLE OF INVENTION: ANTIBODIES AND THEIR USE IN DIAGNOSTIC, THERAPEUTIC AND DISEASE  
; TITLE OF INVENTION: MANAGEMENT OF LUNG CANCER  
; FILE REFERENCE: 705403.4004  
; CURRENT APPLICATION NUMBER: US/10/926,543  
; CURRENT FILING DATE: 2004-08-25  
; PRIOR APPLICATION NUMBER: US 60/497,790  
; PRIOR FILING DATE: 2003-08-25  
; NUMBER OF SEQ ID NOS: 94  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 83  
; LENGTH: 396  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-926-543-83  
Query Match 86.8%; Score 2005; DB 5; Length 396;  
Best Local Similarity 100.0%; Pred. No. 1.2e-136;  
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 53 ELPDHCYRMNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLA 112  
Db 22 ELPDHCYRMNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLA 81  
Qy 113 KRKSDGAFYAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPPFLVGLRYSFQTPKLYFV 172  
Db 82 KRKSDGAFYAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPPFLVGLRYSFQTPKLYFV 141  
Qy 173 LDYVNGGELFFHLQRRERFLEPRARFYAAEVAASVLAIGYLSLNIYRDLKPENILLDCQGH 232  
Db 142 LDYVNGGELFFHLQRRERFLEPRARFYAAEVAASVLAIGYLSLNIYRDLKPENILLDCQGH 201  
Qy 233 VLTDFGLCKEGVEPEDTTSTFCGTPYLAPEVLRKEPYDRAVDWVWCLGAVLYEMLHGLP 292  
Db 202 VLTDFGLCKEGVEPEDTTSTFCGTPYLAPEVLRKEPYDRAVDWVWCLGAVLYEMLHGLP 261  
Qy 293 PFYSQDVSMYENILHQPLOIPGRTVAACDLLOSLLHKDQORQLGSKADFLKIKNVHVF 352  
Db 262 PFYSQDVSMYENILHQPLOIPGRTVAACDLLOSLLHKDQORQLGSKADFLKIKNVHVF 321  
Qy 353 SPINWDDLHKRLTPFPNPNVTGPADLKHPDPEFTQEAUSKSICTPDTVASSSGASSAF 412  
Db 322 SPINWDDLHKRLTPFPNPNVTGPADLKHPDPEFTQEAUSKSICTPDTVASSSGASSAF 381  
Qy 413 LGFSYAPEDDDIILDC 427  
Db 382 LGFSYAPEDDDIILDC 396  
RESULT 5  
US-09-971-118-2  
; Sequence 2, Application US/09971118  
; Patent No. US20020123056A1  
; GENERAL INFORMATION:  
; APPLICANT: DELANEY, ALLEN  
; APPLICANT: YOGANATHAN, THILLAINATHAN  
; TITLE OF INVENTION: SGK2 AND ITS USES  
; FILE REFERENCE: KINE025CIP  
; CURRENT APPLICATION NUMBER: US/09/971,118  
; CURRENT FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: PCT/US01/21479  
; PRIOR FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/237,419  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 367  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-971-118-2  
Query Match 84.6%; Score 1954; DB 3; Length 367;  
Best Local Similarity 100.0%; Pred. No. 5.3e-133;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 61 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLAKRKSDF 120  
Db 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLAKRKSDF 60  
Qy 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPPFLVGLRYSFQTPKLYFVLDYNGGE 180  
Db 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPPFLVGLRYSFQTPKLYFVLDYNGGE 120  
Qy 181 LFFHLQRRERFLEPRARFYAAEVAASVLAIGYLSLNIYRDLKPENILLDCQGHVLTDFGL 240  
Db 121 LFFHLQRRERFLEPRARFYAAEVAASVLAIGYLSLNIYRDLKPENILLDCQGHVLTDFGL 180

QY 241 CKEGVEPEDTTSTFCGTPYLAPEVLKPEPYDRAVDWCLGAVLYEMLHGLPPFYSDQVS 300  
DB 181 CKEGVEPEDTTSTFCGTPYLAPEVLKPEPYDRAVDWCLGAVLYEMLHGLPPFYSDQVS 240  
QY 301 QMYENILHQPLQIPGGRVAAACDLQLSLHKDQRLGSKADPLEIKNVHFFSPINWDDL 360  
DB 241 QMYENILHQPLQIPGGRVAAACDLQLSLHKDQRLGSKADPLEIKNVHFFSPINWDDL 300  
QY 361 YHKRLTPPPNPNVTGPADLKHDFPETOEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 420  
DB 301 YHKRLTPPPNPNVTGPADLKHDFPETOEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360  
QY 421 DDDILDC 427  
DB 361 DDDILDC 367

RESULT 6  
US-10-291-172-256  
; Sequence 256, Application US/10291172  
; Publication No. US20030228584A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-045  
; CURRENT APPLICATION NUMBER: US/10/291,172  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 09/693,267  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 09/665,363  
; PRIOR FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: 09/616,847  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 09/596,193  
; PRIOR FILING DATE: 2000-06-17  
; PRIOR APPLICATION NUMBER: 09/574,454  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: 09/519,705  
; PRIOR FILING DATE: 2000-03-07  
; NUMBER OF SEQ ID NOS: 752  
; SEQ ID NO 256  
; LENGTH: 367  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-291-172-256

Query Match 84.6%; Score 1954; DB 4; Length 367;  
Best Local Similarity 100.0%; Pred. No. 5.3e-133; Mismatches 0; Indels 0; Gaps 0;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 61 MNSSPAGTSPQPSRANGINILGPSANPNAQPTDFDLKVIKGNYGKVLAKRKS DGAF 120  
DB 1 MNSSPAGTSPQPSRANGINILGPSANPNAQPTDFDLKVIKGNYGKVLAKRKS DGAF 60  
QY 121 YAVKVLQKKSILKKKEQSHIMAEBSVLLKNVRHPLVGLRYSQTPEKLYFVLDDYNGGE 180  
DB 61 YAVKVLQKKSILKKKEQSHIMAEBSVLLKNVRHPLVGLRYSQTPEKLYFVLDDYNGGE 120  
QY 181 LFFHLQRRERFLPRARFYAAEVAASAI GYLHLSNIIRDLKPENILLDCQGHVLLTDFGL 240  
DB 121 LFFHLQRRERFLPRARFYAAEVAASAI GYLHLSNIIRDLKPENILLDCQGHVLLTDFGL 180  
QY 241 CKEGVEPEDTTSTFCGTPYLAPEVLKPEPYDRAVDWCLGAVLYEMLHGLPPFYSDQVS 300  
DB 181 CKEGVEPEDTTSTFCGTPYLAPEVLKPEPYDRAVDWCLGAVLYEMLHGLPPFYSDQVS 240  
QY 301 QMYENILHQPLQIPGGRVAAACDLQLSLHKDQRLGSKADPLEIKNVHFFSPINWDDL 360  
DB 241 QMYENILHQPLQIPGGRVAAACDLQLSLHKDQRLGSKADPLEIKNVHFFSPINWDDL 300  
QY 361 YHKRLTPPPNPNVTGPADLKHDFPETOEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 420  
DB 301 YHKRLTPPPNPNVTGPADLKHDFPETOEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360

DB 301 YHKRLTPPPNPNVTGPADLKHDFPETOEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360  
QY 421 DDDILDC 427  
DB 361 DDDILDC 367  
RESULT 7  
US-10-429-160-52  
; Sequence 52, Application US/10429160  
; Publication No. US20040023276A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Teresa R  
; APPLICANT: Mao, Mao  
; APPLICANT: Linsley, Peter S  
; APPLICANT: Lund, Lund  
; TITLE OF INVENTION: LXR Ligand Induced Genes and Proteins  
; FILE REFERENCE: RS0200  
; CURRENT APPLICATION NUMBER: US/10/429,160  
; CURRENT FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: US 60/377,714  
; PRIOR FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 52  
; LENGTH: 367  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-429-160-52

Query Match 84.6%; Score 1954; DB 4; Length 367;  
Best Local Similarity 100.0%; Pred. No. 5.3e-133; Mismatches 0; Indels 0; Gaps 0;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 61 MNSSPAGTSPQPSRANGINILGPSANPNAQPTDFDLKVIKGNYGKVLAKRKS DGAF 120  
DB 1 MNSSPAGTSPQPSRANGINILGPSANPNAQPTDFDLKVIKGNYGKVLAKRKS DGAF 60  
QY 121 YAVKVLQKKSILKKKEQSHIMAEBSVLLKNVRHPLVGLRYSQTPEKLYFVLDDYNGGE 180  
DB 61 YAVKVLQKKSILKKKEQSHIMAEBSVLLKNVRHPLVGLRYSQTPEKLYFVLDDYNGGE 120  
QY 181 LFFHLQRRERFLPRARFYAAEVAASAI GYLHLSNIIRDLKPENILLDCQGHVLLTDFGL 240  
DB 121 LFFHLQRRERFLPRARFYAAEVAASAI GYLHLSNIIRDLKPENILLDCQGHVLLTDFGL 180  
QY 241 CKEGVEPEDTTSTFCGTPYLAPEVLKPEPYDRAVDWCLGAVLYEMLHGLPPFYSDQVS 300  
DB 181 CKEGVEPEDTTSTFCGTPYLAPEVLKPEPYDRAVDWCLGAVLYEMLHGLPPFYSDQVS 240  
QY 301 QMYENILHQPLQIPGGRVAAACDLQLSLHKDQRLGSKADPLEIKNVHFFSPINWDDL 360  
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QY 361 YHKRLTPPPNPNVTGPADLKHDFPETOEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 420  
DB 301 YHKRLTPPPNPNVTGPADLKHDFPETOEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360  
QY 421 DDDILDC 427  
DB 361 DDDILDC 367

RESULT 8  
US-10-221-278-256  
; Sequence 256, Application US/10221278  
; Publication No. US20040034208A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: No. US20040034208A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-045  
; CURRENT APPLICATION NUMBER: US/10/221,278  
; CURRENT FILING DATE: 2002-09-06

; PRIOR APPLICATION NUMBER: 09/693,267  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 09/665,363  
; PRIOR FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: 09/616,847  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 09/596,193  
; PRIOR FILING DATE: 2000-06-17  
; PRIOR APPLICATION NUMBER: 09/574,454  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: 09/519,705  
; PRIOR FILING DATE: 2000-03-07  
; NUMBER OF SEQ ID NOS: 752  
; SEQ ID NO 256  
; LENGTH: 367  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-221-278-256

Query Match 84.6%; Score 1954; DB 4; Length 367;  
Best Local Similarity 100.0%; Pred. No. 5.3e-133;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 61 MNSSPAGTSPQPSRANGNINLGPSANPNNAOPTDFDLKVGKNGYKVLLAKRKSQDAF 120  
Db 1 MNSSPAGTSPQPSRANGNINLGPSANPNNAOPTDFDLKVGKNGYKVLLAKRKSQDAF 60  
Qy 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYVNGGE 180  
Db 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYVNGGE 120  
Qy 181 LFPHLQRRERFLPRARFYAAEVAASAIYGLHLSNIIYRDLKPNILDDCGHVVLDTDFGL 240  
Db 121 LFPHLQRRERFLPRARFYAAEVAASAIYGLHLSNIIYRDLKPNILDDCGHVVLDTDFGL 180  
Qy 241 CKGEVPEPDTTSTFCGTPPEYLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPPFYSDVS 300  
Db 181 CKGEVPEPDTTSTFCGTPPEYLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPPFYSDVS 240  
Qy 301 QMYENILHQPLOIPGGRTVAACDLQSLHDKQORLGSKADFLKTNHVFSPINWDDL 360  
Db 241 QMYENILHQPLOIPGGRTVAACDLQSLHDKQORLGSKADFLKTNHVFSPINWDDL 300  
Qy 361 YHKRLTPFPNPNVTGADLKHPDFTQEAHSVSKSIGCTPTDVTASSGASSAFLGFSYAPE 420  
Db 301 YHKRLTPFPNPNVTGADLKHPDFTQEAHSVSKSIGCTPTDVTASSGASSAFLGFSYAPE 360  
Qy 421 DDDILDC 427  
Db 361 DDDILDC 367

RESULT 9  
US-10-380-235-6  
; Sequence 6, Application US/10380235  
; Publication No. US20040072184A1  
; GENERAL INFORMATION:  
; APPLICANT: Yoganathan, Thillainathan  
; APPLICANT: Delaney, Allen  
; TITLE OF INVENTION: CANCER ASSOCIATED PROTEIN KINASES AND  
; TITLE OF INVENTION: THEIR USES  
; FILE REFERENCE: KINE-024CIP  
; CURRENT APPLICATION NUMBER: US/10/380,235  
; CURRENT FILING DATE: 2003-10-15  
; PRIOR APPLICATION NUMBER: IB01/02237  
; PRIOR FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/290,555  
; PRIOR FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 60/233,999  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: 60/237,419  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,423

; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/238,558  
; PRIOR FILING DATE: 2000-10-04  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 367  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-380-235-6

Query Match 84.6%; Score 1954; DB 4; Length 367;  
Best Local Similarity 100.0%; Pred. No. 5.3e-133;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 61 MNSSPAGTSPQPSRANGNINLGPSANPNNAOPTDFDLKVGKNGYKVLLAKRKSQDAF 120  
Db 1 MNSSPAGTSPQPSRANGNINLGPSANPNNAOPTDFDLKVGKNGYKVLLAKRKSQDAF 60  
Qy 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYVNGGE 180  
Db 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYVNGGE 120  
Qy 181 LFPHLQRRERFLPRARFYAAEVAASAIYGLHLSNIIYRDLKPNILDDCGHVVLDTDFGL 240  
Db 121 LFPHLQRRERFLPRARFYAAEVAASAIYGLHLSNIIYRDLKPNILDDCGHVVLDTDFGL 180  
Qy 241 CKGEVPEPDTTSTFCGTPPEYLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPPFYSDVS 300  
Db 181 CKGEVPEPDTTSTFCGTPPEYLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPPFYSDVS 240  
Qy 301 QMYENILHQPLOIPGGRTVAACDLQSLHDKQORLGSKADFLKTNHVFSPINWDDL 360  
Db 241 QMYENILHQPLOIPGGRTVAACDLQSLHDKQORLGSKADFLKTNHVFSPINWDDL 300  
Qy 361 YHKRLTPFPNPNVTGADLKHPDFTQEAHSVSKSIGCTPTDVTASSGASSAFLGFSYAPE 420  
Db 301 YHKRLTPFPNPNVTGADLKHPDFTQEAHSVSKSIGCTPTDVTASSGASSAFLGFSYAPE 360  
Qy 421 DDDILDC 427  
Db 361 DDDILDC 367

RESULT 10  
US-10-131-410-104  
; Sequence 104, Application US/10131410  
; Publication No. US20030235915A1  
; GENERAL INFORMATION:  
; APPLICANT: SPECHT, THOMAS  
; APPLICANT: HINZMANN, BERND  
; APPLICANT: SCHMITT, ARMIN  
; APPLICANT: PILARSKY, CHRISTIAN  
; APPLICANT: DAHL, EDGAR  
; APPLICANT: ROSENTHAL, ANDRE  
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST  
; TITLE OF INVENTION: TUMORS  
; FILE REFERENCE: SCH-1763  
; CURRENT APPLICATION NUMBER: US/10/131,410  
; CURRENT FILING DATE: 2002-04-25  
; PRIOR APPLICATION NUMBER: 09/646,673  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: PCT/DE99/00908  
; PRIOR FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 202  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 104  
; LENGTH: 388  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-131-410-104  
Query Match 61.5%; Score 1421.5; DB 4; Length 388;



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; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981.353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 3819039CD1
US-09-981-353-7
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Query Match 61.4%; Score 1419; DB 3; Length 431;
Best Local Similarity 68.3%; Pred. No 3e-94;
Matches 267; Conservative 56; Mismatches 54; Indels 14; Gaps 4;

QY 38 PPTFTLSCLLLPVPELPDHCYRMSSPAGTSPQPSRANGINLGFSAAPNAQPTDQDF 97
| : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 52 PEVQSILKISQPOPEL-----MNANP--SPPPSPSQ---QINLGPSSNPHAKPSDFH 100

QY 98 LKVIKGNVGVLLAKRKSDGAFYAVKVLQKKSILKKKEQSHIMASRSVLLKNVRHPLV 157
| : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 101 LKVIKGSFGKVLARHKAEEVFYAVKVLQKKAALKKKEEKTMSERNVLLKNVHPLV 160

QY 158 GLRYSQTPTEKLYFVLDYVNGGELFFHLQREERFLEPRARFYAAEASAIYLHSLNIY 217
| : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 161 GLHFSQTADKLYFVLDYVNGGELFFHLQREERFLEPRARFYAAEASAIYLHSLNIY 220

QY 218 RDLKPNILLDCQGHVLTDFGLCKEGVEPEDTTSTFCGTPPEYLAPEVLKKEPYDRAVDW 277
| : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 221 RDLKPNILLDSQGHVLTDFGLCKENIEHNSTSTFCGTPPEYLAPEVLHQPYDRTVDW 280

QY 278 WCLGAVLYEMLHGLPPFYSDVSQMYENILHQPQTGGRTVAACDLQSLHLDQRQL 337
| : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 281 WCLGAVLYEMLYGLPPFYSRNTAEYDNLINKPLQKPNITNSARHLLGGLQKRTKRL 340

QY 338 GSKADFLKTNVFFSPINWDDLHYKRLTPPNPNVTGPADLKHDPDPEFTQEA VSKSICG 397
| : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 341 GAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNPNVSGPNDLHRHDFEETPEEPVNSIGK 400

QY 398 TPDTV---ASSSGASSAFGLFSYAPEDDDIL 425
| : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 401 SPDSVLVTAASVKEAEAFGLFSYAPPTDSFL 431
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RESULT 14
US-10-403-161-2
; Sequence 2, Application US/10403161
; Publication No. US20040043930A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-573C
; CURRENT APPLICATION NUMBER: US/10/403,161
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/370349
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384543
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/370969
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/403748
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/372019
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/374379
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 09/779679
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181045
; PRIOR FILING DATE: 2000-02-08
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; PRIOR APPLICATION NUMBER: 10/055877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262892
; PRIOR FILING DATE: 2001-01-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 2
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-161-2

Query Match 61.4%; Score 1419; DB 4; Length 431;
Best Local Similarity 68.3%; Pred. No 3e-94;
Matches 267; Conservative 56; Mismatches 54; Indels 14; Gaps 4;

QY 38 PPTFTLSCLLLPVPELPDHCYRMSSPAGTSPQPSRANGINLGFSAAPNAQPTDQDF 97
| : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 52 PEVQSILKISQPOPEL-----MNANP--SPPPSPSQ---QINLGPSSNPHAKPSDFH 100

QY 98 LKVIKGNVGVLLAKRKSDGAFYAVKVLQKKSILKKKEQSHIMASRSVLLKNVRHPLV 157
| : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 101 LKVIKGSFGKVLARHKAEEVFYAVKVLQKKAALKKKEEKTMSERNVLLKNVHPLV 160

QY 158 GLRYSQTPTEKLYFVLDYVNGGELFFHLQREERFLEPRARFYAAEASAIYLHSLNIY 217
| : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 161 GLHFSQTADKLYFVLDYVNGGELFFHLQREERFLEPRARFYAAEASAIYLHSLNIY 220

QY 218 RDLKPNILLDCQGHVLTDFGLCKEGVEPEDTTSTFCGTPPEYLAPEVLKKEPYDRAVDW 277
| : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 221 RDLKPNILLDSQGHVLTDFGLCKENIEHNSTSTFCGTPPEYLAPEVLHQPYDRTVDW 280

QY 278 WCLGAVLYEMLHGLPPFYSDVSQMYENILHQPQTGGRTVAACDLQSLHLDQRQL 337
| : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 281 WCLGAVLYEMLYGLPPFYSRNTAEYDNLINKPLQKPNITNSARHLLGGLQKRTKRL 340

QY 338 GSKADFLKTNVFFSPINWDDLHYKRLTPPNPNVTGPADLKHDPDPEFTQEA VSKSICG 397
| : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 341 GAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNPNVSGPNDLHRHDFEETPEEPVNSIGK 400

QY 398 TPDTV---ASSSGASSAFGLFSYAPEDDDIL 425
| : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 401 SPDSVLVTAASVKEAEAFGLFSYAPPTDSFL 431
```

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RESULT 15
US-10-403-161-4
; Sequence 4, Application US/10403161
; Publication No. US20040043930A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-573C
; CURRENT APPLICATION NUMBER: US/10/403,161
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/370349
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384543
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/370969
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/403748
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/372019
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/374379
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 09/779679
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181045
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 10/055877
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; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262892
; PRIOR FILING DATE: 2001-01-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 4
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-161-4

Query Match      61.4%; Score 1419; DB 4; Length 431;
Best Local Similarity 68.3%; Pred. No. 3e-94;
Matches 267; Conservative 56; Mismatches 54; Indels 14; Gaps 4;

QY 38 PPTPTLSCLLPVPPPELPHDCHYMNSSPAGTSPQPSRANGNINLGPSANPNAPQPTDFDF 97
Db 52 PEVQSILKISQPEPEL-----MNANP--SPFPSPSQ---QINLGFSSNPHAKPSDFHF 100

QY 98 LKVIGKNGYGVLLAKRKSDGAFYAVKVLQKKSILKKKQSHIMABERSVLLKNVRHPFLV 157
Db 101 LKVIGKSGFGKVLARHKAEEVEYAVKVLQKKAILEKKEKHIMSERNVLLKNVHPFLV 160

QY 158 GLRYSQTPEKLYFVLVDYNGGELFHLQREERFLEPRARFYAAEVAISALGYLHSLNIY 217
Db 161 GLHFSQTADKLYFVLVDYNGGELFHLQREERFLEPRARFYAAEIASALGYLHSLNIY 220

QY 218 RDLKPENILLDCQGHVVLTDGFLCKEGVEPEDTSTFCGTPEYLAPEVLKKEPYDRAVDW 277
Db 221 RDLKPENILLDSQGHIVLTDGFLCKENIEHNSTSTFCGTPEYLAPEVLHKQPYDRTVDW 280

QY 278 WCLGAVLYEMLHGLPPFYSDVSQMYENILHQPLOIPGGRTVAACDLLOSLLHKQQRQL 337
Db 281 WCLGAVLYEMLYGLPPFYSRNTAEYDNIILNKPLQLKPNITNSARHLEGLLQKDRTKRL 340

QY 338 GSKADFLKKNHVFSPINWDDLYHKRLTTPPNPNVTGPADLKHFDPEETQEAIVSKSICG 397
Db 341 GAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNPNVSGPNDLRHFDPEETEEPVPNSIGK 400

QY 398 TPDVTV---ASSSGASSAFLGFSYAPEDDDIL 425
Db 401 SPDVLVTASVKEAEAFGLGFSYAPTDSFL 431
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Search completed: January 27, 2006, 23:57:33  
Job time : 74.9264 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2006, 23:32:16 ; Search time 11.0107 Seconds  
(without alignments)  
419.957 Million cell updates/sec

Title: US-09-868-131A-8

Perfect score: 2311

Sequence: 1 MQGLTSGRKPSGGGRCTGR.....ASSAFLGFSYAPEDDDILDC 427

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA New:\*
- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
  - 2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
  - 3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
  - 4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
  - 5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
  - 6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
  - 7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*
  - 8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1419	61.4	543	6	US-10-821-234-1158
2	874.5	37.8	480	7	US-11-109-156-18
3	788.5	34.1	495	6	US-10-770-726-81
4	765	33.1	737	7	US-11-152-366-28
5	722.5	31.3	740	6	US-10-878-556A-129
6	713.5	30.9	942	6	US-10-770-726-76
7	705.5	30.5	341	7	US-11-092-168-4
8	694.5	30.1	343	7	US-11-092-168-3
9	694.5	30.1	351	7	US-11-132-142-13
10	694.5	30.1	462	7	US-11-132-142-10
11	691.5	29.9	331	7	US-11-132-142-14
12	681.5	29.5	350	6	US-10-497-767-4
13	681.5	29.5	381	7	US-11-132-142-9
14	681	29.5	705	6	US-10-995-561-856
15	681	29.5	706	6	US-10-995-561-855
16	681	29.4	706	7	US-11-099-958-1
17	679	29.4	331	7	US-11-099-958-2
18	675	29.2	353	7	US-11-132-142-11
19	672.5	29.1	395	7	US-11-132-142-12
20	670	29.0	515	7	US-11-132-142-8
21	662	28.6	398	7	US-11-132-142-7
22	649.5	28.1	548	7	US-11-132-142-5
23	644	27.9	480	7	US-11-132-142-6
24	547	23.7	637	7	US-11-113-837-4
25	541.5	23.4	1732	6	US-10-055-877-147

26	536	23.2	756	7	US-11-113-837-20	Sequence 20, Appl
27	535.5	23.2	1663	6	US-10-055-877-148	Sequence 148, App
28	532.5	23.0	1590	6	US-10-055-877-146	Sequence 146, App
29	529	22.9	635	7	US-11-113-837-16	Sequence 16, Appl
30	528	22.8	256	6	US-10-877-346-72	Sequence 72, Appl
31	528	22.8	256	6	US-11-113-837-183	Sequence 183, App
32	527.5	22.8	1197	6	US-10-055-877-8	Sequence 8, Appl
33	527.5	22.8	1247	6	US-10-055-877-10	Sequence 10, Appl
34	508	22.0	688	7	US-11-113-837-18	Sequence 18, Appl
35	506	21.9	1613	6	US-10-055-877-145	Sequence 45, Appl
36	506	21.9	1637	6	US-10-055-877-144	Sequence 145, App
37	502.5	21.7	668	7	US-11-113-837-12	Sequence 12, App
38	502	21.7	598	7	US-11-113-837-21	Sequence 21, Appl
39	502	21.7	639	7	US-11-113-837-21	Sequence 48, Appl
40	499	21.6	688	7	US-11-113-837-19	Sequence 19, Appl
41	498.5	21.6	665	7	US-11-113-837-19	Sequence 49, Appl
42	491	21.2	688	7	US-11-125-295-11	Sequence 11, Appl
43	489	21.2	396	7	US-11-125-295-9	Sequence 9, Appl
44	489	21.2	407	7	US-11-113-837-19	Sequence 47, Appl
45	483	20.9	689	7	US-11-113-837-19	Sequence 47, Appl

ALIGNMENTS

RESULT 1

US-10-821-234-1158

; Sequence 1158, Application US/10821234

; Publication No. US20050255114A1

; GENERAL INFORMATION:

; APPLICANT: Labat, Ivan

; APPLICANT: Stache-Crain, Birgit

; APPLICANT: Andarmani, Susan

; APPLICANT: Tang, Y. Tom

; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

; FILE REFERENCE: 821A

; CURRENT APPLICATION NUMBER: US/10/821,234

; CURRENT FILING DATE: 2004-04-07

; PRIOR APPLICATION NUMBER: US 60/462,047

; NUMBER OF SEQ ID NOS: 1704

; SOFTWARE: pt\_seq\_genes Version 1.0

; SEQ ID NO 1158

; LENGTH: 543

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-821-234-1158

Query Match 61.4%; Score 1419; DB 6; Length 543;

Best Local Similarity 68.3%; Pred. No. 1.7e-112;

Matches 267; Conservative 56; Mismatches 54; Indels 14; Gaps 4;

QY 38 PPTPTUSCLLLPVPELPDHCYMNSSPAGTSPQPSRANGNINLGPSANPNQPTDFD 97

Db 164 PEVQSLTKISQPOPEL-----MNANP--SPPPSPSQ---QINLGPSSNPHAKSPDFH 212

QY 98 LKVIKGNVGVKLLAKKSDGAFYAVKVLQKLSILKKQSHIMASRSVLLKNVHPFLV 157

Db 213 LKVIKGNVGVKLLAKKSDGAFYAVKVLQKLSILKKQSHIMASRSVLLKNVHPFLV 272

QY 158 GLRYSQTPEKLYFVLDYVNGGELFPHLQRRERFLPRFARFYAAEASAIYLHSLNIY 217

Db 273 GLHFSQTADKLYFVLDYINGGELFPHLQRRERFLPRFARFYAAEASAIYLHSLNIY 332

QY 218 RDLKPNILLDCOGHVLTDFGLCKEGVPEPTTSTFCGTPPEYLAPEVLKPYDRAVDW 277

Db 333 RDLKPNILLDCOGHVLTDFGLCKEGVPEPTTSTFCGTPPEYLAPEVLKPYDRTVDW 392

QY 278 WCLGAVLYEMHGLPPFYSDVQVSMYENILHQPLOIPGGRTVAACDLQSLHKKDQRL 337

Db 393 WCLGAVLYEMHGLPPFYSDVQVSMYENILHQPLOIPGGRTVAACDLQSLHKKDQRL 452

QY 338 GSKADFLKINHVFFSPINWDDLYHKRLTTPFPNPNVTGPADLKHDFPEFTQEAHSVSGIC 397

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Db 453 GAKDFFWEIKSHVFFSLINWDDLLINKITPPFPNVSGPNDLRHDFEFTPEEPVPSIGK 512
QY 398 TPDVT---ASSSGASSAFLGFSYAPEDDDIL 425
Db 513 SPDSVLVTASVKEAAEAFLGFSYAPPTDSFL 543

RESULT 2
US-11-109-156-18
; Sequence 18, Application US/11109156
; Publication No. US20050250144A1
; GENERAL INFORMATION:
; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-Ichi Yamamoto
; APPLICANT: Shizuko Ishii
; APPLICANT: Tomoyasu Sugiyama
; APPLICANT: Ai Wakamatsu
; APPLICANT: Keiichi Nagai
; APPLICANT: Tetsuji Otsuki
; APPLICANT: Shin-Ichi Funahashi
; APPLICANT: Chiaki Senoo
; APPLICANT: Jun-Ichi Nezu
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
; TITLE OF INVENTION: PHOSPHATASE
; FILE REFERENCE: 06501-099002
; CURRENT APPLICATION NUMBER: US/11/109,156
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: US/10/060,065
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/Jp00/05061
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-109-156-18

Query Match 37.8%; Score 874.5; DB 7; Length 480;
Best Local Similarity 47.5%; Pred. No. 1.5e-66;
Matches 174; Conservative 59; Mismatches 102; Indels 31; Gaps 7;

QY 66 AGTPSPQPSRANGINILGPSANPNAQPT--DPDFLKVIGKNGYKVLAKRKSDBGAFYAV 123
Db 122 SGSPSDNSGAEVSL--AKPKHRTVNEFEYLLKLGKGTGKVLVKEKATGRYAM 178
QY 124 KVLQKSLIKKQSHIMAEVSLLKNVRHPFLVGLRYSFQTPKLYFVLVDYVNGGELFF 183
Db 179 KILKKEVIVAKDEVATLTENRV-LQNSRHPFLTALKYSFQTHDRLCFVMEYANGELFF 237
QY 184 HLQRRERFLPRARFYAAEVASAIYGLHS-LNIIYRDLKPENILDCQGHVLTDFGLCK 242
Db 238 HLSRERVFSDRARFYGAETVSALDYHSEKNVVYRDLKLENMLDKDGHIKITDFGLCK 297
QY 243 EGVPEPDTTSTFCGTPEYLAPEVLRKEPYDRAVDWCLGAVLYEMLHGLPPFYSDVSQM 302
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Db 298 EGKOGATWKTFCGTPEYLAPEVLENDYGRAVDWMLGLGVVYEMMCGRLPFFYNDQHEKL 357
QY 303 YENILHQPLQIPGGRVTAACDLLQSLHLHKDQORL-GSKADFLIEIKNHVFFSFINDDLY 361
Db 358 FELLIMEEIRFRTLGPPEAKSLLSGLLKKDKPRLGGGSEDAKEIQHRRFFAGIVQHVVY 417
QY 362 HKRLTPFPNPNTGPDADLKHDFEFTQEAUVSSKSGICTPDTVASSSGASSAFLGFSYAPED 421
Db 418 EKKLSPPFPQVTSSETDTRYFDEEFTAQMIT----ITP-----PDQ 454
QY 422 DDILDC 427
Db 455 DDSMEC 460

RESULT 3
US-10-770-726-81
; Sequence 81, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: CANCERS
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-81

Query Match 34.1%; Score 788.5; DB 6; Length 495;
Best Local Similarity 45.8%; Pred. No. 3e-59;
Matches 162; Conservative 64; Mismatches 111; Indels 17; Gaps 8;

QY 79 NINLGPSANPNAQPTDFDLKLVIGKNGYKVLAKRKS--GAFYAVKVLQKKSILKK- 134
Db 67 SVNVGPE---RIGPHCFELLRVLGKGYKVFQVRKVGQGTNGLKIYAMKVLRAKIVRNA 123
QY 135 KEQSHIMAEVSLLKNVRHPFLVGLRYSFQTPKLYFVLVDYVNGGELFFHLQRRERFLEP 194
Db 124 KDTAHTRAERNI-LESVKHPFIVELAYAFQTGKLYLILECLSGGELFTHLREGIFLED 182
QY 195 RARFYAAEVASAIYGLHSLNIIYRDLKPENILDCQGHVLTDFGLCKGVEPEDTTSTP 254
Db 183 TACFYLAETITLALGHLHSQGIIRYDLKPENIMLSQSGHIKLTDFGLCKESIHEGAVTHTF 242
QY 255 CGTPEYLAPEVLRKEPYDRAVDWMLGAVLYEMLHGLPPFYSDVSQVMYENILHQPLQIP 314
Db 243 CGTIEYMAPEILVRSGHNRAVDWMLGALMYDMLTGSPPPTAENRRKTKMDKIRGKLALP 302
QY 315 GGRTVAAACDLLQSLHLHKDQORL-GSKADFLIEIKNHVFFSPINWDDLYHKRLTTPFPNV 373
Db 303 PYLTPDARDLVKKFLKBNPSQRIKGGPGDAADVQRHPPFRHNMWDDLLAWRDPVPPRPCL 362
QY 374 TGPADLKHDFEFTQEAUVSSKSGICTPDTVASSSGASSAFLGFSY-APEDDDIIL 426
Db 363 QSEEDVSQPTDTRFTQTPTPVDSD---PDDTALSANQAFLGFTYVAP---SVLD 409

RESULT 4
US-11-152-366-28
; Sequence 28, Application US/11152366
; Publication No. US20060014184A1
; GENERAL INFORMATION:
; APPLICANT: Bvsa, Reginald
; APPLICANT: Vandeghinste, Nick
```

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; APPLICANT: Tomme, Peter H. M.
; TITLE OF INVENTION: Methods For Identification, And Compounds Useful For The
; TITLE OF INVENTION: Treatment Of Degenerative & Inflammatory Diseases
; FILE REFERENCE: P27,980-A USA
; CURRENT APPLICATION NUMBER: US/11/152,366
; CURRENT FILING DATE: 2005-06-14
; PRIOR APPLICATION NUMBER: 60/579,307
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-152-366-28

Query Match      33.1%; Score 765; DB 7; Length 737;
Best Local Similarity 42.3%; Pred. No. 4.8e-57;
Matches 159; Conservative 67; Mismatches 120; Indels 30; Gaps 6;

QY 59 YRMNSSPAG-TPSPQPSRANGNINLGPSANPNQAOTDFDLKVGKGYKVLAKRSD 117
Db 376 HRAASSPDGQLMSP---GENGEVROQAQKRLGLD--EFNFIKVLKGSFGKVMIAELKKG 430
QY 118 GAFYAVKVLQKKSILKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPEKLYFVLDVYN 177
Db 431 DEVYAVKVLKQDVLQDDVDCTMTKRIILALARKHBYLTQLYCCFQTKDRLFFVMEYVN 490
QY 178 GGELFPHLQREFLERPRARFYAAEASAIYGLHSLNIIYRDLKPNILLDCQGHVVLT 237
Db 491 GGDLMFOIQRSRKFDEPRSFYAAEVSALMFLHQHGVYIYRDLKDNILLDAEGHCKLAD 550
QY 238 FGLCKEGVEPEDTTSTFCGTPPEYLAPVLRKEPYDRAVDWVCLGAVLYMLHGLPPYSQ 297
Db 551 FGCKEGLINGVTITFCGTPDIAPILQELVGSVDWVWALGVLMYEMMAQPPPEAD 610
QY 298 DVSQMVENILHQLQIPGGRVTAACDLQSLHLKQRLG---SKADFLFIKHNHVFVFP 354
Db 611 NEDDLFESILHDDVLYPVWLKSAVSLKAFMTKNPKHKLGCVASQNGEDAIKQHPFFE 670
QY 355 INWDDLKHLKLTTPFPNPNVTPADLKHDPPEFTQ-----EAVSKSTGCTPDTVASS 405
Db 671 IDWVLEQKKIKPPFKPRIKTRDANNVDQDFTREBPVLTLDVDAIVKQIN----- 721
QY 406 SGAASSAFLGFSYAPED 421
Db 722 ---QEEFKGFSYGED 734

RESULT 5
US-10-878-556A-129
; Sequence 129, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 740
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw hum/k6a3_human
; DATABASE ENTRY DATE: 1996-10-01
US-10-878-556A-129

Query Match      31.3%; Score 722.5; DB 6; Length 740;
Best Local Similarity 44.4%; Pred. No. 1.9e-53;
Matches 151; Conservative 58; Mismatches 118; Indels 13; Gaps 6;
```

```
QY 90 AQPITDFDLKVGKGYKVLAKRSDG---AFYAVKVLQKKSILKKEQSHIMAERSV 146
Db 63 ADSQSPELLKVLGQSGFGKVLVKKISGSDARQLYANKVL-KKATLKVDRVRYTMRDI 121
QY 147 LLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGSELFFHLQRRERFLPRARFYAAEVASA 206
Db 122 LVE-VNHPFTIVKLHYAFQTEGKLYLILDFLRGDGLFRLSKVMFTBEDVKFYLAELALA 180
QY 207 IGYLHSLNIIYRDLKPNILLDCQGHVVLTDFGLCKEGVEPEDTTSTFCGTPPEYLAPV 266
Db 181 LDHLHSLGIIYRDLKPNILLDEGHILKLTDFGLSKESIDHEKKAVSFCCGTVEYMAPEV 240
QY 267 RKEPYDRAVDWVCLGAVLYMLHGLPPFSQVSYQVYENILHQLQIPGGRVTAACDLQ 326
Db 241 NREGHTQSADWWSFGLVLMFEMLTGTLPPQCKGRKETMTMLKAKLGNPQLSPEAQSLLR 300
QY 327 SLHLKQORQLKSKADFL-EIKNVHFFSPINWDDLYHKRLTTPFPNPNVTPADLKHDPPE 385
Db 301 MLFKNRPNANRLGAGPDGVEIKRHSFSTIDMNKLYRREIHPFPFKPATGRPEDTFFDPE 360
QY 386 FTQEAIVSKSTGCTPDTVASSSGASSAFLGFSYA--PEDDD 423
Db 361 FTAKTPKDSPIGP-----SANAHQLFRGFSFAITSDDE 395

RESULT 6
US-10-770-726-76
; Sequence 76, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATIN
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76
; LENGTH: 942
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-76

Query Match      30.9%; Score 713.5; DB 6; Length 942;
Best Local Similarity 38.5%; Pred. No. 1.5e-52;
Matches 165; Conservative 69; Mismatches 160; Indels 35; Gaps 10;
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QY 3 GLLTSGRKPSGGGRCCTG-----RGGWRGQWCLKPMWGGADPPPTLSCLLLPV----PPE 53
Db 530 GTFSPGASGSEARTTGDISVEKLNLTGTDSSSPQKSSRDPPS-SPSSLSSPIQESTAPE 588
QY 54 LPDHCYRMNSSPAGTSPQPSRANGNINLGPSANPNQAOTDFDLKVGKGYKVLAK 113
Db 589 LP-----SETQTECP-----ALCSPLKSPILTLEDFKFLAVLGHGFGKVLLE 633
QY 114 RKSDGAFYAVKVLQKKSILKKEQSHIMAERSVL--LKNVRHPLVGLRYSFQTPEKLYF 171
Db 634 FRPSGELFAIKALKKGDIVARDEVESLMCEKRIILAAVTSAGHFFLVNLFCCFTPEHVP 693
QY 172 VLDYVNGGELFPHLQRRERFLERPRARFYAAEASAIYGLHSLNIIYRDLKPNILLDCQ 231
Db 694 VMEYSAGDMLHLHISD-VFSEPRATIFYACVVLGQFLHFKHIVYRDLKDLNLLDTEG 752
QY 232 HVVLTDFGLCKEGVEPEDTTSTFCGTPPEYLAPVLRKEPYDRAVDWVCLGAVLYMLHGL 291
Db 753 YKVIADFLCKEGMGYGDRTISTFCGTPPEFLAPEVLTDTSYTRAVDWVWGLGVLYEMLVGE 812
QY 292 PPFYSDVSYQMVENILHQLQIPGGRVTAACDLQSLHLKQRLG-SKADFLFIKHNH 350
```

Db 813 SPFGDDDEEVDSIVNDEVYPRFLSAEAGIMRLLRRNPPRLSSGERDAEDVKQP 872  
QY 351 FSPSPINWDDLYHKRLTPFPNVTGPADLKHFPDPTQEA--VSKSIGCTPDDTVASSGA 408  
Db 873 FFRTLGWEALLARRLPPFPVPTLSGRDVTNSFDEEFTGEAPTILSPPRDARPLTAAE---- 928  
QY 409 SSAFLGFSY 417  
Db 929 QAAFLDQDF 937

## RESULT 7

US-11-092-168-4  
; Sequence 4, Application US/11092168  
; Publication No. US20050277658A1  
; GENERAL INFORMATION:  
; APPLICANT: Arizona Board of Regents on behalf of The University of Arizona  
; APPLICANT: Montigen Pharmaceuticals, Inc.  
; APPLICANT: Hurley, Laurence H.  
; APPLICANT: Mahadevan, Daruka  
; APPLICANT: Han, Haiyong  
; APPLICANT: Bearss, David J.  
; APPLICANT: Vankayalapati, Hariprasad  
; APPLICANT: Bashyam, Sridevi  
; APPLICANT: Munoz, Ruben M.  
; APPLICANT: Warner, Steven L.  
; APPLICANT: Della Croce, Kimiko  
; APPLICANT: Von Hoff, Daniel D.  
; APPLICANT: Grand, Cory L.  
; TITLE OF INVENTION: PROTEIN KINASE INHIBITORS  
; FILE REFERENCE: 920214.00003CONT3  
; CURRENT APPLICATION NUMBER: US/11/092,168  
; CURRENT FILING DATE: 2005-03-29  
; PRIOR APPLICATION NUMBER: US 10/965,313  
; US 60/608,529  
; US 60/511,486  
; US 60/511,489  
; PRIOR FILING DATE: 2004-10-14  
; 2004-09-09  
; 2003-10-14  
; 2003-10-14  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 341  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-092-168-4

Query Match 30.5%; Score 705.5; DB 7; Length 341;  
Best Local Similarity 44.1%; Pred. No. 1.9e-52;  
Matches 138; Conservative 63; Mismatches 105; Indels 7; Gaps 5;  
QY 84 PSANPNAQPTDFDLKVGKNGYKVLAKRKSDGAFYAVKVLQKKSILKKKEQSHIMAE 143  
Db 24 PSQN-TAQLDQPERIKTLGTGSFGRVNLVKHESGNHYAMKLDKQKVKLKQIEHTLNE 82  
QY 144 RSVLLKNVRHPFLVGLRYSFQTEPKLYFVLDYVNGGELFFHLQRRERFLEPRARFYAAEV 203  
Db 83 KRI-LQAVNFPFLVKLEFSFKDNSLNYMVEYVAGGEMFSLRRIGRAEPHARFYAAQI 141  
QY 204 ASAIGVLSLNIYRDLKPNILLDCQGHVLLTDGCLCKEGVEPDTTSTFCGTPEYLAP 263  
Db 142 VLTFEYLSLNIYRDLKPNILLDCQGHVLLTDGCLCKEGVEPDTTSTFCGTPEYLAP 198  
QY 264 EVLRKEPYDRAVDWICGLAVLYEMLHGLPPFYSDVSQVSMYENILHQPLOIPGGRTVAACD 323  
Db 199 EILSKGYNKAVDWWALGVLIYEMAAGYPPFFADQPIQIYEKIVSKVRFPSPHSSDLKD 258  
QY 324 LLOSLLHKDQORLGS-KADFLKIKNVFFSPINWDDLYHKRLTPFPNVTGPADLKH 382  
Db 259 LLRNLLQVLDLTKRFGNLKGVNDIKNKKWFATTDTWIAIYQKVEAPFIPKFKGPGDTSNF 318

QY 383 DPEFTQEAUVSKSI 395  
Db 319 D-DYEEERIRVSI 330  
RESULT 8  
US-11-092-168-3  
; Sequence 3, Application US/11092168  
; Publication No. US20050277658A1  
; GENERAL INFORMATION:  
; APPLICANT: Arizona Board of Regents on behalf of The University of Arizona  
; APPLICANT: Montigen Pharmaceuticals, Inc.  
; APPLICANT: Hurley, Laurence H.  
; APPLICANT: Mahadevan, Daruka  
; APPLICANT: Han, Haiyong  
; APPLICANT: Bearss, David J.  
; APPLICANT: Vankayalapati, Hariprasad  
; APPLICANT: Bashyam, Sridevi  
; APPLICANT: Munoz, Ruben M.  
; APPLICANT: Warner, Steven L.  
; APPLICANT: Della Croce, Kimiko  
; APPLICANT: Von Hoff, Daniel D.  
; APPLICANT: Grand, Cory L.  
; TITLE OF INVENTION: PROTEIN KINASE INHIBITORS  
; FILE REFERENCE: 920214.00003CONT3  
; CURRENT APPLICATION NUMBER: US/11/092,168  
; CURRENT FILING DATE: 2005-03-29  
; PRIOR APPLICATION NUMBER: US 10/965,313  
; US 60/608,529  
; US 60/511,486  
; US 60/511,489  
; PRIOR FILING DATE: 2004-10-14  
; 2004-09-09  
; 2003-10-14  
; 2003-10-14  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 343  
; TYPE: PRT  
; ORGANISM: Bos taurus  
US-11-092-168-3

Query Match 30.1%; Score 694.5; DB 7; Length 343;  
Best Local Similarity 43.1%; Pred. No. 1.6e-51;  
Matches 135; Conservative 66; Mismatches 105; Indels 7; Gaps 5;

QY 84 PSANPNAQPTDFDLKVGKNGYKVLAKRKSDGAFYAVKVLQKKSILKKKEQSHIMAE 143  
Db 26 PAQN-TAHLDOFERIKTLGTGSFGRVNLVKHETGNHFAKILDKQKVKLKQIEHTLNE 84  
QY 144 RSVLLKNVRHPFLVGLRYSFQTEPKLYFVLDYVNGGELFFHLQRRERFLEPRARFYAAEV 203  
Db 85 KRI-LQAVNFPFLVKLEYSFKDNSLNYMVEYVPGGEMFSLRRIGRSEPHARFYAAQI 143  
QY 204 ASAIGVLSLNIYRDLKPNILLDCQGHVLLTDGCLCKEGVEPDTTSTFCGTPEYLAP 263  
Db 144 VLTFEYLSLNIYRDLKPNILLDCQGHVLLTDGCLCKEGVEPDTTSTFCGTPEYLAP 200  
QY 264 EVLRKEPYDRAVDWICGLAVLYEMLHGLPPFYSDVSQVSMYENILHQPLOIPGGRTVAACD 323  
Db 201 EILSKGYNKAVDWWALGVLIYEMAAGYPPFFADQPIQIYEKIVSKVRFPSPHSSDLKD 260  
QY 324 LLOSLLHKDQORLGS-KADFL-EIKNVFFSPINWDDLYHKRLTPFPNVTGPADLKH 382  
Db 261 LLRNLLQVLDLTKRFGNLKGVNDIKNKKWFATTDTWIAIYQKVEAPFIPKFKGPGDTSNF 320  
QY 383 DPEFTQEAUVSKSI 395  
Db 321 D-DYEEERIRVSI 332

## RESULT 9

US-11-132-142-13  
; Sequence 13, Application US/11132142  
; Publication No. US20050276818A1  
; GENERAL INFORMATION:  
; APPLICANT: The Burnham Institute  
; APPLICANT: Sikora, Sergey  
; APPLICANT: Godzik, Adam  
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A  
; FILE REFERENCE: 8014-011-US  
; CURRENT APPLICATION NUMBER: US/11/132,142  
; CURRENT FILING DATE: 2005-05-17  
; PRIOR FILING DATE: 2004-05-17  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 13  
; LENGTH: 351  
; TYPE: PRT  
; ORGANISM: Xenopus sp.  
US-11-132-142-13

Query Match 30.1%; Score 694.5; DB 7; Length 351;  
Best Local Similarity 43.1%; Pred. No. 1.7e-51;  
Matches 135; Conservative 65; Mismatches 106; Indels 7; Gaps 5;  
  
QY 84 PSANPNAQPTDFDLKLVIGKNGYKVLAKRSDGAFYAVKVLQKKSILKKKQSHIMAE 143  
DB 34 PPQN-TASLDDFDMKTLGTGSGFGRVLMVKHGAQYAMKILDKQKVKLQKIEHTLNE 92  
  
QY 144 RSVLLKNVRHPFLVGLRYSFQTPTEKLYFVLDYVNGGELFFHLQRRERFLEPRARFYAAEV 203  
DB 93 KRI-LQAVNPFPLVRLSEYSPKNSNLYMIMEYVPGGEMFSLHRRIGRFSPEHARFYAAQI 151  
  
QY 204 ASAIGYLHSLNIYRDLKPNILLDCQGHVLTDFGLCKEGVEPEDTSTFTCGTPEYLA 263  
DB 152 VLTFFYLHSLDLIYRDLKPNILLIDQGGYIQVTDGFAK---RVKGRWTWLCGTPEYLA 208  
  
QY 264 EVLRKPEPYDRAVDWCLGAVLYEMLHGLPPFYSDVSYOMYENILHQLQIPGGRTVAACD 323  
DB 209 EITLSGYNKAVDWMALGVLYEMAGYPPFADQPIQIYEKIVSGKVRFPFSHSDLDK 268  
  
QY 324 LLOSLLHKDQORLGS-KADFLIKNHVFPSPINWDDLYHKRLTTPFPNPNVTGPAADLKH 382  
DB 269 LLRNLLQVLDLTKRYGNLKNVNDIKNHKWFATTDWIAIYQKVEAPPFKRCRGGTSTNF 328  
  
QY 383 DPEFTQRAVSKI 395  
DB 329 D-DYEBEDIRVSL 340

RESULT 10  
US-11-132-142-10  
; Sequence 10, Application US/11132142  
; Publication No. US20050276818A1  
; GENERAL INFORMATION:  
; APPLICANT: The Burnham Institute  
; APPLICANT: Sikora, Sergey  
; APPLICANT: Godzik, Adam  
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A  
; FILE REFERENCE: 8014-011-US  
; CURRENT APPLICATION NUMBER: US/11/132,142  
; CURRENT FILING DATE: 2005-05-17  
; PRIOR FILING DATE: 2004-05-17  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 10  
; LENGTH: 462  
; TYPE: PRT  
; ORGANISM: Amblyomma  
US-11-132-142-10

Query Match 30.1%; Score 694.5; DB 7; Length 462;  
Best Local Similarity 39.5%; Pred. No. 2.4e-51;  
Matches 147; Conservative 67; Mismatches 133; Indels 25; Gaps 10;  
  
QY 35 GADPTTP-TLSCLLLPVPPPELDPDHCYRMMSSPAGTSPSP---OP-----SRANGNIN-- 81  
DB 86 GLSPPCPQSPAC---TPPATSNNTTASNOATTSDMPPPKPKDFERFLEEARKSPEQK 141  
  
QY 82 -LGPANPNAQPTDFDLKLVIGKNGYKVLAKRSDGAFYAVKVLQKKSILKKKQSHI 140  
DB 142 WTSPPSN-TASLDDFDRITLTGSGFGRVLMVKHGAQYAMKILDKQKVKLQKIEHT 200  
  
QY 141 MAERSVLLKNVRHPFLVGLRYSFQTPTEKLYFVLDYVNGGELFFHLQRRERFLEPRARFYA 200  
DB 201 LNEKRI-LQAVEPFLVLAHFKDNLNLYWVLYVGLGEMFSLHRRIGRFSPEHARFY 259  
  
QY 201 AEVASAIGYLHSLNIYRDLKPNILLDCQGHVLTDFGLCKEGVEPEDTSTFTCGTPEY 260  
DB 260 AQIVLAFQYLHSLDLIYRDLKPNILLIDHTGYIKVTDGFAK---RVKGRWTWLCGTPEY 316  
  
QY 261 LAPEVLKPEPYDRAVDWCLGAVLYEMLHGLPPFYSDVSYOMYENILHQLQIPGGRTVA 320  
DB 317 LAPEIITLSGYNKAVDWMALGVLYEMAGYPPFADQPIQIYEKIVSGKVRFPFSHFTSD 376  
  
QY 321 ACLLSLLHKDQORLGS-KADFLIKNHVFPSPINWDDLYHKRLTTPFPNPNVTGPAADL 379  
DB 377 LKDLNLLQVLDLTKRYGNLKNVNDIKNHKWFATTDWIAIYKKEVEAPPFKCKGPGDT 436  
  
QY 380 KHFDPFTQEA 391  
DB 437 SNFD-EVEBEAL 447

RESULT 11  
US-11-132-142-14  
; Sequence 14, Application US/11132142  
; Publication No. US20050276818A1  
; GENERAL INFORMATION:  
; APPLICANT: The Burnham Institute  
; APPLICANT: Sikora, Sergey  
; APPLICANT: Godzik, Adam  
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A  
; FILE REFERENCE: 8014-011-US  
; CURRENT APPLICATION NUMBER: US/11/132,142  
; CURRENT FILING DATE: 2005-05-17  
; PRIOR FILING DATE: 2004-05-17  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 14  
; LENGTH: 351  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-132-142-14

Query Match 29.9%; Score 691.5; DB 7; Length 351;  
Best Local Similarity 43.1%; Pred. No. 3e-51;  
Matches 135; Conservative 65; Mismatches 106; Indels 7; Gaps 5;  
  
QY 84 PSANPNAQPTDFDLKLVIGKNGYKVLAKRSDGAFYAVKVLQKKSILKKKQSHIMAE 143  
DB 34 PAQN-TAHLDDQFERIKTLGTGSGFGRVLMVKHKTGNHAYAMKILDKQKVKLQKIEHTLNE 92  
  
QY 144 RSVLLKNVRHPFLVGLRYSFQTPTEKLYFVLDYVNGGELFFHLQRRERFLEPRARFYAAEV 203  
DB 93 KRI-LQAVNPFPLVLAHFKDNLNLYWVLYVGLGEMFSLHRRIGRFSPEHARFYAAQI 151  
  
QY 204 ASAIGYLHSLNIYRDLKPNILLDCQGHVLTDFGLCKEGVEPEDTSTFTCGTPEYLA 263  
DB 152 VLTFFYLHSLDLIYRDLKPNILLIDQGGYIQVTDGFAK---RVKGRWTWLCGTPEYLA 208

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Qy 264 EVLRKEPYDRAVDWCLGAVLYEMHLGLPPFFVSQDVDSQMYENILHQPIQIPGCRITVAACD 323
Db 209 EIIISKGYNKAVDMMWALGVLIYEMAAGYVPPFFADQPIQIYEKIVSGKVRFPFHSFSDLKD 268
Qy 324 LLQILLHKDQQRIGLS-KADFELEIKNHVFFSPINDDLYLHKRLTPPFNPNVTGPADLKH 382
Db 269 LLRNLLQVDLTKEFGNLKNGYNDIKNHKWFATTDIAIYQKVEAFPFPKFKGPGDTSNF 328
Qy 383 DPFTQEA VSKSI 395
Db 329 D-DYEEEEIRVSI 340

RESULT 12
US-10-497-767-4
; Sequence 4, Application US/10497767
; Publication No. US20050261836A1
; GENERAL INFORMATION:
; APPLICANT: VERTEX PHARMACEUTICALS INCORPORATED
; APPLICANT: MENG, WUYI
; APPLICANT: SWENSON, LOVOKA
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF MITOGEN-ACTIVATED PROTEIN
; TITLE OF INVENTION: KINASE-ACTIVATED PROTEIN KINASE 2 AND BINDING POCKETS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: VPI/01-13 PCT
; CURRENT APPLICATION NUMBER: US/10/497,767
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/337,513
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (10)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (338)
; OTHER INFORMATION: Variable amino acid
; US-10-497-767-4

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RESULT 13
US-11-132-142-9
; Sequence 9, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; TITLE OF INVENTION: CYCLIC-AMP-DEPENDENT KINASE AND A TARGET FOR SARS THERAPY
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Leishmania sp.
US-11-132-142-9

Query Match          29.5%; Score 681.5; DB 7; Length 381;
Best Local Similarity 42.0%; Pred. No. 2.4e-50;
Matches 136; Conservative 62; Mismatches 113; Indels 13; Gaps 5;

Qy 93 TDFDLKVIQKNGYKGVLLAKRKSDBGAYAVKVLQKSKILKKKQSHMAERSVLLKNVR 152
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 70 SDFELKNTLTGSGFRVRIAHKRGTEYYAIKCLRKRBIIRKKQOQHVAQEKGLIME-LC 128

Qy 153 HPFLVGLRYSFQTEPKLYFVLVDVYNGELPFHLQRRERFLPEPRARFYAAEVAASGYLHS 212
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 129 HPFIVNMCSFQDEKQYFLEDFVNGENFTHLTAGFPNDVAKFYHAELVLAPEYLHS 188

Qy 213 LNIYRDLKPENILLDCQGHVLVTFDGLCKEGVEPDTTTCGTPEYLAPEVLKPEYD 272
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 189 LDVIYRDLKPENILLDNKHGVMTDFGFAK---KVPDRTFTLCGTPEYLAPEVIQSKGHG 245

Qy 273 RAVDWWCLGAVLYEMLHGLPFPYSDYQVMYENILHQPLOIPEGRTVAACDLQSLHLKD 332
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 246 KAVDWWTMGVLLVEFIAGYPPFYDDTTPFRIYEKILAGRLKFPNWDGRARDLVKGLLQTD 305

Qy 333 QRORLGS-KADFLFIKNHVFFSPINDDLYHKRLTPFPNPNVTPADLKHFDPEFTQBAV 391
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 306 HTKELGTLKGPADVKKNHPYFHGANWKLYARYYPAPIPVRVKSPGDTSNFE-KYVPDSPV 364

Qy 392 SKSIGCTPDTVASSSGASSAPLGF 415
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Db 365 DR-----TPALTSAAQAEIKGF 381

RESULT 14
US-10-995-561-856
; Sequence 856, Application US/10995561
; Publication No. US2005027054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 856
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-856

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:12:00 ; Search time 12.622 Seconds  
(without alignments)  
3254.993 Million cell updates/sec

Title: US-09-868-131A-8  
Perfect score: 2311  
Sequence: 1 MQGLTSGRKPSSGGRCTGR.....ASSAFLGFSYAPEDDDILDC 427

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1420	61.4	431	2 A48094	serum and glucocorticoid-regulated kinase - rat
2	983	42.5	422	2 T26334	hypothetical prote
3	891	38.6	479	1 A59380	protein kinase (EC
4	883.5	38.2	462	1 T17287	protein kinase (EC
5	882.5	38.2	454	1 JC4345	protein kinase (EC
6	878.5	38.0	480	1 S33364	protein kinase (EC
7	878.5	38.0	763	1 A40831	gag-akt polyprotei
8	876	37.9	481	1 A46288	protein kinase (EC
9	875.5	37.9	480	1 JC2437	protein kinase (EC
10	874.5	37.8	480	1 A39360	protein kinase (EC
11	866	37.5	680	2 S37955	protein kinase YPK
12	863.5	37.4	480	1 S62117	protein kinase (EC
13	862	37.3	481	1 JC2438	protein kinase (EC
14	854.5	37.0	479	2 A38578	protein kinase 2
15	846	36.6	677	2 JS0178	protein kinase YKR
16	835.5	36.2	611	1 A55888	protein kinase (EC
17	803	34.7	569	2 T50414	probable prolifera
18	799.5	34.6	586	2 A49509	protein kinase C (
19	797	34.5	586	2 A53758	protein kinase C (
20	796	34.4	646	2 T38171	probable serine/th
21	789	34.1	481	2 JE0377	p70 S6 kinase (EC
22	788	34.1	546	1 T43233	protein kinase (EC
23	787	34.1	1016	1 A46079	protein kinase C (
24	783.5	33.9	541	1 T43232	protein kinase (EC
25	782.5	33.9	525	1 A41687	ribosomal protein
26	782.5	33.9	525	1 S12906	probable ribosomal
27	778	33.7	1174	2 T43051	protein kinase C (
28	776	33.6	634	1 B32392	protein kinase C (
29	773.5	33.5	525	1 TVRTK6	ribosomal protein

30 773.5 33.5 736 1 KIRCE  
31 770 33.3 737 1 KIMSCE  
32 769.5 33.3 696 2 S55694  
33 768 33.2 592 2 JN0877  
34 765 33.1 592 1 A30314  
35 765 33.1 592 1 JC1480  
36 765 33.1 1139 1 S28942  
37 763.5 33.0 1139 1 S61918  
38 756 32.7 1096 1 S61917  
39 754 32.6 737 1 KIRCE  
40 753 32.6 735 2 I51901  
41 750 32.5 547 2 T22856  
42 747.5 32.3 528 1 T21523  
43 747 32.3 707 1 A53530  
44 746 32.3 682 1 KIBOGC  
45 745.5 32.3 683 1 S29478

ALIGNMENTS

RESULT 1  
A48094  
serum and glucocorticoid-regulated kinase - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 31-Dec-2004  
C:Accession: A48094  
R:Webster, M.K.; Gojva, L.; Ge, Y.; Maiyar, A.C.; Firestone, G.L.  
Mol. Cell. Biol. 13, 2031-2040, 1993  
A:Title: Characterization of egk, a novel member of the serine/threonine protein kinase  
A:Reference number: A48094; MUID:93204949; PMID:8455596  
A:Accession: A48094  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-431 <WEB>  
A:Cross-references: UNIPARC:UPI000017A3E8  
A:Experimental source: Con8.hdc mammary epithelial tumor cells  
A:Note: sequence extracted from NCBI backbone (NCBIN:127618, NCBIP:127619)  
C:Keywords: ATP  
F:96-355/Domain: protein kinase homology <KIN>  
F:104-112/Region: protein kinase ATP-binding motif

Query Match 61.4%; Score 1420; DB 2; Length 431;  
Best Local Similarity 69.7%; Pred. No. 4.9e-59;  
Matches 265; Conservative 56; Mismatches 45; Indels 14; Gaps 4;  
Qy 49 PVPEPELPHCYRNSSPAGTSPQPSRANGINLGPSANPNAQPTDFDLKVIKGYGK 108  
Db 63 PQPEPEL-----NNANP--SPPEPSQ---QINLGPSSNPHAKPSDFHLKVIKGSFGK 111  
Qy 109 VLLAKKSDGAFYAVKVLQKSKILKKKEQSHIWAERSVLKNVRHPPVLGLRYSFQTPKEK 168  
Db 112 VLLARHKAEAFYAVKVLQKSKILKKKEKHINSEKVNLLKNVHPVLGHLHFSFQADK 171  
Qy 169 LYFVLVDYVNGELFFHQLRRERLEPRAPYAAEVAASIGYLHSLNIYRDLPENILLD 228  
Db 172 LYFVLVDYVNGELFFHQLRRERLEPRAPYAAEVAASIGYLHSLNIYRDLPENILLD 231  
Qy 229 CQHVVLTDFGLCKEGVEPEDTTSTFCGTPPEYLAPEVLKPEYDRAVDWCLGAVLYEML 288  
Db 232 SQGHIVLTDFGLCKENIEHNGTTSTFCGTPPEYLAPEVLKPEYDRTVDWCLGAVLYEML 291  
Qy 289 HGLPPPYSDVSQWYENILHQLQIPGGRVAAACDLQSLHDKDORLQKSGKADFLIKN 348  
Db 292 YGLPPPYSRNTAEYDNLNKLQPLNITNSARHLEGLLQKDRTKRLAKKDDFMKIS 351  
Qy 349 HVFFSPINDDLLYHKELTPFPNPNVTGPADLKHDFEFTQEAIVSKSIGCTPDVT--ASS 405  
Db 352 HIFFSLINDDLLINKITTPFPNPNVSGPSDLRHFDFEFTPEPVPSSIGRSPDSILVTASV 411  
Qy 406 SGASSAFLGFSYAPEDDDIL 425  
Db 412 KEAAEAFGLGFSYAPPMDSFL 431



C;Genetics:  
A;Gene: GDB:AKT3  
A;Cross-references: GDB:9954867  
A;Map position: 1q44-1q44  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating various processes  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k  
F;4-105/Domain: pleckstrin repeat homology <PLK>  
F;146-405/Domain: protein kinase homology <KIN>  
F;154-162/Region: protein kinase ATP-binding motif  
F;177/Active site: Lys #status predicted

Query Match 38.2%; Score 883.5; DB 1; Length 462;  
Best Local Similarity 51.2%; Pred. No. 2.9e-34;  
Matches 173; Conservative 53; Mismatches 99; Indels 13; Gaps 5;

Qy 60 RMSSSPAGTSPQPSRAN--GNINLGSANPNNAOPT--DFDFLKVIGKNGYKVLAKRK 115  
Db 116 RMNCSPT-----SQIDNIGEEEMDASTTHHKRKTWMDFDYLLKLGKGTGKVLVREK 168

Qy 116 SDGAFYAVKVLQKKSILKKKEQSHMAERSVLLKNVHPFLVGLRYSFQTPPEKLYFVLDY 175  
Db 169 ASGKYIAMKILKKEVIAKDEVAHTLSE-SRVLNKTRHPFLTSUKYSFQTKDRLCFVMEY 227

Qy 176 VNGGELFFHLQRRERFLEPRARFYAAEVAASAIGYLHSLNIYRDLKPENILLDCQGHVVL 235  
Db 228 VNGGELFFHLSSRERVSEDRTRFYGAIVSALDYHLHGKIVYRDLKLENMLDKDGHKI 287

Qy 236 TDFGLCKEGVEPEDTTSTFCGTPPYLAPEVLRKEPYDRAVDWVWCLGAVLYEMHLGLPPFY 295  
Db 288 TDFGLCKEGITDAATMTKTCGTPPYLAPEVLENDYGRAVDWVWGLGVVYEMMCGRLPFY 347

Qy 296 SQDVSMYENILHQPLOIPGGRVVAACDLQLSLHKDQORQLGSKADFLKIKHNVFSP 354  
Db 348 NQDEKLFELIMEDIKFPRTLSSDAKSLSLGLLIKDPNKRLLGGPDDPKKIMRHSFSG 407

Qy 355 INWDDLYHKLTTPFPNVNTPGADLKHDFDEFTQEAUS 392  
Db 408 VNWQVYDKLVPPFKPQVTSQVTDTRYFDEEFTAQIT 445

RESULT 5  
JC4345  
protein kinase (EC 2.7.1.37) akt3 [validated] - rat  
N;Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific prote  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C;Accession: J04345  
R;Konishi, H.; Kuroda, S.; Tanaka, M.; Matsuzaki, H.; Ono, Y.; Kameyama, K.; Haga, T.; K  
Biochem. Biophys. Res. Commun. 216, 526-534, 1995  
A;Title: Molecular cloning and characterization of a new member of the RAC protein kinase  
e C subtypes and beta gamma subunits of G proteins.  
A;Reference number: JC4345; MUID:96063640; PMID:7488143  
A;Accession: JC4345  
A;Molecule type: mRNA  
A;Residues: 1-454 <KON>  
A;Cross-references: UNIPROT:Q63484; UNIPARC:UPI000012577F; DDBJ:D49836; NID:g1136777; PI  
A;Experimental source: brain  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating various processes  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k  
F;4-105/Domain: pleckstrin repeat homology <PLK>  
F;146-405/Domain: protein kinase homology <KIN>  
F;154-162/Region: protein kinase ATP-binding motif  
F;177/Active site: Lys #status predicted

Query Match 38.2%; Score 882.5; DB 1; Length 454;  
Best Local Similarity 51.2%; Pred. No. 3.2e-34;  
Matches 173; Conservative 53; Mismatches 99; Indels 13; Gaps 5;

Qy 60 RMSSSPAGTSPQPSRAN--GNINLGSANPNNAOPT--DFDFLKVIGKNGYKVLAKRK 115  
Db 116 RMNCSPT-----SQIDNIGEEEMDASTTHHKRKTWMDFDYLLKLGKGTGKVLVREK 168

Qy 116 SDGAFYAVKVLQKKSILKKKEQSHMAERSVLLKNVHPFLVGLRYSFQTPPEKLYFVLDY 175  
Db 169 ASGKYIAMKILKKEVIAKDEVAHTLSE-SRVLNKTRHPFLTSUKYSFQTKDRLCFVMEY 227

Qy 176 VNGGELFFHLQRRERFLEPRARFYAAEVAASAIGYLHSLNIYRDLKPENILLDCQGHVVL 235  
Db 228 VNGGELFFHLSSRERVSEDRTRFYGAIVSALDYHLHGKIVYRDLKLENMLDKDGHKI 287

Qy 236 TDFGLCKEGVEPEDTTSTFCGTPPYLAPEVLRKEPYDRAVDWVWCLGAVLYEMHLGLPPFY 295  
Db 288 TDFGLCKEGITDAATMTKTCGTPPYLAPEVLENDYGRAVDWVWGLGVVYEMMCGRLPFY 347

Qy 296 SQDVSMYENILHQPLOIPGGRVVAACDLQLSLHKDQORQLGSKADFLKIKHNVFSP 354  
Db 348 NQDEKLFELIMEDIKFPRTLSSDAKSLSLGLLIKDPNKRLLGGPDDPKKIMRHSFSG 407

Qy 355 INWDDLYHKLTTPFPNVNTPGADLKHDFDEFTQEAUS 392  
Db 408 VNWQVYDKLVPPFKPQVTSQVTDTRYFDEEFTAQIT 445

RESULT 6  
S33364  
protein kinase (EC 2.7.1.37) akt1 [similarity] - mouse  
N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prot  
C;Species: Mus musculus (house mouse)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Aug-2004  
C;Accession: S33364  
R;Bellacosa, A.; Franke, T.F.; Gonzalez-Portal, M.E.; Datta, K.; Taguchi, T.; Gardner,  
Oncogene 8, 745-754, 1993  
A;Title: Structure, expression and chromosomal mapping of c-akt: relationship to v-akt  
A;Reference number: S33364; MUID:93173519; PMID:8437858  
A;Accession: S33364  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-480 <BEL>  
A;Cross-references: UNIPROT:P31750; UNIPARC:UPI0000001726; EMBL:X65687; NID:g287806; PI  
C;Genetics:  
A;Gene: MGI:Akt  
A;Cross-references: MGI:87986  
A;Map position: 12  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating various processes  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen  
F;4-106/Domain: pleckstrin repeat homology <PLK>  
F;148-408/Domain: protein kinase homology <KIN>  
F;156-164/Region: protein kinase ATP-binding motif  
F;179/Active site: Lys #status predicted  
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein k  
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predict

Query Match 38.0%; Score 878.5; DB 1; Length 480;  
Best Local Similarity 47.8%; Pred. No. 5.1e-34;  
Matches 175; Conservative 58; Mismatches 102; Indels 31; Gaps 7;

Qy 66 AGTPSPQPSRANGNINLGSANPNNAOPT--DFDFLKVIGKNGYKVLAKRKSDGAPYAV 123  
Db 122 SGSPSPNSGAEMEVSLS--AKPKHVTWNEFEYLLKLGKGTGKVLVREKATGRYAM 178

Qy 124 KVLQKKSILKKKEQSHMAERSVLLKNVHPFLVGLRYSFQTPPEKLYFVLDYVNGGSLFF 183  
Db 179 KILKKEVIAKDEVAHTLTENRV-LQNSRHPFTALKYSFQTHDRLCFVNVYANGGLFF 237

Qy 184 HLQRRERFLEPRARFYAAEVAASAIGYLHSLNIYRDLKPENILLDCQGHVLTDFGLCK 242  
Db 238 HLSRERFVEDRARFYGAIVSALDYHLHGKIVYRDLKLENMLDKDGHKIITDFGLCK 297

QY 243 EGVPEPDTTSTFCGTPYLAPVLRKEPYDRAVDWNCIGAVLYEMHLGLPPFYSDVSQM 302  
DB 298 EGIKDGATWKTCGTPYLAPVLRKEPYDRAVDWNCIGAVLYEMHLGLPPFYSDVSQM 357  
QY 303 YENILHQPLOIPGGRRTVAACDLQSLHKKDQORL--GSKADFLEIKNHVFFSPINWDDLY 361  
DB 358 FEILIMEEIRFPRTLGLPEAKSLLSGLLKKDPTQRLGGSGEDAKEIMQHRFFANIVWQDVI 417  
QY 362 HKRLTPFPNPNVTGADLKHDFEPTQEAIVSKSIGCTPDTVASSSGASSAFLGFSYAPED 421  
DB 418 EKXLSPPFPKQVTSSTDRYDFDEFTAQMIT-----ITP-----PDQ 454  
QY 422 DDILDC 427  
DB 455 DDSMEC 460  
RESULT 7  
A40831  
gag-akt polypotein - AKT8 murine leukemia virus  
N:Contains: amino end of core protein p30; core protein p15; inner coat protein p12; kin  
C:Species: AKT8 murine leukemia virus  
C:Date: 12-Feb-1993 #sequence\_revision 12-May-1994 #text\_change 31-Dec-2004  
C:Accession: A40831, B40931  
R:Bellocosa, A.; Testa, J.R.; Staal, S.P.; Tsichlis, P.N.  
Science 254, 274-277, 1991  
A:Title: A retroviral oncogene, akt, encoding a serine-threonine kinase containing an SH  
A:Reference number: A40831; MUID:92022574; PMID:1833819  
A:Accession: A40831  
A:Molecule type: DNA  
A:Residues: 1-262 <BEL>  
A:Cross-references: UNIPARC:UPI00001725AF; GB:M80675  
A:Accession: B40831  
A:Molecule type: DNA  
A:Residues: 262-763 <BE2>  
A:Cross-references: UNIPARC:UPI00001725B0; GB:M80675  
C:Genetics:  
A:Gene: gag-akt  
A:Keywords: ATP; core protein; glycoprotein; oncogene; phosphoprotein; phosphotransferas  
F:1-129/Product: core protein p15 #status predicted <CP1>  
F:130-214/Product: inner coat protein p12 #status predicted <CP2>  
F:284-763/Product: kinase-related transforming protein akt #status predicted <AKT>  
F:287-389/Domain: pleckstrin repeat homology <PK>  
F:431-691/Domain: protein kinase homology <KIN>  
F:439-447/Region: protein kinase ATP-binding motif  
F:25,337/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:462/Active site: Lys #status predicted  
F:609/Binding site: phosphate (Tyr) (covalent) #status predicted  
Query Match 38.0%; Score 878.5; DB 1; Length 763;  
Best Local Similarity 47.8%; Pred. No. 7.7e-34;  
Matches 175; Conservative 58; Mismatches 102; Indels 31; Gaps 7;  
QY 66 ACTPSQPSRANGNINLGPANFNAOPT--DFDLKVGKNGYGVLLAKRKSDDGAFYAV 123  
DB 405 SGSPSDNSGAEEMEVSL---AKPKHRTVMNEFYLKLLGKGTGKVLVKEKATGRYAM 461  
QY 124 KVLQKSLKQSHQSHIMAEKRSVLLKNVRHPPFLVGLRYSFQTPKLYFVLDYVNGGELFF 183  
DB 462 KILKEVIVAKDEVAHTLTENRV-LQNSRHPPFTALKYSPQTHDRLCFVMEYANGELFF 520  
QY 184 HLQRRFLPRARFYAAEVAASAGYLHS-INIYRDLKPNILDCQGHVLTDFGLCK 242  
DB 521 HLSRERFVSDRARFYGAETVSALDYHSEKNVVRDLKLENMLDKDGHIKITDFGLCK 580  
QY 243 EGVPEPDTTSTFCGTPYLAPVLRKEPYDRAVDWNCIGAVLYEMHLGLPPFYSDVSQM 302  
DB 581 EGIKDGATWKTCGTPYLAPVLRKEPYDRAVDWNCIGAVLYEMHLGLPPFYSDVSQM 460  
QY 303 YENILHQPLOIPGGRRTVAACDLQSLHKKDQORL--GSKADFLEIKNHVFFSPINWDDLY 361  
DB 641 FEILIMEEIRFPRTLGLPEAKSLLSGLLKKDPTQRLGGSGEDAKEIMQHRFFANIVWQDVI 700

QY 362 HKRLTPFPNPNVTGADLKHDFEPTQEAIVSKSIGCTPDTVASSSGASSAFLGFSYAPED 421  
DB 701 EKXLSPPFPKQVTSSTDRYDFDEFTAQMIT-----ITP-----PDQ 737  
QY 422 DDILDC 427  
DB 738 DDSMEC 743  
RESULT 8  
A46288  
protein kinase (EC 2.7.1.37) akt2 - human  
N:Alternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific protei  
C:Species: Homo sapiens (man)  
C:Date: 22-Sep-1993 #sequence\_revision 12-May-1994 #text\_change 16-Aug-2004  
C:Accession: A46288  
R:Cheng, J.Q.; Godwin, A.K.; Bellocosa, A.; Taguchi, T.; Franke, T.F.; Hamilton, T.C.;  
Proc. Natl. Acad. Sci. U.S.A. 89, 9267-9271, 1992  
A:Title: AKT2, a putative oncogene encoding a member of a subfamily of protein-serine/th  
A:Reference number: A46288; MUID:93028445; PMID:1409633  
A:Accession: A46288  
A:Molecule type: mRNA  
A:Residues: 1-481 <CHE>  
A:Cross-references: UNIPROT:P31751; UNIPARC:UPI000049EDB; GB:M95936; NID:g178325; PIDN  
A:Note: sequence extracted from NCBI backbone (NCBIP:115859)  
C:Comment: This protein is amplified in some pancreatic, ovarian, and other carcinomas.  
C:Genetics:  
A:Gene: GDB:AKT2  
A:Cross-references: GDB:135660; OMIM:164731  
A:Map position: 19q13.2-19q13.2  
C:Function:  
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoni  
A:Pathway: signal transduction pathways regulating various processes  
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat  
C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein  
F:4-106/Domain: pleckstrin repeat homology <PK>  
F:150-409/Domain: protein kinase homology <KIN>  
F:158-166/Region: protein kinase ATP-binding motif  
F:181/Active site: Lys #status predicted  
Query Match 37.9%; Score 876; DB 1; Length 481;  
Best Local Similarity 48.9%; Pred. No. 6.7e-34;  
Matches 174; Conservative 57; Mismatches 113; Indels 12; Gaps 5;  
QY 70 SPQPSRANGNINLGPANFNAOPTDFDLKVGKNGYGVLLAKRKSDDGAFYAVVLOK 128  
DB 126 SPDSSTTEMEVAVSKAKAKVTMNDFOYLLKLGKTFGKVLVREKATGRYAMKILRK 185  
QY 129 KSILKKKQSHQSHIMAEKRSVLLKNVRHPPFLVGLRYSFQTPKLYFVLDYVNGGELFFHLQRE 188  
DB 186 EVIIAKDEVAHTVTE-SRVLQNRHPPFTALKYAFQTHDRLCFVMEYANGELFFHLSRE 244  
QY 189 RFLPLPRARFYAAEVAASAGYLHSNIIYRDLKPNILDCQGHVLTDFGLCKEGVEPE 248  
DB 245 RVFTTERARFYGAETVSALDYHSEKNVVRDLKLENMLDKDGHIKITDFGLCKEGISDG 304  
QY 249 DTTSTFCGTPYLAPVLRKEPYDRAVDWNCIGAVLYEMHLGLPPFYSDVSQMYENILH 308  
DB 305 ATMTKFCGTPYLAPVLRKEPYDRAVDWNCIGAVLYEMHLGLPPFYSDVSQMYENILH 364  
QY 309 QFLQIPGGRRTVAACDLQSLHKKDQORL--GSKADFLEIKNHVFFSPINWDDLYHKLTP 367  
DB 365 BEIRFRTLSPKSLAGLKKDPKQRLGGSGSDAKEVMEHRFFLUSINWQDVVQKKLLP 424  
QY 368 PENPNVTGADLKHDFEPTQEAIVSKSIGCTPDTVASSSG-----ASSAFLGFSYA 418  
DB 425 PFKQVTSVDRYDFDEFT-----AQSIITTPDRYDLSGLLELDQTHPPQFSYS 476  
RESULT 9  
JC2437  
protein kinase (EC 2.7.1.37) akt1 [validated] - rat



Db 238 HLSRERVFESDRARFYGAETVSALDYLHSEKNVVYRDLLKLENMLDKDGHKIDTDFGLCK 297

QY 243 EGVEPEDTTSFCGTPEYLAPEVLRKEPYDRAVDMCLGAVLYEMLHGLPPFPYSQDVQSQM 302

Db 298 EGKIDGATMKTFCGTPEYLAPEVLENDYGRAVDWMLGVVYMMCGRLPFYFNQDHEKL 357

QY 303 YENILHQPLOIPGGRITVAACDLLOSLHKKQORQLGSKADFLIEIKNHVFPFSPINWDDLY 361

Db 358 FELIMBEERFPRTLGPEAKSLSLGLKKDPKQRLGGSGSEDAKEIMQHRFFAGIVQHWY 417

QY 362 HKRLTPFPFNPNVTPGADLKHDFPTOEAVSKSIGCTGCTPDTVASSSGASSAFLGFSVAPED 421

Db 418 EKLSLPPFKQVITSETDTRIFDEFTQAQMIT---ITP-----PDQ 454

QY 422 DDLDC 427

Db 455 DDSMEC 460

RESULT 11

S37955

protein kinase YPK1 (EC 2.7.1.1-) - yeast (Saccharomyces cerevisiae)

N;Alternate names: protein YKL126w

C;Species: Saccharomyces cerevisiae

C;Date: 03-May-1994 #sequence.revision 03-May-1994 #text\_change 05-Oct-2004

R;Ramezani Rad, M.; Xu, G.; Kirchrath, L.; Fritz, C.; Keuchel, H.; Hollenberg, C.P. submitted to the Protein Sequence Database, March 1994

A;Reference number: S37953

A;Accession: S37955

A;Molecule type: DNA

A;Residues: 1-680 <RAM>

A;Cross-references: UNIPROT:P12688; UNIPARC:UPI0000113BDF; EMBL:Z28126; NID:G486212; PID:R;Maurer, R.A.

DNA 7, 469-474, 1988

A;Title: Isolation of a yeast protein kinase gene by screening with a mammalian protein

A;Reference number: A31248; MUID:89090805; PMID:2850145

A;Accession: A31248

A;Molecule type: DNA

A;Residues: 1-200, 'L', 202-552, 'I', 554-680 <MAU>

A;Cross-references: UNIPARC:UPI0000168D89; EMBL:M21307; NID:gl72180; PIDN:AAA34880.1; PI

R;Chen, P.; Lee, K.S.; Levin, D.E.

Mol. Gen. Genet. 236, 443-447, 1993

A;Title: A pair of putative protein kinase genes (YPK1 and YPK2) is required for cell gr

A;Reference number: S30903; MUID:93173125; PMID:8437590

A;Accession: S30903

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-200, 'L', 202-226, 'T', 228-552, 'I', 554-680 <CHE>

A;Cross-references: UNIPARC:UPI000017A451

C;Genetics:

A;Gene: SGD:YPK1

A;Cross-references: SGD:S0001609; MIPS:YKL126w

A;Map position: 11L

C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

F;345-602/Domain: protein kinase homology <KIN>

F;353-361/Region: protein kinase ATP-binding motif

F;470/Active site: Asp #status predicted

Query Match 37.5%; Score 866; DB 2; Length 680;

Best Local Similarity 51.5%; Pred. No. 2.6e-33;

Matches 177; Conservative 53; Mismatches 106; Indels 8; Gaps 5;

QY 75 RANGNINLGPSPNAPQPTDFDLKVIKGNKYKVLAKKSGDAFYAVKVLQKKSILKK 134

Db 327 KINISIDYKSRNKPISIDDFDLKVIKGSFGKVMQVRKQTKQYALKAIRKSIYVK 386

QY 135 KEOSHIMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLIDYVNGBGLFFHLQRRERFLEP 194

Db 387 SEVTHTLAERTVLAR-VDCPFIVPLKFSFQSPKLYFVLAFINGBGLFYHLQKEGRFDLS 445

QY 195 RARFYAAEASATGYLHSLNIIRDLKPENILLDCQGHVVLTDFGLCKESGEVEDTTSIF 254

Db 446 RARFYAEILLCALDNLHKLVDVYRDLKPENILLDQGHIALCDFGLCKLNMKDDDKTDF 505

QY 255 CQTPEYLAPEVLRKEPYDRAVDMCLGAVLYEMLHGLPPFPYSQDVQSOMYENILHQLQIP 314

Db 506 CQTPEYLAPELLGLGYTKAVDWTLLGVLLYEMLTGLPEYDEDVPKMYKKILQEPLVFP 565

QY 315 GGRITVAACDLLOSLHKKQORQLGSKADFLIEIKNHVFPFSPINWDDLYHKLRTPPPNPV 373

Db 566 DGFDRDAKOLLTGLLSRDPTRLRLGYNGAD--BIRNHPFESQLSWKRLLMKGVIPPYKPAV 623

QY 374 TGPADLKHDFPTOEAVSKSIGCTGCTPDTVASSSGASSAFLGFSY 417

Db 624 SNSMDSNFEDEFTRE---KPIDSVVDEYLSSES-VQKQFGGWTY 663

RESULT 12

S62117

protein kinase (EC 2.7.1.37) akt1 [similarity] - bovine

N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prot.

C;Species: Bos primigenius taurus (cattle)

C;Date: 10-Sep-1999 #sequence.revision 10-Sep-1999 #text\_change 16-Aug-2004

C;Accession: S62117; S24423; S17999; S15714; S36388

R;Coffer, P.J.; Woodgett, J.R. submitted to the EMBL Data Library, December 1991

A;Reference number: S62117

A;Accession: S62117

A;Molecule type: mRNA

A;Residues: 1-480 <COF>

A;Cross-references: UNIPROT:Q01314; UNIPARC:UPI000012E042; EMBL:X61036; NID:g630; PIDN:R;Coffer, P.J.; Woodgett, J.R.

Eur. J. Biochem. 205, 1217, 1992

A;Reference number: S24423; MUID:92249329; PMID:1533586

A;Contents: erratum

A;Accession: S24423

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 70-78, 'N', 80-145 <COW>

A;Cross-references: UNIPARC:UPI00001725AD; EMBL:X61036

A;Note: this is a revision to the sequence from reference S17999

R;Coffer, P.J.; Woodgett, J.R.

Eur. J. Biochem. 201, 475-481, 1991

A;Title: Molecular cloning and characterisation of a novel putative protein-serine kina

A;Reference number: S17999; MUID:92037600; PMID:1718748

A;Accession: S17999

A;Molecule type: mRNA

A;Residues: 1-70, 'TPSSSAACGPRSSSARSTWRRPSGGVDHRHPDGRRAQEAAGGDDGLPVGLTRRELGGRDGGVAGQ

A;Cross-references: UNIPARC:UPI00001725AE; EMBL:X61036

A;Note: this sequence has been revised in references S62117 and S24423

C;Function:

A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoni

A;Pathway: signal transduction pathways regulating various processes

C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein

C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen

F;4-106/Domain: pleckstrin repeat homology <PLK>

F;148-408/Domain: protein kinase homology <KIN>

F;156-164/Region: protein kinase ATP-binding motif

F;179/Active site: Lys #status predicted

F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein k-

F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predict

Query Match 37.4%; Score 863.5; DB 1; Length 480;

Best Local Similarity 48.2%; Pred. No. 2.5e-33;

Matches 174; Conservative 60; Mismatches 112; Indels 15; Gaps 7;

QY 66 AGTPSPQSPRANGNINLGPSPNAPQPT--DFDFLKVIKGNKYKVLAKKSDGAFYAV 123

Db 122 SGSPGNSGAEMEVSLS---AKPKRVTNNEFEYKVLKLGKGTGKVLVKEKATAAYAM 178

QY 124 KYVLQKKSILKKXEQSHIMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLIDYVNGGELFF 183

Db 179 KILKEIVAKDEVAHTLTENRV-LQNSRHPSLTALKYSFQTHDRLCFQWYANGGELFF 237



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QY 184 HLQERRPLEPRARYAEVASAIGYLSH-LNIIYRDLKPNILLDCQGHVVLDFGLCK 242
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 238 HLSRERFVEDRARFYGAIEIVSALDYLHSEKVVYRDLKLENMLDKDGHKITDFGLCK 297

QY 243 EGVPEDETTSTFCGTPPEYLAPEVRKEPYDRADVWCLGAVLYEMLHGLPPFYSDVSQM 302
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 298 EGKDGATMTKTCGTPPEYLAPEVLENDYGRAVDWMGLGVVYEMMCGRLPFYNQDHEKL 357

QY 303 YENILHOPLOQPGGRTVAACDLLOSLHDKQORL-GSKADFLKKNHVPSPINWDDLY 361
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 358 FELIMREIRPRLSPKASLLSGLLKDPKRLGGSEDAKIMQHRFPASIWQDQVY 417

QY 362 HKRLTPPNPNVTGPADLKHDPFTQEAWSKSGCTPDTVASSSGASSA----FLGFSY 417
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 418 EKLSPPKPKQVTSSETDTRYDDEFTAQMITIT---PPDQDSDMEGVDSERRPFPQFSY 474

QY 418 A 418
:
Db 475 S 475

RESULT 13
JC2438
protein kinase (EC 2.7.1.37) akt2 [validated] - rat
N;Alternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
C;Accession: JC2438
R;Koniishi, H.; Shinomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.
Biochem. Biophys. Res. Commun. 205, 817-825, 1994
A;Title: Molecular cloning of rat RAC protein kinase alpha and beta and their associati
A;Reference number: JC2437; MUID:95091823; PMID:7999118
A;Accession: JC2438
A;Molecule type: mRNA
A;Residues: 1-481 <KON>
A;Cross-references: UNIPROT:P47197; UNIPARC:UPI000012577E; DDBJ:D30041; NID:9485404; PID
A;Experimental source: testis
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Pathway: signal transduction pathways regulating various processes including myoblast
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k
F;4-106/Domain: pleckstrin repeat homology <PLK>
F;150-409/Domain: protein kinase homology <KIN>
F;158-166/Region: protein kinase ATP-binding motif
F;181/Active site: Lys #status predicted

Query Match 37.3%; Score 862; DB 1; Length 481;
Best Local Similarity 48.3%; Pred. No. 3e-33;
Matches 172; Conservative 59; Mismatches 113; Indels 12; Gaps 5;

QY 70 SPOPSRANGNINLGPS-ANPNQAQPTDDFLKVTGKNGYGVKLLAKRSGDGFYAVKVLQK 128
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 126 SPSPSTSENMWEAVSKARAKVTMNDPDKLKGKGTGKVLVREKATGRYVAMKILRK 185

QY 129 KSLIKKKEQSHIMAEVSLKKNVRHPLVGLRYSFQTPKLYFVLDVYNGSEFELHORE 188
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 186 EVLIAKDEVAHTVTE-SRVLQNTRHPELTALKYAFQTHDLRCFVMEYANGDLPFFHLSRE 244

QY 189 RRFLEPRARYAEVASAIGYLSHSLNIIYRDLKPNILLDCQGHVVLDFGLCKEGVEPE 248
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 245 RVFTEDRARFYGAIEIVSALEYLHSTDVVYRDKLENMLDKDGHKITDFGLSKEGISDG 304

QY 249 DTTSTFCGTPPEYLAPEVRKEPYDRADVWCLGAVLYEMLHGLPPFYSDVSQWYENILH 308
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 305 ATMKTCGTPPEYLAPEVLENDYGRAVDWMGLGVVYEMMCGRLPFYNQDHERLFELILM 364

QY 309 QPLQIPGGRITVAACDLLOSLHDKQORL-GSKADFLKKNHVPSPINWDDLYKHKLTP 367
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 365 EBRFPPTLGEAKSLLAGLLKXDKPKQRLGGGSPSDAKENVMEHFFLSINQDQVVKLLP 424

QY 368 PFNPNTGTPADLKHDFDPEFTQEAWSKSGCTPDTVASSSGA----SSAFLGFSYA 418
```

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||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 425 PFKPQVTSEVDTRYFDDEFT---AQSIITTPDRYDSLGSLQDQRTHPFPQFSYS 476

RESULT 14
A38578
protein kinase 2 (EC 2.7.1.1) - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 31-Dec-2004
C;Accession: A38578
R;Haribabu, B.; Dottin, R.P.
Proc. Natl. Acad. Sci. U.S.A. 88, 1115-1119, 1991
A;Title: Identification of a protein kinase multigene family of Dictyostelium discoideu
A;Reference number: A38578; MUID:91142122; PMID:1996312
A;Accession: A38578
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-479 <HAR>
A;Cross-references: UNIPROT:P28178; UNIPARC:UPI0000131858; GB:M59744; NID:g167717; PIDN
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threon
F;151-407/Domain: protein kinase homology <KIN>
F;159-167/Region: protein kinase ATP-binding motif

Query Match 37.0%; Score 854.5; DB 2; Length 479;
Best Local Similarity 46.9%; Pred. No. 6.5e-33;
Matches 175; Conservative 64; Mismatches 118; Indels 16; Gaps 6;

QY 63 SSPACTSPSPSRANGNINLGPSANP-----NAQPTDFDFLKVIGKNGYGVKULLA 112
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 111 ASNEASSSPDSPNGSGNGNDDDEGPEEVIFSKNQSATKDDPELLNVIGKSGFGKVMQV 170

QY 113 KRKSDGAFYAVKVLQKKSILKKEQSHIMAEVSLKKNVRHPLVGLRYSFQTPKLYFV 172
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 171 KKGEKIPFAMKVLKDAIIRAKQVNTSEKTI-LQCISHPIVNLHYAFQTKDKLYMV 229

QY 173 LDYVNGGELFFHLQRRERFLEPRARYAEVASAIGYLSHSLNIIYRDLKPNILLDCQGH 232
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 230 LDFVNGGELFFHLKREGFSEPRVKYAAEIVSALDHLHKQDIVYRDLKPNILLDSEGH 289

QY 233 VLTDTGLCKEGVEPEDETTSTFCGTPPEYLAPEVRKEPYDRADVWCLGAVLYEMLHGLP 292
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 290 ICTDTGLSKK-IETTDGTFTCGTPPEYLAPEVNLGHGCAVDWMSLGLTLLYEMLTGLP 348

QY 293 PFYSQDVQWYENILHOPLOQIPGGRITVAACDLLOSLHDKQORLGSKADFLKKNHVEF 352
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 349 PFYSQWVSTWYQKLNGLKLPITYISPEAKSLLEGLLTREVDRLKGLTKGGG-EVKQHPWF 407

QY 353 SPINWDDLYKHRLTPPPFNPNVTGPADLKHDPFTQEAWSKSGCTPDTVASSSGASSAF 412
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 408 KNIDWEKLDKKEVEVHFVKPKVKSQGTDISQIDPVFTQERPMDSLVET-SALGDAMGKDTSF 466

QY 413 LGFSYAPEDDDIL 425
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 467 EGFTYVA--DSIL 477
```

```
RESULT 15
JS0178
protein kinase YKR2 (EC 2.7.1.1) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YM9718.03c; protein YMR104c
C;Species: Saccharomyces cerevisiae
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 05-Oct-2004
C;Accession: JS0178; S30904; S54565
R;Kubo, K.; Ono, S.; Matsumoto, S.; Yahara, I.; Suzuki, K.
Gene 76, 177-180, 1989
A;Title: A novel yeast gene coding for a putative protein kinase.
A;Reference number: JS0178; MUID:89306654; PMID:2663649
A;Accession: JS0178
A;Molecule type: DNA
A;Residues: 1-677 <KUB>
A;Cross-references: UNIPROT:P18961; UNIPARC:UPI000013BDFF; EMBL:M24929; NID:G295680; PI
R;Chen, P.; Lee, K.S.; Levin, D.E.
Mol. Gen. Genet. 236, 443-447, 1993
```

A;Title: A pair of putative protein kinase genes (YPK1 and YPK2) is required for cell growth  
A;Reference number: S30903; MUID:93173125; PMID:8437590  
A;Accession: S30904  
A;Status: nucleic acid sequence not shown; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-677 <CHE>  
A;Cross-references: UNIPARC:UPI000013BDFF  
R;Hunt, S.; Bowman, S.  
submitted to the EMBL Data Library, May 1995  
A;Reference number: S54510  
A;Accession: S54565  
A;Molecule type: DNA  
A;Residues: 1-677 <HUN>  
A;Cross-references: UNIPARC:UPI000013BDFF; EMBL:Z49702; NID:9817859; PIDN:CAA89740.1; PIR:PIR000013BDFF  
C;Genetics:  
A;Gene: SGD:YPK2; YKR2  
A;Cross-references: SGD:S0004710; MIPS:YMR104C  
A;Map position: 13R  
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase  
F;35-57/Region: histidine-rich  
F;342-599/Domain: protein kinase homology <KIN>  
F;350-358/Region: protein kinase ATP-binding motif  
F;351-375/Region: ATP binding #status predicted  
F;466-512/Region: catalytic #status predicted

Query Match 36.6%; Score 846; DB 2; Length 677;  
Best Local Similarity 49.9%; Pred. No. 2.2e-32;  
Matches 175; Conservative 50; Mismatches 116; Indels 10; Gaps 5;

Qy	75	RANGINL-----GPSANPNAQPTDFDLKVIKGNVCKVLLAKRKSQDGFAYAVKVLQKKS	130
Db	320	RGYKGLNITVDYKPSKNKPLSIDDFDLKVIKGSFGKVMQVRKKDTQKIYALKLRKAY	379
Qy	131	ILKKKEQSHIMASRSLKKNVRHPLVGLRYSQTPEKLYFVLDYVNGGELFFHLQERR	190
Db	380	IVSKCEVTHLAERTVLAR-VDCFFIVPLKFSQSEKLYLVLAFLNGGELFFYHLOEGR	438
Qy	191	FLEPRARFYAAEVASAIQYHLSNIIYRDLKPNILLDCQGHVVLTDGFLCKEGVPEPT	250
Db	439	FSLARSFYIAELLCALDSLKLKLDVIYRDLKPNILLDYQGHIALCDFGLCKLNMKDNDK	498
Qy	251	TSTPCGTPEYLAPEVLRKEPYDRAVDWMCIGAVLYEMLHGLPPFYSDYVSQMYENILHQP	310
Db	499	TDTFCGTPEYLAPEILLGQGYTKTVDMWTGLILLYEMMTGLPPYDENVPMYKKILQQP	558
Qy	311	LQIPGGRTVAACDLQLSLHKDQRLGSKADFLKKNHVFFSPINWDDLYHKRLTPPFN	370
Db	559	LLFPDGFDPAAKDLLLGLLSRDPSSRLGVNGTD-EIENHPFFKDISWKKLLKGYIPPYK	617
Qy	371	PNTVGPADLKHDPFTQEAQVSKSIGCTPDTVASSGASSAFIGFSYAPED	421
Db	618	PIVKSEIDTANFDQFTKE---KPIDSVVDVDEYLSAS-IQKQFGGWTYIGDE	664

Search completed: January 27, 2006, 23:32:06  
Job time : 13.622 secs



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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:08:15 ; Search time 69.5554 Seconds  
(without alignments)  
4331.236 Million cell updates/sec

Title: US-09-868-131A-8

Perfect score: 2311

Sequence: 1 MQGLLTSGRKPSGGGRCTGR.....ASSAFLGSVAPEDDDILD 427

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2311	100.0	427	1	SGK2 HUMAN
2	2311	100.0	427	2	Q5H8Y6 HUMAN
3	2064	89.3	393	2	Q52PK5 HUMAN
4	1947	84.2	367	2	Q5T2R3 HUMAN
5	1938.5	83.9	366	2	Q5H821 HUMAN
6	1932	83.6	367	2	Q5RD29_PONPY
7	1848	80.0	367	1	SGK2 MOUSE
8	1540	66.6	302	1	SGK2 RAT
9	1497	64.8	285	2	Q5H8Y4 HUMAN
10	1450.5	62.8	350	2	Q4S7Y9_TETNG
11	1445.5	62.5	431	2	Q5Q0U5_FUNHE
12	1440.5	62.3	433	2	Q7ZTW4_BRARE
13	1427	61.7	432	2	Q6UI19_CHICK
14	1425.5	61.7	434	2	Q93524_XENLA
15	1423	61.6	431	1	SGK1 RABIT
16	1422.5	61.6	434	2	Q6GPN6_XENLA
17	1420	61.4	431	2	Q68G05_RAT
18	1419	61.4	421	2	Q5TCN4_HUMAN
19	1419	61.4	431	2	Q5TCN3_HUMAN
20	1419	61.4	445	2	Q5TCN2_HUMAN
21	1419	61.4	526	2	Q5V765_HUMAN
22	1418.5	61.4	418	2	Q5BKX4_XENTR
23	1416	61.3	431	1	SGK3_MOUSE
24	1416	61.3	519	2	Q6N6S5_MOUSE
25	1415	61.2	431	1	SGK1 HUMAN
26	1414	61.2	431	2	Q4R633_MACFA
27	1411.5	61.1	430	1	SGK1 RAT
28	1404.5	60.8	490	2	Q4RR91_TETNG
29	1399	60.5	434	2	Q6GLY8_XENLA
30	1392	60.2	594	2	Q73927_SQUAC
31	1390.5	60.2	433	2	Q73926_squalus aca

32 1338.5 57.9 429 2 Q8VEK1 MOUSE  
33 1338.5 57.9 496 1 SGK3\_MOUSE  
34 1328.5 57.5 429 2 Q6FHV7\_HUMAN  
35 1328.5 57.5 496 1 SGK3\_HUMAN  
36 1328.5 57.5 496 2 Q53EW6\_HUMAN  
37 1328.5 57.5 496 2 Q5R7A7\_PONPY  
38 1323.5 57.1 496 2 Q5H9Q5\_HUMAN  
39 1320.5 57.1 518 2 Q4SFC2\_TETNG  
40 1319.5 52.1 490 2 Q5ZJQ4\_CHICK  
41 1213 52.5 1114 2 Q4SVX7\_TETNG  
42 1063 46.0 316 2 Q4RI65\_TETNG  
43 1035 44.8 1550 2 Q4SYI0\_TETNG  
44 1025.5 44.4 198 2 Q5H8Y5\_HUMAN  
45 984 42.6 423 2 Q613H2\_CAEBR

#### ALIGNMENTS

RESULT 1  
SGK2\_HUMAN STANDARD; PRT; 427 AA.  
AC Q8VEK1; Q9UKG6;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DE 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Serine/threonine-protein kinase Sgk2 (EC 2.7.1.37)  
DE (Serum/glucocorticoid regulated kinase 2).  
GN Name=SGK2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2), PHOSPHORYLATION SITE THR-253,  
RP AND MUTAGENESIS OF SER-416.  
RX MEDLINE=2018032; PubMed=10548550; DOI=10.1042/0264-6021:3440189;  
RA Kobayashi T., Deak M., Morrice N., Cohen P.;  
RT "Characterization of the structure and regulation of two novel  
RT isoforms of serum- and glucocorticoid-induced protein kinase.";  
RL Biochem. J. 344:189-197(1999).  
[2]  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] (ISOFORM 1).  
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;  
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,  
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,  
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
RA Lenvaestlahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
RA Marsh V.L., Martin S.L., McConachie L.J., McLeay K., McMurray A.A.,  
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Rameay H.,  
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,  
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
Rogers J.;  
RT "The DNA sequence and comparative analysis of human chromosome 20.";  
RL Nature 414:865-871(2001).  
[3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
RC TISSUE=Brain, and Colon;  
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares R.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Haie S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Hong D.E.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [4]  
RP FUNCTION.  
RX MEDLINE=22284526; PubMed=12397388; DOI=10.1007/s00424-002-0873-2;  
RA Gamber N., Fillon S., Feng Y., Friedrich B., Lang P.A., Henke G.,  
RA Huber S.M., Kobayashi T., Cohen P., Lang F.;  
RT "K(+) channel activation by all three isoforms of serum- and  
RT glucocorticoid-dependent protein kinase SGK.";  
RL Pflugers Arch. 445:60-66(2002).  
CC -!- FUNCTION: Involved in the activation of potassium channels.  
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Names=2; Synonyms=beta;  
CC IsoId=Q9HBY8-1; Sequence=Displayed;  
CC Name=1; Synonyms=alpha;  
CC IsoId=Q9HBY8-2; Sequence=VSP\_004932;  
CC -!- TISSUE SPECIFICITY: Highly expressed in liver, kidney and  
CC pancreas, and at lower levels in brain.  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
CC -!- CAUTION: Not regulated by serum or glucocorticoids.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC ENBL; AF186470; AAG17012.1; -; mRNA.  
CC ENBL; AF169034; AAF12757.2; -; mRNA.  
CC ENBL; Z98752; CAC18509.1; -; Genomic DNA.  
CC ENBL; BC014037; AAH14037.2; ALT SEQ; mRNA.  
CC ENBL; BC065511; AAH65511.1; -; mRNA.  
CC HSSP; P31751; 1GZK.  
CC Ensembl; ENSG00000101049; Homo sapiens.  
CC HGNC; HGNC:13900; SGK2.  
CC MIM; 607589; -;  
CC GO; GO:0015459; F:potassium channel regulator activity; IDA.  
CC GO; GO:0004682; F:protein kinase CK2 activity; NAS.  
CC GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.  
CC GO; GO:0017080; F:sodium channel regulator activity; NAS.  
CC GO; GO:0004668; F:protein amino acid phosphorylation; NAS.  
CC GO; GO:0007243; P:protein kinase cascade; TAS.  
CC GO; GO:0006979; P:response to oxidative stress; TAS.  
CC InterPro; IPR000961; Kinase.C  
CC InterPro; IPR000715; Prot\_kinase.  
CC InterPro; IPR008271; Ser\_Thr\_kin\_AS.  
CC InterPro; IPR002290; Ser\_Thr\_kinase.  
CC Pfam; PF00069; Pkinase; 1.  
CC Pfam; PF00433; Pkinase C; 1.  
CC ProDom; PD000001; Prot\_kinase; 1.

DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TKC; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW Alternative splicing; ATP-binding; Kinase; Nucleotide-binding;  
KW Phosphorylation; Serine/threonine-protein kinase; Transferase.  
FT DOMAIN 95 352 Protein kinase.  
FT NP\_BIND 101 109 ATP (By similarity).  
FT MOTIF 128 138 Nuclear localization signal (By similarity).  
FT ACT\_SITE 219 219 Proton acceptor (By similarity).  
FT BINDING 124 124 ATP (By similarity).  
FT MOD\_RES 253 253 Phosphothreonine (By PPK1).  
FT VARSPPLIC 1 60 Missing (in isoform 1).  
FT MUTAGEN 416 416 S->D: Increased activation.  
SQ SEQUENCE 427 AA; 47604 MW; D8F0FA6DF54B1370 CRC64;  
Query Match 100.0%; Score 2311; DB 1; Length 427;  
Best Local Similarity 100.0%; Pred. No. 3.2e-145;  
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MQGLLTSGRKPSSGGGRCCTGCGWGWCLKPMWGGADPTPTLSCLLLPVPPELPDHCYR 60  
DB 1 MQGLLTSGRKPSSGGGRCCTGCGWGWCLKPMWGGADPTPTLSCLLLPVPPELPDHCYR 60  
QY 61 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNYGKVLAKRKS DGAF 120  
DB 61 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNYGKVLAKRKS DGAF 120  
QY 121 YAVKVLQKKSILKKKEQSHIMAEVSLLKNVHPFLVGLRYSFQTEPKLYFVLDYNGGE 180  
DB 121 YAVKVLQKKSILKKKEQSHIMAEVSLLKNVHPFLVGLRYSFQTEPKLYFVLDYNGGE 180  
QY 181 LFFHLQRRERFLEPRARFYAAEVASAGVLSHLSNIIYRDLKPNILLDCQGHVVLDFGL 240  
DB 181 LFFHLQRRERFLEPRARFYAAEVASAGVLSHLSNIIYRDLKPNILLDCQGHVVLDFGL 240  
QY 241 CKEGVEPEDTTSTFCGTPPEYLAPEVLKPEPYDRAVDMWCLGAVLYEMLHGLPFYSDVS 300  
DB 241 CKEGVEPEDTTSTFCGTPPEYLAPEVLKPEPYDRAVDMWCLGAVLYEMLHGLPFYSDVS 300  
QY 301 QMYENILHQPLOIPGGRITVAACDLLOSLLHKQORQLGSKADFLKKNHVFSPINWDDL 360  
DB 301 QMYENILHQPLOIPGGRITVAACDLLOSLLHKQORQLGSKADFLKKNHVFSPINWDDL 360  
QY 361 YHKRLTPPPNPVNTGPAHLKHPDPEPTQEA VSKSIGCTPDTVASSSGASSAFGLFSYAPE 420  
DB 361 YHKRLTPPPNPVNTGPAHLKHPDPEPTQEA VSKSIGCTPDTVASSSGASSAFGLFSYAPE 420  
QY 421 DDDILDC 427  
DB 421 DDDILDC 427  
RESULT 2  
Q5H8Y6 HUMAN  
ID Q5H8Y6 HUMAN PRELIMINARY; PRT; 427 AA.  
AC Q5H8Y6;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE OTTHUMP00000031703.  
GN Name=SGK2; ORFNames=RP1-138B7.2-002;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Beasley H.;

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RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z98752; CA142312.1; -, Genomic DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
SQ SEQUENCE 427 AA; 47604 MW; D8F0FA6DF54B1370 CRC64;

Query Match 100.0%; Score 2311; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 3.2e-145;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQGLLTSGRKPSGGGRCCTGRGGWRGQWCLKPMWGGADPPTTSLCLLLPVPELPDHCYR 60
DB 1 MQGLLTSGRKPSGGGRCCTGRGGWRGQWCLKPMWGGADPPTTSLCLLLPVPELPDHCYR 60
QY 61 MNSSPAGTSPQPSRANGNINLGSANPNAPQTFDFLKVIGKNGYKVLAKRKSQDGF 120
DB 61 MNSSPAGTSPQPSRANGNINLGSANPNAPQTFDFLKVIGKNGYKVLAKRKSQDGF 120
QY 121 YAVKVLQKSKILKKQSHIMAERSVLLKNVRPFLVGLRYSQTPEKLYFVLIDYNGGE 180
DB 121 YAVKVLQKSKILKKQSHIMAERSVLLKNVRPFLVGLRYSQTPEKLYFVLIDYNGGE 180
QY 181 LFPHLQRRERFLPRARFYAAEVAASAIQYLHLSNLIYRDLKPNILLDCQGHVVLDTFGL 240
DB 181 LFPHLQRRERFLPRARFYAAEVAASAIQYLHLSNLIYRDLKPNILLDCQGHVVLDTFGL 240
QY 241 CKGEVPEDDTTSTFCGTPPEYLAPEVLKPEPYDRAVDWMCIGAVLYEMLHGLPPFYSDVS 300
DB 241 CKGEVPEDDTTSTFCGTPPEYLAPEVLKPEPYDRAVDWMCIGAVLYEMLHGLPPFYSDVS 300
QY 301 QMYENILHQPLQIPGGRTVAACDLLOSLLHKQORQLGSKADFLKINHVFFSPINWDDL 360
DB 301 QMYENILHQPLQIPGGRTVAACDLLOSLLHKQORQLGSKADFLKINHVFFSPINWDDL 360
QY 361 YHKRLTPFPNPNVTGPADLKHFDPEFTQEAHSVKSIGCTPDTVASSSGASSAFGLGFSVAPE 420
DB 361 YHKRLTPFPNPNVTGPADLKHFDPEFTQEAHSVKSIGCTPDTVASSSGASSAFGLGFSVAPE 420
QY 421 DDILDC 427
DB 421 DDILDC 427

RESULT 3
Q52PK5 HUMAN
ID Q52PK5 HUMAN PRELIMINARY; PRT; 393 AA.
AC Q52PK5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Serum/glucocorticoid regulated kinase 2.
GN Name-SGK2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
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RP NUCLEOTIDE SEQUENCE.
RA Li H., Nong W., Zhou G., Ke R., Shen C., Zhong G., Zheng Z., Liang M.,
RA Xiao W., Lin L., Yang S.;
RT "Direct Submission.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY987010; AAX88805.1; -, mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 393 AA; 43962 MW; B9931E71A8B998D6 CRC64;

Query Match 89.3%; Score 2064; DB 2; Length 393;
Best Local Similarity 91.6%; Pred. No. 7.3e-129;
Matches 391; Conservative 1; Mismatches 1; Indels 34; Gaps 1;

QY 1 MQGLLTSGRKPSGGGRCCTGRGGWRGQWCLKPMWGGADPPTTSLCLLLPVPELPDHCYR 60
DB 1 MQGLLTSGRKPSGGGRCCTGRGGWRGQWCLKPMWGGADPPTTSLCLLLPVPELPDHCYR 26
QY 61 MNSSPAGTSPQPSRANGNINLGSANPNAPQTFDFLKVIGKNGYKVLAKRKSQDGF 120
DB 27 MNSSPAGTSPQPSRANGNINLGSANPNAPQTFDFLKVIGKNGYKVLAKRKSQDGF 86
QY 121 YAVKVLQKSKILKKQSHIMAERSVLLKNVRPFLVGLRYSQTPEKLYFVLIDYNGGE 180
DB 87 YAVKVLQKSKILKKQSHIMAERSVLLKNVRPFLVGLRYSQTPEKLYFVLIDYNGGE 146
QY 181 LFPHLQRRERFLPRARFYAAEVAASAIQYLHLSNLIYRDLKPNILLDCQGHVVLDTFGL 240
DB 147 LFPHLQRRERFLPRARFYAAEVAASAIQYLHLSNLIYRDLKPNILLDCQGHVVLDTFGL 206
QY 241 CKGEVPEDDTTSTFCGTPPEYLAPEVLKPEPYDRAVDWMCIGAVLYEMLHGLPPFYSDVS 300
DB 207 CKGEVPEDDTTSTFCGTPPEYLAPEVLKPEPYDRAVDWMCIGAVLYEMLHGLPPFYSDVS 266
QY 301 QMYENILHQPLQIPGGRTVAACDLLOSLLHKQORQLGSKADFLKINHVFFSPINWDDL 360
DB 267 QMYENILHQPLQIPGGRTVAACDLLOSLLHKQORQLGSKADFLKINHVFFSPINWDDL 326
QY 361 YHKRLTPFPNPNVTGPADLKHFDPEFTQEAHSVKSIGCTPDTVASSSGASSAFGLGFSVAPE 420
DB 327 YHKRLTPFPNPNVTGPADLKHFDPEFTQEAHSVKSIGCTPDTVASSSGASSAFGLGFSVAPE 386
QY 421 DDILDC 427
DB 387 DDILDC 393

RESULT 4
Q52ZK3 HUMAN
ID Q52ZK3 HUMAN PRELIMINARY; PRT; 367 AA.
AC Q52ZK3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Serum/glucocorticoid regulated kinase 2.
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN NUCLEOTIDE SEQUENCE.  
RP Kaundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,  
RA Phelan M., Farmer A.;  
RA "Cloning of human full-length cDNAs in BD Creator(TM) System Donor  
RT vector."  
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BT020098; AAV38901.1; -; mRNA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000961; Pkinase C.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_Thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_Thr\_pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; Pkinase; 1.  
DR Pfam; PF00433; Pkinase C; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TKG; 1.  
DR SMART; SM00219; TyrKG; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW Kinase.  
SQ SEQUENCE 367 AA; 41233 MW; C91DD892C4C2486B CRC64;  
  
Query Match 84.2%; Score 1947; DB 2; Length 367;  
Best Local Similarity 99.7%; Pred. No. 3.9e-121;  
Matches 366; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 61 MNSSPAGTSPQPSRANGNINLGPSANPNQAQPTDFLKVIGKNGYKVLAKRKSDGAF 120  
DB 1 MNSSPAGTSPQPSRANGNINLGPSANPNQAQPTDFLKVIGKNGYKVLAKRKSDGAF 60  
  
QY 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPELVGLRYSFQTPEKLYFVLDYVNGGE 180  
DB 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPELVGLRYSFQTPEKLYFVLDYVNGGE 120  
  
QY 181 LFFHLQRRERFLEPRARFYAAEVAASAIYGLHSLNIYRDLKPNILLLDCCGHVLTDFGL 240  
DB 121 LFFHLQRRERFLEPRARFYAAEVAASAIYGLHSLNIYRDLKPNILLLDCCGHVLTDFGL 180  
  
QY 241 CKEGVEPEDTTTFCGTPEYLAPEVLKPEYDRAVDWNCGLGAVLYEMLHGLPPFYSQDVS 300  
DB 181 CKEGVEPEDTTTFCGTPEYLAPEVLKPEYDRAVDWNCGLGAVLYEMLHGLPPFYSQDVS 240  
  
QY 301 QMYENILHQPLOIPGERTVAACDLQSLHKQORQLGSKADFLKKNHVFSPINWDDL 360  
DB 241 QMYENILHQPLOIPGERTVAACDLQSLHKQORQLGSKADFLKKNHVFSPINWDDL 300  
  
QY 361 YHKRLTPFPNPNVTGPADLKHDFPEFTQEA VSKSIGCTPTDVASSGASSAF LGFSYAPE 420  
DB 301 YHKRLTPFPNPNVTGPADLKHDFPEFTQEA VSKSIGCTPTDVASSGASSAF LGFSYAPE 360  
  
QY 421 DDILDC 427  
DB 361 DDILDC 367

RESULT 5  
QSH821\_HUMAN  
ID QSH821\_HUMAN PRELIMINARY; PRT; 366 AA.  
AC QSH821;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE OTTHUMP000000311706.  
GN Name=SGK2; ORFNames=RP1-138B7.2-006;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN NUCLEOTIDE SEQUENCE.  
RP Beasley H.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z98752; CAI42315.1; -; Genomic\_DNA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000961; Pkinase C.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_Thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_Thr\_pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; Pkinase; 1.  
DR Pfam; PF00433; Pkinase C; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TKG; 1.  
DR SMART; SM00219; TyrKG; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
SQ SEQUENCE 366 AA; 41047 MW; 8B8546894C23571F CRC64;  
  
Query Match 83.9%; Score 1938.5; DB 2; Length 366;  
Best Local Similarity 99.7%; Pred. No. 1.4e-120;  
Matches 366; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
  
QY 61 MNSSPAGTSPQPSRANGNINLGPSANPNQAQPTDFLKVIGKNGYKVLAKRKSDGAF 120  
DB 1 MNSSPAGTSPQPSRANGNINLGPSANPNQAQPTDFLKVIGKNGYKVLAKRKSDGAF 60  
  
QY 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPELVGLRYSFQTPEKLYFVLDYVNGGE 180  
DB 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPELVGLRYSFQTPEKLYFVLDYVNGGE 119  
  
QY 181 LFFHLQRRERFLEPRARFYAAEVAASAIYGLHSLNIYRDLKPNILLLDCCGHVLTDFGL 240  
DB 120 LFFHLQRRERFLEPRARFYAAEVAASAIYGLHSLNIYRDLKPNILLLDCCGHVLTDFGL 179  
  
QY 241 CKEGVEPEDTTTFCGTPEYLAPEVLKPEYDRAVDWNCGLGAVLYEMLHGLPPFYSQDVS 300  
DB 180 CKEGVEPEDTTTFCGTPEYLAPEVLKPEYDRAVDWNCGLGAVLYEMLHGLPPFYSQDVS 239  
  
QY 301 QMYENILHQPLOIPGERTVAACDLQSLHKQORQLGSKADFLKKNHVFSPINWDDL 360  
DB 240 QMYENILHQPLOIPGERTVAACDLQSLHKQORQLGSKADFLKKNHVFSPINWDDL 299  
  
QY 361 YHKRLTPFPNPNVTGPADLKHDFPEFTQEA VSKSIGCTPTDVASSGASSAF LGFSYAPE 420  
DB 300 YHKRLTPFPNPNVTGPADLKHDFPEFTQEA VSKSIGCTPTDVASSGASSAF LGFSYAPE 359  
  
QY 421 DDILDC 427  
DB 360 DDILDC 366

RESULT 6  
QSRDZ9\_PONPY  
ID QSRDZ9\_PONPY PRELIMINARY; PRT; 367 AA.  
AC QSRDZ9;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

DE Hypothetical protein DKFZp469N2435.  
GN Name=DKFZp469N2435;  
OS Pongo pygmaeus (orangutan).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Pongo.  
OX NCBI\_TaxID=9600;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Kidney;  
RG The German cDNA Consortium;  
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,  
RA Mewes H.W., Weil B., Amid C., Oeanger A., Pobo G., Han M., Wiemann S.;  
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL: CR857741; CAH90008.1; -; mRNA.  
DR GO: GO:0005524; F:ATP binding; IEA.  
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro: IPR000961; Pkinase C.  
DR InterPro: IPR000719; Prot kinase.  
DR InterPro: IPR008271; Ser Thr pkin AS.  
DR InterPro: IPR002290; Ser\_thr\_kinase.  
DR InterPro: IPR001245; Tyr\_kinase.  
DR Pfam: PF00069; Pkinase; 1.  
DR Pfam: PF00433; Pkinase C; 1.  
DR ProDom: PD000001; Prot kinase; 1.  
DR SMART: SM00133; S\_TK\_X; 1.  
DR SMART: SM00220; S\_TK; 1.  
DR SMART: SM00219; Tyr\_K; 1.  
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 367 AA; 41218 MW; 61128B6CC0519B73 CRC64;  
  
Query Match 1 83.6%; Score 1932; DB 2; Length 367;  
Best Local Similarity 98.6%; Pred. No. 3.9e-120;  
Matches 362; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
QY 61 MNSSPAGTSPQPSRANGNINLGPSPNPNARPTDFDLKVGKNGKVLAKRKSDGAF 120  
DB 1 MNSSPAGTSPQPSRANGNINLGPSPNPNARPTDFDLKVGKNGKVLAKRKSDGTF 60  
  
QY 121 YAVKVLQKSLKKSQSHIMARSVLLKNVRHPELVGLRYSFQTEKLYFVLVDYNGGE 180  
DB 61 YAVKVLQKSLKKSQSHIMARSVLLKNVRHPELVGLRYSFQTEKLYFVLVDYNGGE 120  
  
QY 181 LPFHLQRERFLPRARFYAAEVAASAIQYLHSLNIIVRDLPENILLDCQGHVLTDFGL 240  
DB 121 LPFHLQRERFLPRARFYAAEVAASAIQYLHSLNIIVRDLPENILLDCQGHVLTDFGL 180  
  
QY 241 CKGVSPEDTSTFCGTPEYLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPPFYSDVS 300  
DB 181 CKGVSPEDTSTFCGTPEYLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPPFYSDVS 240  
  
QY 301 QMVENILHQLQIPGGRITVAACDLQSLHKKQORLQSGKADFLKKNHVFSPINWDDL 360  
DB 241 QMVENILHQLQIPGGRITVAACDLQSLHKKQORLQSGKADFLKKNHVFSPINWDDL 300  
  
QY 361 YHKRLTPFPNPNVTPGADLKHDFEFTQEAIVSKSIGCTPDTVASSGASSAFIGFSYAPE 420  
DB 301 YHKRLTPFPNPNVTPGADLKHDFEFTQEAIVSKSIGCTPDTVASSGASSAFIGFSYAPE 360  
  
QY 421 DDDILDC 427  
DB 361 DDDILDC 367  
  
RESULT 7  
SGK2\_MOUSE  
ID SGK2\_MOUSE STANDARD; PRT; 367 AA.  
AC Q9QZS5; Q8R0P6;

DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Serine/threonine-protein kinase Sgk2 (EC 2.7.1.37)  
DE (Serum/glucocorticoid regulated kinase 2).  
GN Name=Sgk2;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).  
RX MEDLINE=20018032; PubMed=10548550; DOI=10.1042/0264-6021:3440189;  
RA Kobayashi T., Deak M., Morrice N., Cohen P.;  
RT "Characterization of the structure and regulation of two novel  
RT isoforms of serum- and glucocorticoid-induced protein kinase.";  
RL Biochem. J. 344:189-197(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).  
RC STRAIN=C57BL/6J; TISSUE=Kidney;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schorbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzieraki R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shirokawa T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume M., Inotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
RC TISSUE=Kidney;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zengberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butlerfield Y.S.N., Krzywicki M.I., Skalek U., Smalls D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences. ";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: Involved in the activation of potassium channels (By similarity).

CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=Q9QZS5-1; Sequence=Displayed;

CC Name=2;

CC IsoId=Q9QZS5-2; Sequence=VSP\_004933;

CC Note=No experimental confirmation available;

CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

CC -!- CAUTION: Not regulated by serum or glucocorticoids.

CC -----

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CC -----

DR EMBL; AF169033; AAF12756.1; -; mRNA.

DR EMBL; AK050009; BAC34031.1; -; mRNA.

DR EMBL; BC026549; AAH26549.1; -; mRNA.

DR HSP; P31751; IGZK.

DR Ensembl; ENSMUSG0000017868; Mus musculus.

DR MGI; MGI:131318; Sgk2.

DR GO; GO:0015459; F:potassium channel regulator activity; ISS.

DR GO; GO:0004682; F:protein kinase CK2 activity; ISS.

DR GO; GO:0017080; F:sodium channel regulator activity; ISS.

DR GO; GO:0006468; P:protein amino acid phosphorylation; ISS.

DR InterPro; IPR000961; Pkinase\_C.

DR InterPro; IPR000719; Prot\_kinase.

DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.

DR InterPro; IPR002290; Ser\_thr\_pkinase.

DR Pfam; PF00069; Pkinase\_I.

DR Pfam; PF00433; Pkinase\_C; 1.

DR ProDom; PD000001; Prot\_kinase; 1.

DR SMART; SM00133; S\_TK\_X; 1.

DR SMART; SM00220; S\_TK; 1.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.

KW Alternative splicing; ATP-binding; Kinase; Nucleotide-binding;

KW Phosphorylation; Serine/threonine-protein kinase; Transferase.

FT DOMAIN 35 292

FT NP\_BIND 41 49 ATP (By similarity).

FT MOTIF 68 78 Nuclear localization signal (By similarity).

FT ACT\_SITE 159 159 Proton acceptor (By similarity).

FT BINDING 64 64 ATP (By similarity).

FT MOD\_RES 193 193 Phosphothreonine (by PDPK1) (By similarity).

FT VARSPLIC 171 199 Missing (in isoform 2).

FT CONFLICT 77 77 Missing (in Ref. 3).

SQ SEQUENCE 367 AA; 41359 MW; 668C04B1AE9E33A CRC64;

Query Match 80.0%; Score 1848; DB 1; Length 367;

Best Local Similarity 94.3%; Pred. No. 1; Se-114;

Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 61 MNSPAGTPSPQSRANGNTNLGSPANPNAPQTFDFLKVIGKNGYGVLLAKRKSDGAF 120

Db 1 MASSPVGPSPQSRANGNTNLGSPANPNARPTDFDLKVIGKNGYGVLLAKRKSDGAF 60

QY 121 YAVKVLQKSIILKKQESHMAERSVLLKNVRPFLVGLRYSQTPEKLYFVLDYNGGE 180

Db 61 YAVKVLQKSIILKKQEQNHMAERNVLLKNVRPFLVGLRYSQTPEKLYFVLDYNGGE 120

QY 181 LFPHLQRRFLPRLPRPFYAAEVASAIYLHLSNIYRDLKPNILLDCQGHVLTDFGL 240

Db 121 LFPHLQRRFLPRLPRPFYAAEVASAIYLHLSNIYRDLKPNILLDCQGHVLTDFGL 180

QY 241 CKEGVEPEDTTSTFCGTPEYLAPEVLURKEPYDRAVDWVWCLGAVLYEMLHGLPPFYSDVVS 300

Db 181 CKCEVEPEETTTSTFCGTPEYLAPEVLURKEPYDRAVDWVWCLGAVLYEMLHGLPPFFNTDVA 240

QY 301 QMVENILHOPLOIPGGRTVAACDLQLSLHKQORQLGSKADPFLKIKNVFFSPINWDDL 360

Db 241 QMVENILHOPLOIPGGRTVAACDLQLGLLHKQORQLGSKEDFLDKNVHFFSPINWDDL 300

QY 361 YHKRLTPPNPNVTGPPADLKHFDPEFTQBAVSKSIGCTPDTVASSSGASSAFLGFSYAE 420

Db 301 YHKRLTPPNPNVEGPA DLKHFDPEFTQBAVSKSIGCTPDTVASSSGASSAFLGFSYAQD 360

QY 421 DDDILD 426

Db 361 DDDILD 366

RESULT 8

SGK2\_RAT

ID SGK2\_RAT STANDARD; PRT; 302 AA.

AC Q8R4U9;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Serine/threonine-protein kinase Sgk2 (EC 2.7.1.37)

DE (Serum/glucocorticoid regulated kinase 2) (Fragment).

DE Name=Sgk2;

DE Rattus norvegicus (Rat).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Muridae; Murinae; Rattus.

OX NCBI\_TaxId=10116;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA STRAIN=Sprague-Dawley; TISSUE=Kidney;

RA Peng Y.X., Huber S.M., Waerntges S., Lang F.;

RT "SGK2 and SGK3 mRNA expression in rat kidney.";

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Involved in the activation of potassium channels (By similarity).

CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

CC -----

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CC -----

DR EMBL; AF361756; AAL91351.1; -; mRNA.

DR HSP; P31751; IGZK.

DR Ensembl; ENSRNOG0000033573; Rattus norvegicus.

DR RGD; 620232; Sgk2.

DR GO; GO:0015459; F:potassium channel regulator activity; ISS.

DR GO; GO:0004682; F:protein kinase CK2 activity; ISS.

DR GO; GO:0017080; F:sodium channel regulator activity; ISS.

DR GO; GO:0006468; P:protein amino acid phosphorylation; ISS.

DR InterPro; IPR000719; Prot\_kinase.

DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.

DR InterPro; IPR002290; Ser\_thr\_pkinase.

DR Pfam; PF00069; Pkinase; 1.

DR ProDom; PD000001; Prot\_kinase; 1.

DR SMART; SM00220; S\_TK; 1.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.

KW ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;

KW Serine/threonine-protein kinase; Transferase.

FT DOMAIN 18 275

FT NP\_BIND 24 32 ATP (By similarity).

FT MOTIF 51 61 Nuclear localization signal (By similarity).

FT ACT\_SITE 142 142 Proton acceptor (By similarity).  
FT BINDING 47 47 ATP (By similarity).  
FT MOD\_RES 176 176 Phosphothreonine (by PDPK1) (By  
FT similarity).  
FT NON\_TER 1 1  
FT NON\_TER 302 302  
SQ SEQUENCE 302 AA; 34622 MW; A74EE3F424283D66 CRC64;  
Query Match 66.6%; Score 1540; DB 1; Length 302;  
Best Local Similarity 94.7%; Pred. No. 3.2e-94;  
Matches 286; Conservative 8; Mismatches 8; Indels 0; Gaps 0;  
Qy 78 GNINLGSANNAOPTDFDLKVTGKGNVGVLLAKRSGDGAFAVAVKVLQKXILKXKEQ 137  
Db 1 GNINLGSANNAOPTDFDLKVTGKGNVGVLLAKRSGDGAFAVAVKVLQKXILKXKEQ 60  
Qy 138 SHIAERSVLLKNVRHPFLVGLRYSFOTPEKLYFVLDVYNGGELFFHLQREHREPRAR 197  
Db 61 SHIAERNVLLKNVRHPFLVGLRYSFOTPEKLYFVLDVYNGGELFFHLQREHREPRAR 120  
Qy 198 FYAAEVASAIYLHSLNIIYRDLKPNILLDCQGHVVLTDGLCKEGVEPEDTSTFCGT 257  
Db 121 FYTAEVASAIGYLSHSLNIIYRDLKPNILLDCQGHVVLTDGLCKEGVEPEDTSTFCGT 180  
Qy 258 PEYLAPEVLRKEPYDRAVDMWCLGAVLYEMHLGLPPFYSDVDSQMYENILHQPQLIPGGR 317  
Db 181 PEYLAPEVLRKEPYDRAVDMWCLGAVLYEMHLGLPPFYSDVDSQMYENILHQPQLIPGGR 240  
Qy 318 TVAACDLLOSLHDKQRLGSKADFLKIKHNVFFSPINWDDLHYKRLTPFPNPNVTGPA 377  
Db 241 TVAACDLLOSLHDKQRLGSKADFLKIKHNVFFSPINWDDLHYKRLTPFPNPNVTGPA 300  
Qy 378 DL 379  
Db 301 DL 302  
RESULT 9  
Q5H8Y4\_HUMAN  
ID Q5H8Y4\_HUMAN PRELIMINARY; PRT; 285 AA.  
AC Q5H8Y4;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE OTTHUMP0000031704.  
GN Name=SGK2; ORFNames=RPI-138B7.2-004;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Beasley H.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
DR EMBL; Z98752; CAI42314.1; -, Genomic\_DNA.  
DR GO; GO:000524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_Thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_Thr\_pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; Pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR SMART; SM00219; TykC; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS0011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.

KW ATP-binding; Kinase; Nucleotide-binding;  
KW Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 285 AA; 32130 MW; A3493A701ABB4542 CRC64;  
Query Match 64.8%; Score 1497; DB 2; Length 285;  
Best Local Similarity 99.6%; Pred. No. 2.1e-91;  
Matches 283; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 61 MNSGPACTPSPQPSRANGNINLGSANPNNAOPTDFDLKVTGKGNVGVLLAKRSGDGA 120  
Db 1 MNSGPACTPSPQPSRANGNINLGSANPNNAOPTDFDLKVTGKGNVGVLLAKRSGDGA 60  
Qy 121 YAVKVLQKXILKXKEQSHIAERSVLLKNVRHPFLVGLRYSFOTPEKLYFVLDVYNGGE 180  
Db 61 YAVKVLQKXILKXKEQSHIAERSVLLKNVRHPFLVGLRYSFOTPEKLYFVLDVYNGGE 120  
Qy 181 LFPHLQREHREPRARFYAAEVASAIYLHSLNIIYRDLKPNILLDCQGHVVLTDGL 240  
Db 121 LFPHLQREHREPRARFYAAEVASAIYLHSLNIIYRDLKPNILLDCQGHVVLTDGL 180  
Qy 241 CKGVPEPDITSTFCGTPEYLAPEVLRKEPYDRAVDMWCLGAVLYEMHLGLPPFYSDVDS 300  
Db 181 CKGVPEPDITSTFCGTPEYLAPEVLRKEPYDRAVDMWCLGAVLYEMHLGLPPFYSDVDS 240  
Qy 301 QMYENILHQPQLIPGGRITVAACDLLOSLHDKQRLGSKADFL 344  
Db 241 QMYENILHQPQLIPGGRITVAACDLLOSLHDKQRLGSKADFL 284

RESULT 10  
Q4S7Y9\_TETNG  
ID Q4S7Y9\_TETNG PRELIMINARY; PRT; 350 AA.  
AC Q4S7Y9;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Chromosome 9 SCAF14710, whole genome shotgun sequence.  
DE (Fragment).  
GN ORFNames=GSTENG00022577001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=99883;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
RA Mauceli E., Bounneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
RA Biemont C., Skalll Z., Cattolico L., Poulain J., De Berardinis V.,  
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet P., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
RA Winkler P., Lander E.S., Weissbach J., Roest Crallius H.;  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
the early vertebrate proto-karyotype.";  
RN Nature 431:946-957(2004).  
[2]  
RP NUCLEOTIDE SEQUENCE.  
RG Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC -1- FUNCTION: Plays a key role in the control of the eukaryotic cell  
CC cycle. It is required in higher cells for entry into S-phase and  
CC mitosis. Component of the kinase complex that phosphorylates the  
CC repetitive C-terminus of RNA polymerase II. Catalytic component of



CC MPF (By similarity)  
CC -1- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in  
CC mature oocytes (By similarity).  
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
DR EMBL: CAAE01014710; CAG03243.1; -; Genomic\_DNA.  
DR InterPro: IPR000961; Pkinase.C.  
DR InterPro: IPR000719; Prot\_kinase.  
DR InterPro: IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00069; Pkinase; 1.  
DR Pfam: PF00433; Pkinase.C; 1.  
DR ProDom: PD000001; Prot\_kinase; 1.  
DR SMART: SM00133; S\_TK\_A; 1.  
DR SMART: SM00220; S\_TK; 1.  
DR SMART: SM00219; TyrK; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Nucleotide-binding;  
KW Serine/threonine-protein kinase; Transferase.  
FT NON TER 1  
SQ SEQUENCE 350 AA; 39571 MW; 56BF9C5C2889D924 CRC64;

Query Match 62.8%; Score 1450.5; DB 2; Length 350;  
Best Local Similarity 77.1%; Pred. No. 3.3e-88;  
Matches 270; Conservative 36; Mismatches 43; Indels 1; Gaps 1;  
QY 76 ANGININLPSANQAQPTDFDLKVGKNGYKVLAKRSDGAFYAVKVLQKKILKKK 135  
DB 2 SHDDVNLGPNANPHARTDFDLAVIGKGTGFKVLLAKHTDSFVAVKVLQKKILKKK 61  
QY 136 EQSHMAERSVLLKNVRHPLVGLRYSFQPEKLYFVLDVYNGGELFFHLQRRRFLR 195  
DB 62 EQKNMAERNVLLKSLKHPFLVRLHYSFQAEKLYFVLDVYNGGELFFHLQRRCFSEPR 121  
QY 196 ARFYAAEVAISAIGYLHSLNIYRDLPENILLDCQGHVLTDFGLCKEGVEPDTSTFC 255  
DB 122 ARFYAAEVAISAIGYLHSLNIYRDLPENILLDCQGHVLTDFGLCKEGVEPDTSTFC 181  
QY 256 GTEPYLAPEVLKPEPYDRAVDWVCLGAVLYEMHLGLPPFYSDQVSMYENILHQPILQIPG 315  
DB 182 GTEPYLAPEVLKPEPYDRTVDWVCLGAVLYEMIYSLPPFYSDRVGVWYDGLHKPLQLPP 241  
QY 316 GRTVAACDLLOSLLHKDQORLQSGKADFLKHNHVFSPINWDDLYHKRLTTPFPNPNVTG 375  
DB 242 GKSDAVCSLLVGLLQKQDHRRLGAIDFLKHNHVFSPINWDDLYHKRLTTPFPNPNVVG 301  
QY 376 PADLKHPDPTQEAQVSKSIGCTPDTVASSSGASSAFLGFSYAPEDDDIL 425  
DB 302 PADTQHIDPFTREVMVSSSVSQTPFTASAS-ASNAFNGFSFVATEDSFL 350

RESULT 11  
Q5Q0U5\_FUNHE PRELIMINARY; PRT; 431 AA.  
AC Q5Q0U5;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DE 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Serum and glucocorticoid-regulated kinase.  
GN Names:SGK;  
OS Fundulus heteroclitus (Killifish) (Mummichog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;  
OC Cyprinodontiformes; Fundulidae; Fundulus.  
OC NCBI\_TaxID=8078;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Liver;  
RA Sato J.D., Clarke C.C., Stanton B.A.;  
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY800243; AAV80429.1; -; mRNA.  
DR GO: GO:000524; F:ATP binding; IEA.  
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO: GO:0004648; P:protein amino acid phosphorylation; IEA.  
DR InterPro: IPR000961; Pkinase.C.  
DR InterPro: IPR000719; Prot\_kinase.  
DR InterPro: IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00069; Pkinase; 1.  
DR Pfam: PF00433; Pkinase.C; 1.  
DR ProDom: PD000001; Prot\_kinase; 1.  
DR SMART: SM00133; S\_TK\_A; 1.  
DR SMART: SM00220; S\_TK; 1.  
DR SMART: SM00219; TyrK; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW Kinase.  
SQ SEQUENCE 431 AA; 48870 MW; 91C80821F64B454D CRC64;  
Query Match 62.5%; Score 1445.5; DB 2; Length 431;  
Best Local Similarity 69.6%; Pred. No. 9.2e-88;  
Matches 270; Conservative 51; Mismatches 56; Indels 11; Gaps 4;  
QY 41 PTLSCLLLPVPELPHDHCYRMNSPAGTSPQSPRANGNINLGPSSANPNAQPTDFDLKV 100  
DB 52 PEVQSILNLTTPQDPE--LMNSNP--SPPPSPSQ--QINLGPSSNPSPAKPSDFHLKV 103  
QY 101 IKGNGYKVLAKRSDGAFYAVKVLQKKILKKEQSHMAERSVLLKNVRHPLVGLR 160  
DB 104 IKGSGFGKVLARHRTDQDFYAVKVLQKAILKKKEKHIMSERNVLLKNVRHPLVGLH 163  
QY 161 YSFQPEKLYFVLDVYNGGELFFHLQRRRFLRPRFYAAEVAISAIGYLHSLNIYRD 220  
DB 164 YSFQADKLYFVLDVYNGGELFFHLQRRCFLEPRARFYSAEIASALGYLHSLNIYRD 223  
QY 221 KPENILDCQGHVLTDFGLCKEGVEPDTSTFCGTPPYLAPEVLKPEPYDRAVDWVCL 280  
DB 224 KPENILDSQGHILITDFGLCKENTPNGTSTFCGTPPYLAPEVLHQPILQIPGRTVAACDLLOSLLHKDQORLQSGK 283  
QY 281 GAVLYEMHLGLPPFYSDQVSMYENILHQPILQIPGRTVAACDLLOSLLHKDQORLQSGK 340  
DB 284 GAVLYEMLYGLPPFYSDRYSRNTAEYDNLNKLQKPNISYARHLEGLQKDKTKRLGCK 343  
QY 341 ADLFLETKHNHVFSPINWDDLYHKRLTTPFPNPNVTGPAFLKHPDPTQEAQVSKSIGCTPD 400  
DB 344 DDFTEIKHNHVFSPINWDDLYNAKMTTPFPNPNVTGENDLRHFDPEFTDPEVPSSIGCSPD 403  
QY 401 ---TVASSSGASSAFLGFSYAPEDDDIL 425  
DB 404 CALATASIKEAAEAFVGFSYAPSMDSYL 431

RESULT 12  
Q7ZTW4\_BRARE PRELIMINARY; PRT; 433 AA.  
AC Q7ZTW4;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 13-SEP-2003 (TrEMBLrel. 31, Last annotation update)  
DE Serum/glucocorticoid regulated kinase.  
GN Names:sgk;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OC NCBI\_TaxID=7955;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Kidney, and Whole body;  
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RX



	R	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshylyki S., Carninci P., Prange C., Rana S.S., Joquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.N., Kravynski M.I., Skalska U., Smailius D.E., Schnersch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human rat mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
	[2]	
NR	NNUCLEOTIDE SEQUENCE.	
RP	NTISSUE=whole body;	
RG	NIH MGC Project;	
RL	Submitted (MAY-2003) to the ENBL/GenBank/DDBJ databases.	
RR	[3]	
NNUCLEOTIDE SEQUENCE.		
RP	TISSUE=Kidney;	
RG	NIH MGC Project;	
RL	Submitted (MAR-2004) to the ENBL/GenBank/DDBJ databases.	
CC -1-	CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.	
CC -1-	SUBCELLULAR LOCATION: Cytoplasmic (inactive holoenzyme and monomeric catalytic subunit). Translocates into the nucleus (monomeric catalytic subunit). By similarity)	
-1-	SIMILARITY: Belongs to the Ser/thr protein kinase family.	
ENBL; BC052134;	AAH52134.1; -- mRNA.	
ENBL; BC067618;	AHH67618.1; -- mRNA.	
HSSP; P31751;	IMRY.	
D	Ensembl; ENSDARGO0000025522; Danio rerio.	
ZFIN; ZDR-GENE-030131;-2860;	sgk.	
GO; GO:0005524;	F:ATP binding; IEA.	
GO; GO:0004574;	F:protein serine/threonine kinase activity; IEA.	
GO; GO:0006468;	P:protein amino acid phosphorylation; IEA.	
InterPro; IPR000961;	Kkinase_C.	
InterPro; IPR000719;	Prot_kinase.	
InterPro; IPR008271;	Ser Thr pkin AS.	
InterPro; IPR002290;	Ser_thr_pkinase.	
Pfam; PF00069;	Pkinase_1.	
Pfam; PF00433;	Pkinase_C; 1.	
PRODom; PD000001;	Prot_kinase; 1.	
SMART; SM00133;	S TK_X; 1.	
SMART; SM00220;	S_TKG; 1.	
PROSITE; PS00107;	PROTEIN_KINASE_ATP; 1.	
PROSITE; PS00011;	PROTEIN_KINASE_DOM; 1.	
PROSITE; PS00108;	PROTEIN_KINASE_ST; 1.	
KW	ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;	
KW	Serine/threonine-protein kinase; Transferase; CAMP.	
SQ	SEQUENCE 433 AA; 48983 MW; F2AA477IE245FF56 CRC64;	
Query Match	62.3%; Score 1440.5; DB 2; Length 433;	
Best Local Similarity	69.8%; Pred. No. 2e+87;	
Matches	271; Conservative 49; Mismatches 57; Indels 11; Gaps 4;	
QY	41 PTLSCLLPVPPELPHDCHYRMNSPPAGTPSPQRSANGNINIGPSANPAQTDFDLKV 100   : ::::  :::     :  :::   :::	
Db	54 PFVQSILNLTPPO---DVLMNSNP--SPPPSPSQ----QIINLGSSNPTAKPSDFDLKV 105   : ::::  :::     :  :::   :::	
QY	101 IGKNGYGVLLAKRKSDCAFYAVVLQKKSLIKKEQHSHMAERSVILLKNVRHPFLVGIR 160   : ::::  :::     :  :::   :::	
Db	106 IGKSGFGVKLLARRSRDEKFYAVVLQKKAILKKEEKIHMSERNVLLKNVKHFPFLGLH 165   : ::::  :::     :  :::   :::	
QY	161 YSFQTPEKLIFYLDLVNYGSELFFHLQRERAPLRPFARYAEVASAIGYLHSINIYNDL 220   : ::::  :::     :  :::   :::	

Db 162 GLHFSQTDKLVFLVDYINGGELFYHLQRCFCLEPRARFYAAETASALGYLHSLNIVY 221  
QY 218 RDLKPNENILDCQHVLTDFGLCKGVEPEDTTSTFCGTPEYLAPEVLKPEYDRADVW 277  
Db 222 RDLKPNENILDCQHVLTDFGLCKENIEHNGTTSTFCGTPEYLAPEVLKQPYDRVDW 281  
QY 278 WCLGAVLYEMLHGLPPYSQDVSMYENILHQPLOIPGGRTVAAACDLQSLHKKQORL 337  
Db 282 WCLGAVLYEMLGLPPYSRNTAEYNDILNKPLQKPNITNARGHLEGLLQKRTKRL 341  
QY 338 GSKADLEIKNHFVFPINWDDLYHKRLTPPFPNVTGPADLKHFDPEFTQEAVSIGC 397  
Db 342 GAKEDFEIKNHFVFPINWDDLYHKRLTPPFPNVTGPADLKHFDPEFTQEAVSIGC 401  
QY 398 TPDVT---ASSGASSAFGLGSYAPEDDDIL 425  
Db 402 SPDSILITASVKEAAEAFGLGSYAPPVDSPL 432  
RESULT 14  
O93524 XENLA PRELIMINARY; PRT; 434 AA.  
ID AC O93524;  
DT 01-NOV-1998 (T-EMBLrel. 08, Created)  
DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)  
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Renal tubule;  
RX MEDLINE=99161637; PubMed=10051674; DOI=10.1073/pnas.96.5.2514;  
RA Chen S.-Y., Bhargava A., Mastroberardino L., Meijer O.C., Wang J.,  
Buse P., Firestone G.L., Verrey F., Pearce D.;  
RT "Epithelial sodium channel regulated by aldosterone-induced protein  
sgk.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:2514-2519(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Renal tubule;  
RA Chen S.-Y., Pearce D.;  
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (inactive holoenzyme and  
monomeric catalytic subunit). Translocates into the nucleus  
(monomeric catalytic subunit) (By similarity).  
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
DR EMBL; AF057138; AAC62398.1; -; mRNA.  
DR HSSP; P31751; 1MRV.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000961; Pkinase C.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR Pfam; PF00069; Pkinase; I.  
DR Pfam; PF00433; Pkinase C; I.  
DR PRODOM; PD000001; Prot\_kinase; I.  
DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TK; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS00011; PROTEIN KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN KINASE\_ST; 1.  
KW ATP-binding; Cell cycle; Cell division; Hypothetical protein; Kinase;  
KW Nuclear protein; Nucleotide-binding; Serine/threonine-protein kinase;  
KW Transferase; camp.  
SQ SEQUENCE 434 AA; 49130 MW; 4A061E3B86AA6F61 CRC64;

Query Match 61.7%; Score 1425.5; DB 2; Length 434;  
Best Local Similarity 69.0%; Pred. No. 28-86;  
Matches 261; Conservative 59; Mismatches 47; Indels 11; Gaps 3;  
QY 51 PPELDHCHYRMNSSPAGTPSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNYGKVL 110  
Db 65 PPQEP-LLNENSSPPSPSQ-----INLGSSNPHAKPSDFQFLIKGSGFGKVL 116  
QY 111 LAKRSDGAFYAVKVLQKKSILKKQESHIMAEVSLLKNVRHPLVGLRYSFQTEPKLY 170  
Db 117 LARHOSDEKFAVKVLQKAILKKKEKHIMSEKRVLLKNVHPFLVGLHFSFQTTSLRY 176  
QY 171 FVLDDYNGGELFPHLQRRERFLEPRARFYAAVSAIGVLSNIIYRLKPNENILDCQ 230  
Db 177 FLDYINGGELFYHLQRCFCLEPRARFYAAETASALGYLHSLNIVYRLKPNENILDCQ 236  
QY 231 GHVLTDFGLCKGVEPEDTTSTFCGTPEYLAPEVLKPEYDRADVWMLCGAVLYEMLHG 290  
Db 237 GHVLTDFGLCKENIEPNTTSTFCGTPEYLAPEVLKQPYDRTVDMWMLCGAVLYEMLYG 296  
QY 291 LPFFYSQDVSMYENILHQPLOIPGGRTVAAACDLQSLHKKQORLQSKADFLKHNHV 350  
Db 297 LPFFYSRNTAEYNDILNKPLQKPNITNARGHLEGLLQKRTKRIKANDFMEIKNHI 356  
QY 351 FESPINWDDLYHKRLTPPFPNVTGPADLKHFDPEFTQEAVSIGCTPDVT---ASSSG 407  
Db 357 FESPINWDDLYHKRLTPPFPNVTGPADLKHFDPEFTQEAVSIGCTPDVT---ASSSG 416  
QY 408 ASSAFGLGSYAPEDDDIL 425  
Db 417 AAETAFGLGSYAPPVDSPL 434  
RESULT 15  
SGK1 RABIT STANDARD; PRT; 431 AA.  
ID AC O9XT18;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Serine/threonine-protein kinase Sgk1 (EC 2.7.1.37)  
DE (Serum/glucocorticoid-regulated kinase 1).  
GN Name-SGK; Synonym-SGK1;  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;  
OC Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=New Zealand white;  
RX MEDLINE=99287894; PubMed=10358046; DOI=10.1074/jbc.274.24.16973;  
RA Naray-Fejes-Toth A., Canessa C., Cleaveland E.S., Aldrich G.,  
Fejes-Toth G.;  
RT "sgk is an aldosterone-induced kinase in the renal collecting duct.  
Effects on epithelial Na+ channels.";  
RL J. Biol. Chem. 274:16973-16978(1999).  
CC -1- FUNCTION: Protein kinase that plays an important role in  
activating certain potassium, sodium, and chloride channels,  
suggesting an involvement in the regulation of processes such as  
cell survival, neuronal excitability, and renal sodium excretion.  
CC May be a key component of cellular stress response. Phosphorylates  
NEDD4L, which leads to its inactivation and to the subsequent  
activation of various channels and transporters such as ENAC,  
Kv1.3, or EAAT1 (By similarity).  
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -1- SUBUNIT: Interacts with NEDD4 and NEDD4L (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear, upon  
phosphorylation (By similarity).  
CC -1- PTM: Regulated by phosphorylation. Phosphoinositide 3-kinase (PI3-  
kinase) pathway promotes phosphorylation at Ser-422 which in turn  
increases the phosphorylation of Thr-256 by PDPK1 (By similarity).  
CC -1- PTM: Ubiquitinated by NEDD4L; which promotes proteasomal

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CC      degradation (By similarity).
CC      -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      EMBL; AF139633; AAD43303.1; -; mRNA.
CC      HSP; P31751; 1GZK.
CC      InterPro; IPR000961; Pkinase_C.
CC      InterPro; IPR000719; Prot_kinase.
CC      InterPro; IPR008271; Ser_thr_pkin_AS.
CC      InterPro; IPR002290; Ser_thr_pkinase.
CC      Pfam; PF00069; Pkinase; 1.
CC      Pfam; PF00433; Pkinase_C; 1.
CC      ProDom; PD000001; Prot_kinase; 1.
CC      SMART; SM00133; S_TK_X; 1.
CC      SMART; SM00220; S_TKC; 1.
CC      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC      PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC      Apoptosis; ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
CC      Phosphorylation; Serine/threonine-protein kinase; Transferase;
CC      Ub1 conjugation.
CC      DOMAIN 98      Protein kinase.
CC      NP_BIND 104 112  ATP (By similarity).
CC      MOTIF 131 141  Nuclear localization signal (By
CC      similarity).
CC      ACT_SITE 222 222  Proton acceptor (By similarity).
CC      BINDING 127 127  ATP (By similarity).
CC      MOD_RES 256 256  Phosphothreonine (by PDPK1) (By
CC      similarity).
CC      MOD_RES 422 422  Phosphoserine (By similarity).
CC      SEQUENCE 431 AA; 48999 MW; 354898A77E8E38FD CRC64;
Query Match      61.6%; Score 1423; DB 1; Length 431;
Best Local Similarity 70.0%; Pred. No. 2.9e-86;
Matches 266; Conservative 55; Mismatches 45; Indels 14; Gaps 4;
QY 49  PVPPELDPHCVRMNSSPAGTSPQPSRANGNINLPSANPNAQPTDFDLKVGKGYGK 108
DB 63  PQEPEL-----MNANP--SPPSPSQ---QINLGPSSNPFAKPSDFHLKVIKGSFGK 111
QY 109 VLLAKRKDGAFYAVKVLQKSLKKKEQSHMAERSVLLKNVHPHVLGLRYSPOTPEK 168
DB 112 VLLARHAEAFYAVKVLQKKAALKKKKEKHMSERNVLLKNVHPHVLGLHFSFQADK 171
QY 169 LYFVLDYVNGELFFHLQRRERFLEPRARFYAAEVAASAGYLHSLNIIYRDLKPENILLD 228
DB 172 LYFVLDYINGELFYHLQRECFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLD 231
QY 229 CQGHVLTDFGLCKGEVEPDTTSTFCGTPYLAPEVLRKEPYDRAVDWVWCLGAVLYEML 288
DB 232 SQGHVLTDFGLCKENIEHNGTTSTFCGTPYLAPEVLRKEPYDRTVDWVWCLGAVLYEML 291
QY 289 HGLPPFYSDVQMYENILHQLQI PGGRVVAACDLQLQSLHKKDQRORLGSKADFLKIN 348
DB 292 YGLPPFYSRNTAEYMDNINLKNLQLEKNTITNSARHLLGLEQLQDRTKRLGAKDDFMEIRN 351
QY 349 HVFFSPINWDDLXKRLTPFPNPNVTGPADLKHFDPDETOEAVSKSIGCTPDTV---ASS 405
DB 352 HVFFSLINWDDLXKRLTPFPNPNVSGPSDLRHFDPEFTEPVPSSIGRSPDSILITASV 411
QY 406 SGASSAFLGFSYAPEDDDIL 425
DB 412 KEAAEAFLGFSYAPPMDSFL 431

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